

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 94..339

&lt;221&gt; sig\_peptide

&lt;222&gt; 94..216

&lt;223&gt; Von Heijne matrix

score 4.90000009536743

seq LSLVSHAPGEALA/RA

&lt;400&gt; 409

```

gtgttgacaga aatccggcaa tcgacctgag gacttgcgag ccgctcagct cccgggacgt      60
ttggagctgc tgctaaataa tttctgctca gcc atg tcg ccg gct cca gat gca      114
                                Met Ser Pro Ala Pro Asp Ala
                                -40 -35
gcc ccg gct cct gcg tcg atc tcc ctg ttt gac ctc agc gcg gat gct      162
Ala Pro Ala Pro Ala Ser Ile Ser Leu Phe Asp Leu Ser Ala Asp Ala
                                -30 -25 -20
ccg gtc ttt cag ggc ctg agc ctg gtg agc cac gcg cct ggg gag gct      210
Pro Val Phe Gln Gly Leu Ser Leu Val Ser His Ala Pro Gly Glu Ala
                                -15 -10 -5
ctg gcc ccg gct ccg cgt act tcc tgt tca ggc tca ggg gag aga gaa      258
Leu Ala Arg Ala Pro Arg Thr Ser Cys Ser Gly Ser Gly Glu Arg Glu
                                1 5 10
agc cca gaa aga aag cta ctc cag ggt cct atg gat att tca gag aag      306
Ser Pro Glu Arg Lys Leu Leu Gln Gly Pro Met Asp Ile Ser Glu Lys
15 20 25 30
tta ttt tgt tca act tgt gac cag acc ttc cag aa      341
Leu Phe Cys Ser Thr Cys Asp Gln Thr Phe Gln
                                35 40

```

&lt;210&gt; 410

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 153..320

&lt;221&gt; sig\_peptide

&lt;222&gt; 153..257

&lt;223&gt; Von Heijne matrix

score 4.90000009536743

seq LFIFIGSLQPVPT/RF

&lt;400&gt; 410

```

cacacacaaa ctctcaagtg gcctaattcc ctctcaccaa accaatcaca atacagataa      60
aagagaataa cttgtgttca tttttgtaca aacaaaaaag atataaattg tgaatgrtgc      120
atgrttttta awtwwccaag taaactgggc aa atg ctt ctg cat tat tta aag      173
                                Met Leu Leu His Tyr Leu Lys
                                -35 -30
cta aaa ggt gat cag tgg aaa ctt tcc tct gtt agt act cta ata ctt      221
Leu Lys Gly Asp Gln Trp Lys Leu Ser Ser Val Ser Thr Leu Ile Leu
                                -25 -20 -15
ttt ata ttt atc ggc tca cta caa cct gtg cct acc agg ttc aag cga      269
Phe Ile Phe Ile Gly Ser Leu Gln Pro Val Pro Thr Arg Phe Lys Arg
                                -10 -5 1
ttc tcc tgt ctc gdc cac ctg agt agc cga gac cac agg caa gca cta      317
Phe Ser Cys Leu Xaa His Leu Ser Ser Arg Asp His Arg Gln Ala Leu

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5 10 15 20 321

cgg g  
Arg

<210> 411  
<211> 635  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 84..635

<221> sig\_peptide  
<222> 84..542  
<223> Von Heijne matrix  
score 4.90000009536743  
seq MIVSLAAVAWVGQ/QV

<400> 411  
gggttggtggt tgggtgtgcgg gtttcgggttg gaggactcgt tggggaggtg gcctgcgctt 60  
gtagagactg catccccgag acg atg gcg gag gga gat aat cgc agc acc aac 113  
Met Ala Glu Gly Asp Asn Arg Ser Thr Asn  
-150 -145  
ctg ctg gct gca gag act gca agt ctg gaa gaa cag ctg caa gga tgg 161  
Leu Leu Ala Ala Glu Thr Ala Ser Leu Glu Glu Gln Leu Gln Gly Trp  
-140 -135 -130  
gga gaa gtg atg ctg atg gct gat aaa gtc ctc cga tgg gaa aga gcc 209  
Gly Glu Val Met Leu Met Ala Asp Lys Val Leu Arg Trp Glu Arg Ala  
-125 -120 -115  
tgg ttt cca cct gcc atc atg ggt gtg gtt tct ttg gtg ttt ctg att 257  
Trp Phe Pro Pro Ala Ile Met Gly Val Val Ser Leu Val Phe Leu Ile  
-110 -105 -100  
atc tac tat cta gat cca tct gtt ctg tcc ggc gtt tcc tgt ttt gtt 305  
Ile Tyr Tyr Leu Asp Pro Ser Val Leu Ser Gly Val Ser Cys Phe Val  
-95 -90 -85 -80  
atg ttt ttg tgc ttg gct gac tac ctt gtt ccc att cta gcg cct aga 353  
Met Phe Leu Cys Leu Ala Asp Tyr Leu Val Pro Ile Leu Ala Pro Arg  
-75 -70 -65  
att ttt ggc tcc aat aaa tgg acc act gaa caa cag caa aga ttc cat 401  
Ile Phe Gly Ser Asn Lys Trp Thr Thr Glu Gln Gln Gln Arg Phe His  
-60 -55 -50  
gaa att tgc agc aat cta gta aaa act cga cgc aga gct gtg ggt tgg 449  
Glu Ile Cys Ser Asn Leu Val Lys Thr Arg Arg Arg Ala Val Gly Trp  
-45 -40 -35  
tgg aaa cgc ctc ttc aca cta aag gaa gaa aaa cct aag atg tac ttc 497  
Trp Lys Arg Leu Phe Thr Leu Lys Glu Glu Lys Pro Lys Met Tyr Phe  
-30 -25 -20  
atg acc atg atc gtt tcc ctt gct gcg gtt gct tgg gtg gga caa caa 545  
Met Thr Met Ile Val Ser Leu Ala Ala Val Ala Trp Val Gly Gln Gln  
-15 -10 -5 1  
gtc cac aac ctg ctt ctc acc tac ctg ata gtg act tcc tta cta ttg 593  
Val His Asn Leu Leu Leu Thr Tyr Leu Ile Val Thr Ser Leu Leu Leu  
5 10 15  
ctt cct gga cta aac caa cat gga atc att ttg aag tac att 635  
Leu Pro Gly Leu Asn Gln His Gly Ile Ile Leu Lys Tyr Ile  
20 25 30

<210> 412  
<211> 335  
<212> DNA  
<213> Homo sapiens

**<220>**

<221> CDS

<222> 33...335

<221> sig peptide

<222> 33..110

### <223> Von Heine matrix

score 4.900000009536743

seq LLRGLLAGPAATS/WS

<400> 412

aatggacgag	aggtcagggt	aggtttttga	ag	atg	gcg	gcc	ctc	aag	gct	ctg	53
				Met	Ala	Ala	Leu	Lys	Ala	Leu	
					-25					-20	
gtg	tcc	ggc	tgt	ggg	cgg	ctt	ctc	cgt	ggg	cta	101
Val	Ser	Gly	Cys	Gly	Arg	Leu	Leu	Arg	Gly	Leu	
				-15						-5	
gcg	acc	agc	tgg	tct	cgg	ctt	cca	gct	cgc	ttc	149
Ala	Thr	Ser	Trp	Ser	Arg	Leu	Pro	Ala	Arg	Gly	
			1				5			10	
gag	acc	caa	gaa	ggg	aag	aca	act	ata	att	gaa	197
Glu	Thr	Gln	Glu	Gly	Lys	Thr	Thr	Ile	Ile	Glu	
			15				20			25	
act	ccc	aag	gag	agt	cca	aat	cct	cct	aac	ccc	245
Thr	Pro	Lys	Glu	Ser	Pro	Asn	Pro	Pro	Asn	Pro	
30					35				40		
atc	tgc	cgt	tgg	aac	ctg	aag	cac	aag	tat	aac	293
Ile	Cys	Arg	Trp	Asn	Leu	Lys	His	Lys	Tyr	Asn	
				50					55		
ctg	ctt	agc	cag	ttc	atc	cgg	cct	cat	gga	ggc	335
Leu	Leu	Ser	Gln	Phe	Ile	Arg	Pro	His	Gly	Gly	
			65					70		75	

<210> 413

<211> 158

<212> DNA

<213> Homo sapiens

**<220>**

<221> CDS

<222> 25..156

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<221> sig peptide
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<222> 25.93

### <223> Von Heijne matrix

score 4.900000009536743

seq LVGFKQVVAWTFA/SD

<221> misc feature

<222> 17

<223> n=a, g, c or t

<400> 413

agaaactgac atttg <b>b</b> ntgt t <b>t</b> ta atg ggg tcc ctg ctg ttc atc agg cag	51
Met Gly Ser Leu Leu Phe Ile Arg Gln	
-20 -15	
aca ctt gtg ggc ttt aaa cag gtc gtt gct tgg acc ttt gct tct gat	99
Thr Leu Val Gly Phe Lys Gln Val Val Ala Trp Thr Phe Ala Ser Asp	
-10 -5 1	
tca cat tgt gsa aaw gtg gww atg gtd wtc tws agt cag ttg arw aat	147
Ser His Cys Xaa Xaa Val Xaa Met Val Xaa Xaa Ser Gln Leu Xaa Asn	
5 10 15	

ccc cca ctg gg  
Pro Pro Leu  
20

158

<210> 414  
<211> 202  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 59..202

<221> sig\_peptide  
<222> 59..130  
<223> Von Heijne matrix  
score 4.90000009536743  
seq LLRGSLLASXRA/XX

<221> misc\_feature  
<222> 160  
<223> n=a, g, c or t

<400> 414  
ctgggagcga cgcctccgct cgtctcgttg gttccggagg tcgctgcggc ggtgggaa 58  
atg ctg gcg cgc gcg gcg gag grc act ggg gcc ctt ttg ctg agg ggc 106  
Met Leu Ala Arg Ala Ala Glu Xaa Thr Gly Ala Leu Leu Leu Arg Gly  
-20 -15 -10  
tct cta ctg gct tct grc cgc gck ycg sys vcg cct cct ctg gga ttg 154  
Ser Leu Leu Ala Ser Xaa Arg Ala Xaa Xaa Xaa Pro Pro Leu Gly Leu  
-5 1 5  
scc cgn aac acc gwt ggt act gtt cgt gcc gca gca gga ggc ctg ggt 202  
Xaa Arg Asn Thr Xaa Gly Thr Val Arg Ala Ala Ala Gly Gly Leu Gly  
10 15 20

<210> 415  
<211> 229  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 146..229

<221> sig\_peptide  
<222> 146..196  
<223> Von Heijne matrix  
score 4.90000009536743  
seq LLSFCLCSDFISQ/DA

<400> 415  
gtmaaaactcc cgcagacttc tctgtagatc gctgagcgat actttcggca gcacctcctt 60  
gattctcagt tttgctggag gccgcaacca ggccctactc aaccctcctt cccaggaggc 120  
ccaggccccc aagctcagat ccccc atg aat gcc tcc ctg ttg tct ttc tgc 172  
Met Asn Ala Ser Leu Leu Ser Phe Cys  
-15 -10  
ctt tgt tca gat ttc atc tct caa gat gcc ctg ctt ctg act gtc ata 220  
Leu Cys Ser Asp Phe Ile Ser Gln Asp Ala Leu Leu Leu Thr Val Ile  
-5 1 5  
ttt cct ccc 229  
Phe Pro Pro  
10

<210> 416  
 <211> 265  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 27..263

<221> sig\_peptide  
 <222> 27..206  
 <223> Von Heijne matrix  
 score 4.90000009536743  
 seq LVGVIVHSGQAHA/GH

<400> 416  
 atgatgaaca aataagggttt ccctgg atg cta aac atg gag cct tac aca gtt 53  
 Met Leu Asn Met Glu Pro Tyr Thr Val  
 -60 -55  
 tca gga atg gct cgc caa gat tct tct tct gaa gtt ggg gaa aat ggg 101  
 Ser Gly Met Ala Arg Gln Asp Ser Ser Ser Glu Val Gly Glu Asn Gly  
 -50 -45 -40  
 cga agt gtg gat cag ggc ggt gga gga tcc cca cga aaa aag gtt gcc 149  
 Arg Ser Val Asp Gln Gly Gly Gly Gly Ser Pro Arg Lys Lys Val Ala  
 -35 -30 -25 -20  
 ctc aca gaa aac tat gaa ctt gtc ggt gtc atc gta cac agt ggg cag 197  
 Leu Thr Glu Asn Tyr Glu Leu Val Gly Val Ile Val His Ser Gly Gln  
 -15 -10 -5  
 gca cac gca ggc cac tac tat tcc ttc att aag gac agg cga ggg tgt 245  
 Ala His Ala Gly His Tyr Tyr Ser Phe Ile Lys Asp Arg Arg Gly Cys  
 1 5 10  
 gga aaa gga aag tgg ctg gg 265  
 Gly Lys Gly Lys Trp Leu  
 15

<210> 417  
 <211> 228  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 160..228

<221> sig\_peptide  
 <222> 160..219  
 <223> Von Heijne matrix  
 score 4.90000009536743  
 seq LHLXSSRXPPILA/SP

<221> misc\_feature  
 <222> 166..167,190  
 <223> n=a, g, c or t

<400> 417  
 ttgtctgtct taggcctgga cactgttggt gacttatttc cagatttttaa tttctctttg 60  
 gttgaagact gccactgtc tcatagagtg tttgatattat ttatttatty athtwgacat 120  
 gaggwykctc tctgcmaacc caggctggak tgcagtgac atg atv nng gct cac 174  
 Met Xaa Xaa Ala His  
 -20  
 ttc agc ctc cac ctc nkg agc tca agg art cck ccc atc tta gcc tcc 222

227

Phe Ser Leu His Leu Xaa Ser Ser Arg Xaa Pro Pro Ile Leu Ala Ser  
 -15 -10 -5 1  
 cca gta  
 Pro Val

228

<210> 418  
 <211> 225  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 125..223

<221> sig\_peptide  
 <222> 125..175  
 <223> Von Heijne matrix  
 score 4.90000009536743  
 seq VCELSIFFTYVLA/IY

<400> 418  
 aaaagtttgt aataagttgc actttcatca agactgtatt agggagtcca gtctccccac 60  
 atccttgta gacgggatg acatcagtct tttaaattctt accaacttat tgggaaaaaa 120  
 aaaa atg ata cgt cct gtt tgt gaa ttg agc att ttt ttc acc tat gta 169  
 Met Ile Arg Pro Val Cys Glu Leu Ser Ile Phe Phe Thr Tyr Val  
 -15 -10 -5  
 cta gcc att tac ata tct cct tct gtg aat tgt ctg ttt ata tcc ttt 217  
 Leu Ala Ile Tyr Ile Ser Pro Ser Val Asn Cys Leu Phe Ile Ser Phe  
 1 5 10  
 cct gcg gg 225  
 Pro Ala  
 15

<210> 419  
 <211> 293  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 42..293

<221> sig\_peptide  
 <222> 42..128  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq LLSARLLSQEKRA/AE

<400> 419  
 gtgctctatg gagctattgc ggccgtgggt ggtcgcgggc r atg cgg ggc tgc cag 56  
 Met Arg Gly Cys Gln  
 -25  
 ctc ctc ggg ctt cgt agc tct tgg ccc ggg gac cta cta agt gct cgg 104  
 Leu Leu Gly Leu Arg Ser Ser Trp Pro Gly Asp Leu Leu Ser Ala Arg  
 -20 -15 -10  
 ctc ttg tcc caa gag aag cgg gca gcg gaa acg cac ttt ggg ttt gag 152  
 Leu Leu Ser Gln Glu Lys Arg Ala Ala Glu Thr His Phe Gly Phe Glu  
 -5 1 5  
 act gtg tcg gaa gag gag aag agg ggg gac tta aca tca gtt gta agt 200  
 Thr Val Ser Glu Glu Glu Lys Arg Gly Asp Leu Thr Ser Val Val Ser  
 10 15 20  
 cta gag tac cct gaa gtg caa tta cag ggt caa agg gtc tat gcm ttc 248  
 Leu Glu Tyr Pro Glu Val Gln Leu Gln Gly Gln Arg Val Tyr Ala Phe

228  
 25 30 35 40 293  
 ctg tca ccc att tgt acc tat ggc tct gag gga tgc agc ctc aag  
 Leu Ser Pro Ile Cys Thr Tyr Gly Ser Glu Gly Cys Ser Leu Lys  
 45 50 55

<210> 420  
 <211> 194  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 30..194

<221> sig\_peptide  
 <222> 30..134  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq PWVLDIFLTLVFA/LG

<400> 420  
 agttgctaga aagcaatgcg cctattcac atg gag aat ctt ccc ttt cct cta 53  
 Met Glu Asn Leu Pro Phe Pro Leu  
 -35 -30  
 aaa tta ctt agt gcc tca tca cta aac acc ccc agc tcc aca cca tgg 101  
 Lys Leu Leu Ser Ala Ser Ser Leu Asn Thr Pro Ser Ser Thr Pro Trp  
 -25 -20 -15  
 gtg ttg gat atc ttc ctc acc ttg gtg ttt gcc ctg ggg ttc ttc ttc 149  
 Val Leu Asp Ile Phe Leu Thr Leu Val Phe Ala Leu Gly Phe Phe Phe  
 -10 -5 1 5  
 cta tta ctc ccc tac ttc tct tac ctc cgt tgt gac aac cca cca 194  
 Leu Leu Leu Pro Tyr Phe Ser Tyr Leu Arg Cys Asp Asn Pro Pro  
 10 15 20

<210> 421  
 <211> 90  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 29..88

<221> sig\_peptide  
 <222> 29..67  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq MCVCVFAIFGVRC/CV

<221> misc\_feature  
 <222> 61  
 <223> n=a, g, c or t

<400> 421  
 tatttgaggat ttgttgctct gtgtgtat atg tgc gtg tgt gtg ttt gct ata 52  
 Met Cys Val Cys Val Phe Ala Ile  
 -10  
 ttt ggg gtn cgt tgc tgt gtg tgt gtc cgc tgt att tg 90  
 Phe Gly Val Arg Cys Cys Val Cys Val Arg Cys Ile  
 -5 1 5

<210> 422

<211> 161  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 22..159

<221> sig\_peptide  
 <222> 22..153  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq XPCPLLFPACFP/CP

<400> 422  
 tcatttgggt ttttatttaa t atg att tgc ata ttt tac tct aag att tcc 51  
 Met Ile Cys Ile Phe Tyr Ser Lys Ile Ser  
 -40 -35  
 atc tct gtc ggc tgt ggg agg aca gca gcc gag caa gtt gga tgt aaa 99  
 Ile Ser Val Gly Cys Gly Arg Thr Ala Ala Glu Gln Val Gly Cys Lys  
 -30 -25 -20  
 cag agg tca ttt cac ckc ccy tgc cct ctg ctg ttt cct ggt gcd tgc 147  
 Gln Arg Ser Phe His Xaa Pro Cys Pro Leu Leu Phe Pro Gly Ala Cys  
 -15 -10 -5  
 ttt ccc tgc cca ac 161  
 Phe Pro Cys Pro  
 1

<210> 423  
 <211> 420  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 333..419

<221> sig\_peptide  
 <222> 333..380  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq ICVSLMASDGASS/PV

<221> misc\_feature  
 <222> 323..324,328  
 <223> n=a, g, c or t

<400> 423  
 ctgccgcygg acacgggttc ttccagcttt tggctattgt gaataacgct gctatggaca 60  
 tgaatgtaca aacatccctt cagatcctcc ttccagttct tgtgggtaca taccctgagt 120  
 ggaactgtgg catcatatgg taactctgtg tttaacattt tgaggaacca ccctactgct 180  
 tcccacagag gctgtaccag tttacttccc accaacagtg caaggattcc aatttctcca 240  
 catccgtgcc aacactatth tctttttgtc gctgtttgtc ttgtttgtct ggaaaatagc 300  
 catgctgagg ggtgagaggt grnnghanrg tt atg aat ttg att tgc gtt tcc 353  
 Met Asn Leu Ile Cys Val Ser  
 -15 -10  
 ctg atg gcc agt gat ggg gca tct tcc cct gtg ctt ggt ggc tct tca 401  
 Leu Met Ala Ser Asp Gly Ala Ser Ser Pro Val Leu Gly Gly Ser Ser  
 -5 1 5  
 cac tct tcc tcc cwt rgg g 420  
 His Ser Ser Ser Xaa Xaa  
 10

<210> 424  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 256..432

<221> sig\_peptide  
 <222> 256..396  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq LVSA LPQASFSSS/SE

<400> 424  
 agtgaggagt carggaggtg tgtgtgagag agagagagaa aagagagaga cagagacggg 60  
 gagagagaga gggagagaga agagagggag gaggggaagaa gaaaagacgg agggaggtga 120  
 ggaggaaggg agggggagag acagagacct agaggggctg aagaccaga cagagctggc 180  
 agagctactg agaagaggac tggagcgctc tgagagcctc tcaagatctt ttgggggagc 240  
 ccaataaatg tgaac atg gga tct gtc acr gga gct gtc ctc aag acg cta 291  
 Met Gly Ser Val Thr Gly Ala Val Leu Lys Thr Leu  
 -45 -40  
 ctt ctg tta tct act caa aat tgg aac aga gtc gaa gct ggg aat tcc 339  
 Leu Leu Leu Ser Thr Gln Asn Trp Asn Arg Val Glu Ala Gly Asn Ser  
 -35 -30 -25 -20  
 tat gac tgt gat gat cct ctt gtg tct gcc ttg cct cag gca tcc ttc 387  
 Tyr Asp Cys Asp Asp Pro Leu Val Ser Ala Leu Pro Gln Ala Ser Phe  
 -15 -10 -5  
 agc agt tct tcc gag ctc tcc agc agt cat agt cct gga ttt gca 432  
 Ser Ser Ser Ser Glu Leu Ser Ser Ser His Ser Pro Gly Phe Ala  
 1 5 10

<210> 425  
 <211> 419  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 278..418

<221> sig\_peptide  
 <222> 278..370  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq FFLFLFSSCDVP/VP

<400> 425  
 ccgaattatt ttagtggttac ttatctttga ataaaatgta ttttcttg atcaattagt 60  
 tgcagcacgt tcttaggaat ggaatagaga agcatcctaa gccagaagga tttttttttt 120  
 tctagatcac agtgaagctt taatatggkk ggatatttgt ccagcccaa atcccatgct 180  
 gaattgaaac ccctagtgtc ggaggtgggg cctggtggaa ggtgtttgga tcatgaggac 240  
 acatctctga tgaatggcct agctcatcct cttagtgt atg atg agt gag tyc tca 295  
 Met Met Ser Glu Xaa Ser  
 -30  
 caa gat ctg gtt gta aag tgt gcc cca cca csg cca ttc ttt ctc ttg 343  
 Gln Asp Leu Val Val Lys Cys Ala Pro Pro Xaa Pro Phe Phe Leu Leu  
 -25 -20 -15 -10  
 ttc ctg ttt tct tca tgt gat gtg cct gtt ccc ctt cac ctt ctg caa 391  
 Phe Leu Phe Ser Ser Cys Asp Val Pro Val Pro Leu His Leu Leu Gln  
 -5 1 5

tgg ctg caa agc ttc ctg agg cct agg g 419  
 Trp Leu Gln Ser Phe Leu Arg Pro Arg  
 10 15

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<210> 426
<211> 232 .
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 54..230

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<221> sig_peptide
<222> 54..134
<223> Von Heijne matrix
      score 4.80000019073486
      seq VLLTSGVKPQTFA/VS
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<400> 426																			
gcagtgagtg ttacagttct taaagatggg gtgtccggag tttgttcctt cca atg																		56	
																Met			
ttc aga tgt gtc cgg ttt ctt cct tct ggc ggg ttc gtg gtc ttg ctg																		104	
Phe Arg Cys Val Arg Phe Leu Pro Ser Gly Gly Phe Val Val Leu Leu																			
-25				-20				-15											
act tca gga gtg aag cca caa acc ttc gca gtg agt gtt aca gct ctt																		152	
Thr Ser Gly Val Lys Pro Gln Thr Phe Ala Val Ser Val Thr Ala Leu																			
-10				-5				1				5							
aaa ggt ggc atg ccc gga gtt gtt cat tcc tcc ggt ggg ttc gtg gtt																		200	
Lys Gly Gly Met Pro Gly Val Val His Ser Ser Gly Gly Phe Val Val																			
10				15				20											
ttg cta act tca gga gcg aas tgc aga cct tc																		232	
Leu Leu Thr Ser Gly Ala Xaa Cys Arg Pro																			
25				30															

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<210> 427
<211> 383
<212> DNA
<213> Homo sapiens
```

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<220>  
<221> CDS  
<222> 226..381
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<221> sig_peptide
<222> 226..315
<223> Von Heijne matrix
      score 4.80000019073486
      seq CLFLNARLAGTLC/QL
```

[illegible]

232

ttt ggc cgc cta gga aac acc gag agt cac cta cat ggg ctg gct ggg 381  
 Phe Gly Arg Leu Gly Asn Thr Glu Ser His Leu His Gly Leu Ala Gly  
           10                          15                          20

gg 383

<210> 428

<211> 132

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 32..130

<221> sig\_peptide

<222> 32..124

<223> Von Heijne matrix

score 4.80000019073486

seq LLCPLTCPHHSLS/TV

<400> 428

ttcaacaaat gagtcatagt gttttcgtat t atg tat ttt gat atc cag att 52  
   Met Tyr Phe Asp Ile Gln Ile  
   -30                          -25

gtc tca gat gtg gtc agc ggg att ccc ttc aaa ctt ctg tgc cct tta 100  
 Val Ser Asp Val Val Ser Gly Ile Pro Phe Lys Leu Leu Cys Pro Leu  
                           -20                          -15                          -10

aca tgt ccc cat cat tct ctg agc acc gtg gg 132  
 Thr Cys Pro His His Ser Leu Ser Thr Val  
                   -5                          1

<210> 429

<211> 165

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 25..165

<221> sig\_peptide

<222> 25..117

<223> Von Heijne matrix

score 4.80000019073486

seq FSPFLPSLPLLEA/ER

<400> 429

caaaactgttg aaaagttaac tctt atg tta ttt ata ttt tca gac ata gat 51  
   Met Leu Phe Ile Phe Ser Asp Ile Asp  
   -30                          -25

tgg aag atg gac tta tgc ttt ttc tct ttc tct cct ttc ctt ccc tcc 99  
 Trp Lys Met Asp Leu Cys Phe Phe Ser Phe Ser Pro Phe Leu Pro Ser  
                   -20                          -15                          -10

ctt cct ttg ttg gag gct gaa aga atg agg gtc agt gat caa ctt cag 147  
 Leu Pro Leu Leu Glu Ala Glu Arg Met Arg Val Ser Asp Gln Leu Gln  
           -5                          1                          5                          10

tat acc act gga kac ggg 165  
 Tyr Thr Thr Gly Xaa Gly  
                   15

<210> 430

<211> 236

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 52..234

<221> sig\_peptide

<222> 52..159

<223> Von Heijne matrix

score 4.80000019073486

seq VLLAIGMFFTAWF/FV

<400> 430

```

gccgacgtgt tcttccggtg gcggasggcg gattagcctt cgcggggcaa a atg gag      57
                                         Met Glu
                                         -35
ctc gag gcc atg agc aga tat acc agc cca gtg aac cca gct gtc ttc      105
Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe
          -30                      -25                      -20
ccc cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc gcc      153
Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala
          -15                      -10                      -5
tgg ttc ttc gtt tac gag gtc acc tct acc aag tac act cgt gat atc      201
Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile
          1                      5                      10
tat aaa gag ctc ctc atc tcc tta gtg gcc cga gg                        236
Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Arg
15                      20                      25

```

<210> 431

<211> 354

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 239..352

<221> sig\_peptide

<222> 239..289

<223> Von Heijne matrix

score 4.80000019073486

seq LKLISTNFSLCQS/VQ

<221> misc\_feature

<222> 345

<223> n=a, g, c or t

<400> 431

```

aggccttctg agtgcagctg gcaccatggg tgtgctccag agcaacttct gcttgctctg      60
agccccctgc cctgcctccc ctttcacat gtttctctg acaagatttt aagtacagca      120
attcaagaag atttctcctc ctaaacgaca tttatctgaa gtctattgcc tcttgattgc      180
tggaagagad tcttaaaatc atttcaaaag taacttataa acaaacttat taaaagtg      238
atg aaa gga gca ttg aaa tta att agc act aat ttt tca ctg tgc caa      286
Met Lys Gly Ala Leu Lys Leu Ile Ser Thr Asn Phe Ser Leu Cys Gln
          -15                      -10                      -5
agt gtg cag tgt cct tca gag gaa aca ata aca gat ctg gtg agt gtg      334
Ser Val Gln Cys Pro Ser Glu Glu Thr Ile Thr Asp Leu Val Ser Val
          1                      5                      10                      15
cca tgc cag tng gga ctg gg                        354
Pro Cys Gln Xaa Gly Leu
          20

```

<210> 432  
 <211> 431  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 153..431

<221> sig\_peptide  
 <222> 153..359  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq MMVLSLGIILASA/SF

<400> 432  
 gtaaaaaaac actggaataa ggaagggctg atgactttca gaagatgaag gtaagtagaa 60  
 accgttgatg ggactgagaa accagagtta aaacctcttt ggagcttctg aggactcagc 120  
 tggaaaccaac gggcacagtt ggcaacacca tc atg aca tca caa cct gtt ccc 173  
 Met Thr Ser Gln Pro Val Pro  
 -65  
 aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa 221  
 Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln  
 -60 -55 -50  
 gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa 269  
 Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys  
 -45 -40 -35  
 cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt 317  
 His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys  
 -30 -25 -20 -15  
 ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc 365  
 Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe  
 -10 -5 1  
 tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac 413  
 Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr  
 5 10 15  
 cca ttc ata gga ccc ggg 431  
 Pro Phe Ile Gly Pro Gly  
 20

<210> 433  
 <211> 201  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 37..201

<221> sig\_peptide  
 <222> 37..156  
 <223> Von Heijne matrix  
 score 4.80000019073486  
 seq IVSAACKCGSSQA/AI

<400> 433  
 aatatttatg aagcagtttg gaaccaaagg ggtagt atg gta gac gag tgt ctt 54  
 Met Val Asp Glu Cys Leu  
 -40 -35  
 aca gag cct gtg tgg gga agc aaa agg caa ggg tgt agt tca cag gca 102  
 Thr Glu Pro Val Trp Gly Ser Lys Arg Gln Gly Cys Ser Ser Gln Ala  
 -30 -25 -20

235

```

gaa gcg agc tgt gac att gtc agt gca gcg tgt aag tgt ggc tcc tca      150
Glu Ala Ser Cys Asp Ile Val Ser Ala Ala Cys Lys Cys Gly Ser Ser
      -15      -10      -5
cag gcg gcc att gat tgt gag acc tca tct tgc tct gaa gat ttc ccg      198
Gln Ala Ala Ile Asp Cys Glu Thr Ser Ser Cys Ser Glu Asp Phe Pro
      1      5      10
gtg
Val
15

```

&lt;210&gt; 434

&lt;211&gt; 334

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 242..334

&lt;221&gt; sig\_peptide

&lt;222&gt; 242..283

&lt;223&gt; Von Heijne matrix

score 4.80000019073486

seq AWWFSGTFPLTHP/CS

&lt;400&gt; 434

```

aagctgtact ctttcagcac atttcctttc atctcccct tcttccctct tctgtgtctt      60
caagactttc cccctcttgc tgccacagat gcagtgaagc ctgccatata taagggtacaa      120
tgtgtggcaa ctctgcaggt ggggtctatg caagctacag acccctctga gtgtggtcag      180
tgccttagcc tggcctggat gcctaccagg ccccaaccaac acctagctgc tggatattat      240
a atg gca tgg tgg ttt tct gga acc ttc cca cta act cac ccc tgc agc      289
  Met Ala Trp Trp Phe Ser Gly Thr Phe Pro Leu Thr His Pro Cys Ser
      -10      -5      1
gga tac ggc tct ctg atg gct cct tct agc cct acc cct tct ggg      334
Gly Tyr Gly Ser Leu Met Ala Pro Ser Ser Pro Thr Pro Ser Gly
      5      10      15

```

&lt;210&gt; 435

&lt;211&gt; 386

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 152..385

&lt;221&gt; sig\_peptide

&lt;222&gt; 152..322

&lt;223&gt; Von Heijne matrix

score 4.80000019073486

seq VTSLANLIPPVKA/TP

&lt;400&gt; 435

```

agtcgagtc tgcccggtc gaagccggct gtcggtctcc gtgtcgccgc cgccgcccg      60
catcgtggag ctggggcccc cttttgctg ggagttttgt agtcgcctag ggtcagcggt      120
gacatcccaa agggcaggcc cggcagccgc c atg gtg gcc aag gat tac ccc      172
  Met Val Ala Lys Asp Tyr Pro
      -55
ttc tac ctc acg gtc aag aga gcg aac tgc agc ctg gag cta cct ccg      220
Phe Tyr Leu Thr Val Lys Arg Ala Asn Cys Ser Leu Glu Leu Pro Pro
-50      -45      -40      -35
gcc agc ggt ccg gcc aag gac gct gag gag cct agt aat aaa cgg gtc      268
Ala Ser Gly Pro Ala Lys Asp Ala Glu Glu Pro Ser Asn Lys Arg Val

```

236

-30	-25	-20	
aaa ccc ctt tcc cga gtc acg tcg cta gca aac ctc atc ccg ccc gtg			316
Lys Pro Leu Ser Arg Val Thr Ser Leu Ala Asn Leu Ile Pro Pro Val			
-15	-10	-5	
aag gcc acg cca tta aag cgc ttc agt caa acc ctg cag cgc tcc att			364
Lys Ala Thr Pro Leu Lys Arg Phe Ser Gln Thr Leu Gln Arg Ser Ile			
1	5	10	
agc ttc cgc agt gag agc gcc t			386
Ser Phe Arg Ser Glu Ser Ala			
15	20		

&lt;210&gt; 436

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 191..472

&lt;221&gt; sig\_peptide

&lt;222&gt; 191..274

&lt;223&gt; Von Heijne matrix

score 4.80000019073486

seq GVLLEPFVHQVGG/HS

&lt;400&gt; 436

tttttttgggt gcgagagaaa caataggacg gaaacgccga ggaacccggc tgaggcggca		60
gcgagcatcc tggccagaac aagccaagga gccaagacga gagggacaca cggacaaaaca		120
acagacagaa gacgtactgg ccgctggact ccgctgcctc ccccatctcc ccgccatctg		180
cgccccggagg atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc		229
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg		
-25	-20	
gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac		277
Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His		
-15	-10	-5
tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc		
Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val		325
5	10	15
cca agg gaa cat cag ttc tac gag acc ctc cct gct gag atg cgc aaa		373
Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys		
20	25	30
ttc act ccc cag tac aaa gga caa agc caa agg ccc ctt gtt agc tgg		421
Phe Thr Pro Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp		
35	40	45
cca tcc ctg ccc cat ttt ttc ccc tgg tcc ttt ccc ctg tgg cca cag		469
Pro Ser Leu Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln		
50	55	60
gga		472
Gly		

&lt;210&gt; 437

&lt;211&gt; 469

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 213..467

&lt;221&gt; sig\_peptide

&lt;222&gt; 213..314

&lt;223&gt; Von Heijne matrix

score 4.80000019073486  
seq ILAFLQSPRAILP/GN

<221> misc\_feature  
<222> 432..433  
<223> n=a, g, c or t

<400> 437  
ggattccgcgcccagggtttctaaatccagacattcccgtttggctgagcactctaggcc60  
tacatccatgaagctaggagagcgacactcaagactgcactattgagagaagctaacgt120  
taaaggcagtgaaatatattcgggagtccagctccggaaccggggagctcttttagtggga180  
ggggcggcgtgatggcgcttctggcctccgaatgcta ggg ggc gct gtg atc233  
Met Leu Gly Gly Ala Val Ile  
-30  
gcc ggg cgg cct ctt ggg cgc tgg gag tcc acc gcg caa ssc atc ctg281  
Ala Gly Arg Pro Leu Gly Arg Trp Glu Ser Thr Ala Gln Xaa Ile Leu  
-25 -20 -15  
gcc ttt ctt cag tcc cca cgt gcg atc ctt ccc ggc aac ttt ttc gag329  
Ala Phe Leu Gln Ser Pro Arg Ala Ile Leu Pro Gly Asn Phe Phe Glu  
-10 -5 1 5  
aaa aat gcc caa att caa ggc ggc ccg tgg ggt ggg ggg tca gga aaa377  
Lys Asn Ala Gln Ile Gln Gly Gly Pro Trp Gly Gly Gly Ser Gly Lys  
10 15 20  
aca tgc gcc cct ggc cga tsa gat cct ggc tgg gaa tgc ggt gcg ggc425  
Thr Cys Ala Pro Gly Arg Xaa Asp Pro Gly Trp Glu Cys Gly Ala Gly  
25 30 35  
ggg ggt nng gga gaa gcg gcg ggg tcg cgg gam agg ara agc gg469  
Gly Gly Xaa Gly Glu Ala Ala Gly Ser Arg Xaa Arg Xaa Ser  
40 45 50

<210> 438  
<211> 169  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 77..169

<221> sig\_peptide  
<222> 77..124  
<223> Von Heijne matrix  
score 4.80000019073486  
seq ACFHFLVSSLIS/FE

<400> 438  
ttgataggaa tagcattgaa tctgtaaatt gctttgggca ctatggccat ttaataata60  
ttgattcttc ctatcc atg agc atg gca tgt ttt ttc cat ttg ttt gtg tca112  
Met Ser Met Ala Cys Phe Phe His Leu Phe Val Ser  
-15 -10 -5  
tct ctg att tcc ttt gag cag tgt ttt gka atg cta aga aaa ttg ctt160  
Ser Leu Ile Ser Phe Glu Gln Cys Phe Xaa Met Leu Arg Lys Leu Leu  
1 5 10  
aaa att ata169  
Lys Ile Ile  
15

<210> 439  
<211> 447  
<212> DNA  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 211..447

&lt;221&gt; sig\_peptide

&lt;222&gt; 211..345

&lt;223&gt; Von Heijne matrix

score 4.69999980926514

seq PWLEVGLFFWLHA/AP

&lt;400&gt; 439

```

agaacaatgc tgcttggtc cctgaattca gcacccttcc tagggaatgt atgggtggat      60
cttttgctt gcaggattct ttttcattct tgcagggact tctggggccg gagtatgtaa      120
aactcctggg tctctgtgtg tgcttgagtg gctgctctac tgagactctg catacacagc      180
tctgtatatc ggacccawgg ccctgggtggc atg ggc tca cga gga gat ccc ctg      234
                               Met Gly Ser Arg Gly Asp Pro Leu
                               -45                               -40

atc tgt ggg ttg caa aga tct gtg gga gaa gtg tgg ttt cct gga tgg      282
Ile Cys Gly Leu Gln Arg Ser Val Gly Glu Val Trp Phe Pro Gly Trp
      -35                               -30                               -25

ggg cac aca atc act cac tgc ttc cct tgg ctg gag gtg ggg ctt ttt      330
Gly His Thr Ile Thr His Cys Phe Pro Trp Leu Glu Val Gly Leu Phe
      -20                               -15                               -10

ttt tgg ctc cat gct gct cct ggg cgg gcg att gcc cta ccc cat ttt      378
Phe Trp Leu His Ala Ala Pro Gly Arg Ala Ile Ala Leu Pro His Phe
      -5                               1                               5                               10

tct tca ttc tct gtg ggt caa gdb gtt cac ttg gtc agt cca ttg tgr      426
Ser Ser Phe Ser Val Gly Gln Xaa Val His Leu Val Ser Pro Leu Xaa
      15                               20                               25

gam ctg gat att tca gtt gaa      447
Xaa Leu Asp Ile Ser Val Glu
      30

```

&lt;210&gt; 440

&lt;211&gt; 340

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 176..340

&lt;221&gt; sig\_peptide

&lt;222&gt; 176..232

&lt;223&gt; Von Heijne matrix

score 4.69999980926514

seq ELLLLLPRGLCQV/CP

&lt;221&gt; misc\_feature

&lt;222&gt; 20,279..281

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 440

```

agaaaagcag ccgcagttgn gccgctccac cagcgcgtcc ggggtgggcct agcagtcgct      60
ccatttatcg cttgagatct ccagccttac cgcggctcga aatggacccc aactgctcct      120
gcaccactgg tgtctccwrc gcctgcaccg gctcctgcac gtgcaaagag tgcaa atg      178
                               Met

cac ctc ctg caa gaa gag ctg ctg ctc ctg ctg ccc cgt ggg ctg tgc      226
His Leu Leu Gln Glu Glu Leu Leu Leu Leu Pro Arg Gly Leu Cys
      -15                               -10                               -5

caa gtg tgc cca cgg ctg tgt ctg caa agg gmc gtt gga gaa ctg cag      274
Gln Val Cys Pro Arg Leu Cys Leu Gln Arg Xaa Val Gly Glu Leu Gln

```

239

1	5	10	
mtg cnn nky cct gat	gtg gga aca gct ctt ctc	cca gat gtt aat aga	322
Xaa Xaa Xaa Pro Asp	Val Gly Thr Ala Leu Leu	Pro Asp Val Asn Arg	
15	20	25	30
aca agc tgc aca acc tgg			340
Thr Ser Cys Thr Thr Trp			
	35		

&lt;210&gt; 441

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 292..408

&lt;221&gt; sig\_peptide

&lt;222&gt; 292..375

&lt;223&gt; Von Heijne matrix

score 4.69999980926514

seq QLVTRLLLSPSQS/TQ

&lt;400&gt; 441

agaagatggg gaaagaggaa ggaaaggatg cccagatata	gggagcttta gcgatgtagt	60
gaacggacag aagatcagga acaagttgag ttcattgtgt	ggagatggca rraagatgga	120
gattggtgag ctgagtggag aagtgccata gageggtgtt	ttgccagagt gtctgcggat	180
tgctcatacc tgggaaggat tctttgtatg gttcccttag	gctgagggag ggtatcagct	240
ttacagacct tgtgggatta caaaagggcc accacacact	cttcaaccaa t atg tgt	297
	Met Cys	

cta tct tgc att caa ggc tca ttc ttt gtt gaa att ttg cag ttg gtc	345
Leu Ser Cys Ile Gln Gly Ser Phe Phe Val Glu Ile Leu Gln Leu Val	
-25 -20 -15	

act agg cta ttg tta tct cca tct caa agt aca cag aca cac aca cac	393
Thr Arg Leu Leu Leu Ser Pro Ser Gln Ser Thr Gln Thr His Thr His	
-10 -5 1 5	

aca cac aca cac aca a	409
Thr His Thr His Thr	
10	

&lt;210&gt; 442

&lt;211&gt; 320

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 203..319

&lt;221&gt; sig\_peptide

&lt;222&gt; 203..298

&lt;223&gt; Von Heijne matrix

score 4.69999980926514

seq AILLLVXVSDKNE/QQ

&lt;221&gt; misc\_feature

&lt;222&gt; 225..227,279

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 442

cacactagaa tagactggaa caacttggat ttagtgattc	cgatgcttat caggaaggtc	60
tctgttcttt tataggaaga aaaaacatag ttatttttct	tttatgatac aaaggtatgc	120

240

```

tttctatgca agctggatac cagaccaaga ataataaatc acaatttcat aaggtttcta 180
agacttgata ttatatgggg at atg acc att ttg agg gaa atg tnn nca tca 232
                        Met Thr Ile Leu Arg Glu Met Xaa Xaa Ser
                        -30 -25
ctt tat gta ctt gaa gct aag gat act gct atc tta ttg ctt gtt tna 280
Leu Tyr Val Leu Glu Ala Lys Asp Thr Ala Ile Leu Leu Leu Val Xaa
-20 -15 -10
gtg agc gat aag aat gaa cag cag ctt ggg agg ggc gtg g 320
Val Ser Asp Lys Asn Glu Gln Gln Leu Gly Arg Gly Val
-5 1 5

```

<210> 443  
 <211> 256  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 102..254

<221> sig\_peptide  
 <222> 102..188  
 <223> Von Heijne matrix  
 score 4.69999980926514  
 seq ICCNLYFLLFCRS/SF

```

<400> 443
cttctttgta actcctgcat atacctttgc atttatgtag cttctggagg gcacatggag 60
gtagctcacc atggttttaa ttgcatttc tctgataatg a atg aga ctt agt tct 116
                        Met Arg Leu Ser Ser
                        -25
tcc tgt ggg ttg cct gtt aag act ttg cca ttt atc tgt tgc aat ctt 164
Ser Cys Gly Leu Pro Val Lys Thr Leu Pro Phe Ile Cys Cys Asn Leu
-20 -15 -10
tat ttc ttg ctg ttt tgt agg agt tct ttt tta tat ttt gga tat gat 212
Tyr Phe Leu Leu Phe Cys Arg Ser Ser Phe Leu Tyr Phe Gly Tyr Asp
-5 1 5
ccc att aat act tac atg tat tac aat gtt ttc tcc cac tcg gg 256
Pro Ile Asn Thr Tyr Met Tyr Tyr Asn Val Phe Ser His Ser
10 15 20

```

<210> 444  
 <211> 284  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 17..283

<221> sig\_peptide  
 <222> 17..220  
 <223> Von Heijne matrix  
 score 4.69999980926514  
 seq GCLLXPLLVSCLG/SL

```

<400> 444
tagatggcga ctccct atg tta ctg acg aga ccg gcg gtg agt gcg gga ggc 52
                        Met Leu Leu Thr Arg Pro Ala Val Ser Ala Gly Gly
                        -65 -60
gcg gas cgc ttc tct ccg ggc tct cgg ggc agg ggt tcg gac ttg gaa 100
Ala Xaa Arg Phe Ser Pro Gly Ser Arg Gly Arg Gly Ser Asp Leu Glu
-55 -50 -45

```

241

```

agg ggt ctg tgc ccc gcc cat ccc ggg gcc cct cct ttg ccc cgc ccc      148
Arg Gly Leu Cys Pro Ala His Pro Gly Ala Pro Pro Leu Pro Arg Pro
-40                               -35                               -30                               -25
ccg gac cgc ctt ccc cat tca ttc tct cct acg ggg tgt ctc ctg hgc      196
Pro Asp Arg Leu Pro His Ser Phe Ser Pro Thr Gly Cys Leu Leu Xaa
-20                               -15                               -10
ccc ctt ctg gtc tcg tgt ttg ggg tct ctg ctt ccg gtc acc caa acc      244
Pro Leu Leu Val Ser Cys Leu Gly Ser Leu Leu Pro Val Thr Gln Thr
-5                               1                               5
ctg ggg tcc ttc agt gct ggt ccc tgc ttc agg acc ctc a                284
Leu Gly Ser Phe Ser Ala Gly Pro Cys Phe Arg Thr Leu
10                               15                               20

```

<210> 445  
 <211> 240  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 103..240

<221> sig\_peptide  
 <222> 103..177  
 <223> Von Heijne matrix  
 score 4.69999980926514  
 seq ILXSLSSSVPSRA/GS

```

<400> 445
tctttttgtaa tgaagcatgg cagccaggcc tagcacactt ccctctgcac accatcctgc      60
tcaggcctct gtgcctcggc tgtgctgttc cttctgcttg ga atg cat tca ctg      114
                               Met His Ser Leu
                               -25
tgt cca ctt agc caa ttc cta cct att ctt tma agc ctc agt tcc agt      162
Cys Pro Leu Ser Gln Phe Leu Pro Ile Leu Xaa Ser Leu Ser Ser Ser
-20                               -15                               -10
gtc ccc tcg agg gca ggc agt gct ttc cca tct gcc cta ggt cca ctc      210
Val Pro Ser Arg Ala Gly Ser Ala Phe Pro Ser Ala Leu Gly Pro Leu
-5                               1                               5                               10
tac cag cct cta ctt ggg ccc cca gca tgg                                240
Tyr Gln Pro Leu Leu Gly Pro Pro Ala Trp
15                               20

```

<210> 446  
 <211> 184  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 8..184

<221> sig\_peptide  
 <222> 8..139  
 <223> Von Heijne matrix  
 score 4.69999980926514  
 seq LVFLSVXLLFLLF/LV

```

<400> 446
tcctttt atg cga aca caa gta tat gag ggg ttg tgt aaa aat tat ttt      49
Met Arg Thr Gln Val Tyr Glu Gly Leu Cys Lys Asn Tyr Phe
-40                               -35
tct ctt gct gta cta caa aga gat aga atc aaa ctg ctt ttt ttc gac      97

```

242

```

Ser Leu Ala Val Leu Gln Arg Asp Arg Ile Lys Leu Leu Phe Phe Asp
-30          -25          -20          -15
ata ctg gtt ttt ctt tct gtt tww ctt ctc ttt ctt cta ttt ctt gtg      145
Ile Leu Val Phe Leu Ser Val Xaa Leu Leu Phe Leu Leu Phe Leu Val
          -10          -5          1
gat atw atg gct aat adc aca aca agt tta ggg agg ccc      184
Asp Ile Met Ala Asn Xaa Thr Thr Ser Leu Gly Arg Pro
      5          10          15

```

<210> 447  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 34..360

<221> sig\_peptide  
 <222> 34..168  
 <223> Von Heijne matrix  
       score 4.69999980926514  
       seq LLSLAQTTTKTTA/TT

<221> misc\_feature  
 <222> 280  
 <223> n=a, g, c or t

```

<400> 447
aaaaactctt ttctttatcc tctttccaga aaa atg ggc caa ttc aca gct gca      54
                               Met Gly Gln Phe Thr Ala Ala
                               -45          -40
atg gtt ggg aga att tcc tgt ctg gga gtc tgg aaa ctg cca aga gtg      102
Met Val Gly Arg Ile Ser Cys Leu Gly Val Trp Lys Leu Pro Arg Val
          -35          -30          -25
gaa agc tgc agc cag cca gcg agg cct ctg ttg tca ctg gcc caa aca      150
Glu Ser Cys Ser Gln Pro Ala Arg Pro Leu Leu Ser Leu Ala Gln Thr
          -20          -15          -10
aca aca aaa aca acc gca aca aca aca aca aca aaa cat gcc acg      198
Thr Thr Lys Thr Thr Ala Thr Thr Thr Thr Thr Thr Lys His Ala Thr
          -5          1          5          10
tgt gca ctg gca tat aca aac acg ccc aca gaa cca vrc caa gcg gac      246
Cys Ala Leu Ala Tyr Thr Asn Thr Pro Thr Glu Pro Xaa Gln Ala Asp
          15          20          25
aag gct tca agg aga gct tct ggg ahv ctc rwv ncc gcg gcg agg cat      294
Lys Ala Ser Arg Arg Ala Ser Gly Xaa Leu Xaa Xaa Ala Ala Arg His
          30          35          40
atc cct tgg cat ggt gcc act gca gcc cag ctc cca gcc ccc ccg cca      342
Ile Pro Trp His Gly Ala Thr Ala Ala Gln Leu Pro Ala Pro Pro Pro
          45          50          55
tct gtc atc agc gct ctg      360
Ser Val Ile Ser Ala Leu
      60

```

<210> 448  
 <211> 123  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 39..122

```

<221> sig_peptide
<222> 39..92
<223> Von Heijne matrix
      score 4.69999980926514
      seq IAILFPNSGSCFA/FS

<400> 448
cttatctgat tcacagcccg tattcagatt tgccaatt atg ttg att ttc att att      56
                                   Met Leu Ile Phe Ile Ile
                                   -15
gct att tta ttt ccc aat tca gga tca tgc ttt gca ttt agt tgt cat      104
Ala Ile Leu Phe Pro Asn Ser Gly Ser Cys Phe Ala Phe Ser Cys His
      -10                               -5                               1
gtc tcc ttt ttt ttt ttt t      123
Val Ser Phe Phe Phe Phe
5                               10

<210> 449
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 18..191

<221> sig_peptide
<222> 18..62
<223> Von Heijne matrix
      score 4.69999980926514
      seq RCACFPFFPFAFC/HD

<400> 449
ctctctcctg ttcggtc atg gtg aga tgt gct tgc ttc ccc ttc ttc ccc      50
                                   Met Val Arg Cys Ala Cys Phe Pro Phe Phe Pro
                                   -15                               -10                               -5
ttc gcc ttc tgc cat gac tgt aag ttt ctt ggg gcc tcc cag tca tgc      98
Phe Ala Phe Cys His Asp Cys Lys Phe Leu Gly Ala Ser Gln Ser Cys
      1                               5                               10
ttc ttg tta agc cgg caa aac tgt gta agc aca gga kga cct tca tcc      146
Phe Leu Leu Ser Arg Gln Asn Cys Val Ser Thr Gly Xaa Pro Ser Ser
      15                               20                               25
aaa tct gat atc aac tca agg tct gga tct tgt tca ctg gca agg gg      193
Lys Ser Asp Ile Asn Ser Arg Ser Gly Ser Cys Ser Leu Ala Arg
      30                               35                               40

<210> 450
<211> 302
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..301

<221> sig_peptide
<222> 8..88
<223> Von Heijne matrix
      score 4.69999980926514
      seq LAPLXLVFISLLP/AP

<221> misc_feature

```

&lt;222&gt; 292

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 450

```

ccagcaa atg gtg agt ttg agg gta ggg gcc tct cca ttt cgg ttc cca      49
      Met Val Ser Leu Arg Val Gly Ala Ser Pro Phe Arg Phe Pro
            -25                    -20                    -15
ctg gcc ccc ctc tbt ttg gtt ttc atc tct ctt ctc cca gcc cca ttt      97
Leu Ala Pro Leu Xaa Leu Val Phe Ile Ser Leu Leu Pro Ala Pro Phe
            -10                    -5                    1
ttt cct act ctt tcg ttt cct tgt tgc tgt gtg tcc tgg ctc ttt tct      145
Phe Pro Thr Leu Ser Phe Pro Cys Cys Cys Val Ser Trp Leu Phe Ser
      5                    10                    15
ctt tct gtg vtt gtc tct ctg cgt ctc agt ctt tbt gtg tcc tgt tta      193
Leu Ser Val Xaa Val Ser Leu Arg Leu Ser Leu Xaa Val Ser Cys Leu
20                    25                    30                    35
tct ctc tgg tgt ctc ttg gta ttg ttt ctc tct ccc act ctg tat gtc      241
Ser Leu Trp Cys Leu Leu Val Leu Phe Leu Ser Pro Thr Leu Tyr Val
            40                    45                    50
tct gac tca ttc tgc tca ttc tgt gtc ctc cct att gct ctc tgt ccc      289
Ser Asp Ser Phe Cys Ser Phe Cys Val Leu Pro Ile Ala Leu Cys Pro
            55                    60                    65
can gct cgt tct t
Xaa Ala Arg Ser
      70

```

&lt;210&gt; 451

&lt;211&gt; 367

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 150..365

&lt;221&gt; sig\_peptide

&lt;222&gt; 150..311

&lt;223&gt; Von Heijne matrix

score 4.69999980926514

seq PGLAFLAILTVLA/KP

&lt;400&gt; 451

```

aaaatgatcc atgcacacag cctctatagg aaagaaaaaa aatatccaat tgattttctt      60
cccttttctg cttctaaagt ataccaaatt tcactgtgat cttaatatcc cccagaacag      120
acacctctga gcagagagca ggccttaga atg gcc cac ccc tgt tta gct cca      173
                        Met Ala His Pro Cys Leu Ala Pro
                                -50
gca gaa cct tct act ctt tca caa acc kcc cat cca att caa aga acc      221
Ala Glu Pro Ser Thr Leu Ser Gln Thr Xaa His Pro Ile Gln Arg Thr
      -45                    -40                    -35
ctg aca act ttc cct cag gct tgg gtt cta acc agc agc ttt tcc ata      269
Leu Thr Thr Phe Pro Gln Ala Trp Val Leu Thr Ser Ser Phe Ser Ile
      -30                    -25                    -20                    -15
cag cca ggc ctt gca ttc cta gcc att ctc acc gtg tta gcc aaa ccc      317
Gln Pro Gly Leu Ala Phe Leu Ala Ile Leu Thr Val Leu Ala Lys Pro
            -10                    -5                    1
ggs tcc tct amc tgg agt cct ggt cag ttc aca cca cac tcc ctg ctg      365
Gly Ser Ser Xaa Trp Ser Pro Gly Gln Phe Thr Pro His Ser Leu Leu
      5                    10                    15
gg

```

&lt;210&gt; 452

<211> 349  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 244..348

<221> sig\_peptide  
 <222> 244..336  
 <223> Von Heijne matrix  
 score 4.69999980926514  
 seq HLYXSLFSSFLCS/TP

<400> 452  
 ttctttcark tcttactact catccttcat ttatctcctg gatcattgcc cagagaatga 60  
 aagaaattgc cagtcaagcc agccaggtag gttaaatacta tcttggcagt cctggagact 120  
 gctgcagact gactgcctga tgtccgtgcc cactgggggtt tttccctttt cagaaaggat 180  
 ttctccctga tctctcccca caaactctgg ctttgctttt tcatttccta agagcaactc 240  
 aat atg cat ttc ccc atc caa gct acc ttc sac tat tcc cct act gat 288  
 Met His Phe Pro Ile Gln Ala Thr Phe Xaa Tyr Ser Pro Thr Asp  
 -30 -25 -20  
 tct ctc tgt cat tta tat ttk tca ctc ttc tct tcc ttt ctc tgc tct 336  
 Ser Leu Cys His Leu Tyr Xaa Ser Leu Phe Ser Ser Phe Leu Cys Ser  
 -15 -10 -5  
 acc cct gcc cgg g 349  
 Thr Pro Ala Arg  
 1

<210> 453  
 <211> 270  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 87..269

<221> sig\_peptide  
 <222> 87..194  
 <223> Von Heijne matrix  
 score 4.69999980926514  
 seq SCFVPSLVTGALQ/QS

<400> 453  
 agcagtccag agaagtgaat tgacttgcct gaagccacag agcctgcaag tgcgagggct 60  
 gggattccaa tccaagctct gggcca atg gct ttg cat atc cta gaa tgc gag 113  
 Met Ala Leu His Ile Leu Glu Cys Glu  
 -35 -30  
 agg aac gtt tgt ttt gta gca gtt aga cag cct gct cat gaa agc tgc 161  
 Arg Asn Val Cys Phe Val Ala Val Arg Gln Pro Ala His Glu Ser Cys  
 -25 -20 -15  
 ttt gtg ccc agc ctt gtg aca ggt gct tta caa caa tcc cag aca cag 209  
 Phe Val Pro Ser Leu Val Thr Gly Ala Leu Gln Gln Ser Gln Thr Gln  
 -10 -5 1 5  
 cac cca cct tgg gtt tgc cct cag gta cag ggc tcc tat cca tcc tgg 257  
 His Pro Pro Trp Val Cys Pro Gln Val Gln Gly Ser Tyr Pro Ser Trp  
 10 15 20  
 aag aac aga ggg a 270  
 Lys Asn Arg Gly  
 25

<210> 454

<211> 492  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 317..490

<221> sig\_peptide  
 <222> 317..412  
 <223> Von Heijne matrix  
 score 4.69999980926514  
 seq RVLXLCNSRVST/RX

<221> misc\_feature  
 <222> 415..416  
 <223> n=a, g, c or t

<400> 454  
 taaggatatt acaaaacatt ttataaacac gtgggtctct tatgaagtac aatccaaagt 60  
 ttgcatacaa tttaaaacaa aagcaagaaa tgtcacgctt tgggaacact gtttktctca 120  
 cactaaaatg ttctatctga agcaagggga agtgtccaaa ttatagttca caaaatacct 180  
 ttattttctc acaacaaaat catccctagt cagcggecca acattactca tttctgtcat 240  
 caaaaacacc ctttctgtgg gttggtatga aatatccgca ggcatcacia gtactataag 300  
 aaagggtctt ttcaaa atg tcc tgt act cac tcc tct tct aac ctg ggt aag 352  
 Met Ser Cys Thr His Ser Ser Ser Asn Leu Gly Lys  
 -30 -25  
 ttt tct gta cac aga gag tac cgt gtc ctc mta ctg tgt aac agt agg 400  
 Phe Ser Val His Arg Glu Tyr Arg Val Leu Xaa Leu Cys Asn Ser Arg  
 -20 -15 -10 -5  
 gtc tct ttc act cgn ntc cat gtg aag aga cca cca wac agg cta tgt 448  
 Val Ser Phe Thr Arg Xaa His Val Lys Arg Pro Pro Xaa Arg Leu Cys  
 1 5 10  
 gtg agc agc aaa ggc tgt tta ttt cac ctg ggt gca ggc agg ct 492  
 Val Ser Ser Lys Gly Cys Leu Phe His Leu Gly Ala Gly Arg  
 15 20 25

<210> 455  
 <211> 177  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 56..175

<221> sig\_peptide  
 <222> 56..112  
 <223> Von Heijne matrix  
 score 4.69999980926514  
 seq AFPLLLVIILLFQ/KQ

<400> 455  
 cacattcata agtatgagct taggctgagg atatatatcc agtgggggat gaaac atg 58  
 Met  
 ctt aag aaa ttg agt gca ttt cct tta tta ttg gtt att att ttg cta 106  
 Leu Lys Lys Leu Ser Ala Phe Pro Leu Leu Leu Val Ile Ile Leu Leu  
 -15 -10 -5  
 ttt caa aaa caa wtt gga ctt tta aaa aat tat amt tca cca cag aga 154  
 Phe Gln Lys Gln Xaa Gly Leu Leu Lys Asn Tyr Xaa Ser Pro Gln Arg  
 1 5 10  
 cag gtg ttg ttt tgt aat cga ag 177

Gln Val Leu Phe Cys Asn Arg  
15 20

<210> 456  
<211> 102  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 14..100

<221> sig\_peptide  
<222> 14..67  
<223> Von Heijne matrix  
score 4.69999980926514  
seq CIFLAVLISKISWA/VN

<400> 456  
ctaattgaaa agg atg tcc tat ttc cga tgt ata ttt ttg gca gtt ttg 49  
Met Ser Tyr Phe Arg Cys Ile Phe Leu Ala Val Leu  
-15 -10  
tca aaa atc agt tgg gct gta aat atg tgc agt ctt att tct ggg tcc 97  
Ser Lys Ile Ser Trp Ala Val Asn Met Cys Ser Leu Ile Ser Gly Ser  
-5 1 5 10  
tcg gg 102  
Ser

<210> 457  
<211> 151  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 35..151

<221> sig\_peptide  
<222> 35..136  
<223> Von Heijne matrix  
score 4.59999990463257  
seq LFLSISLITLYYS/SE

<400> 457  
tgagttaaatt tagacaactg taagagaaaa attt atg ctt tgt ata atg ttt ggt 55  
Met Leu Cys Ile Met Phe Gly  
-30  
att gaa act aat gaa att acc aag atg aca atg tct ttt ctt ttg ttt 103  
Ile Glu Thr Asn Glu Ile Thr Lys Met Thr Met Ser Phe Leu Leu Phe  
-25 -20 -15  
cta agt atc agt ttg ata act tta tat tat tcc tca gaa gca tgt ggg 151  
Leu Ser Ile Ser Leu Ile Thr Leu Tyr Tyr Ser Ser Glu Ala Cys Gly  
-10 -5 1 5

<210> 458  
<211> 285  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 16..285

<221> sig\_peptide

<222> 16..132

<223> Von Heijne matrix

score 4.59999990463257

seq YVFXLLAPFLTRS/SP

<221> misc\_feature

<222> 251

<223> n=a, g, c or t

<400> 458

```

agacctccag aaacc atg tgt caa gct cgg att gcc tta gac agg tgc aat      51
          Met Cys Gln Ala Arg Ile Ala Leu Asp Arg Cys Asn
                    -35                    -30
tta aga aca gct ttc atc ctc ttt kct ctc ata ttg tca cac tat gtg      99
Leu Arg Thr Ala Phe Ile Leu Phe Xaa Leu Ile Leu Ser His Tyr Val
          -25                    -20                    -15
ttc yga ctt ctg gct cct ttc ctc aca aga agc tca ccc agc tgg aac      147
Phe Xaa Leu Leu Ala Pro Phe Leu Thr Arg Ser Ser Pro Ser Trp Asn
          -10                    -5                    1                    5
tct tat ggg acc ttg gca cca gag acc aca aat tcc tct ttg aag ttt      195
Ser Tyr Gly Thr Leu Ala Pro Glu Thr Thr Asn Ser Ser Leu Lys Phe
                    10                    15                    20
tct aac agc aac aat ggt att tct gac ttg gct twc ttg tat ttc tcd      243
Ser Asn Ser Asn Asn Gly Ile Ser Asp Leu Ala Xaa Leu Tyr Phe Ser
                    25                    30                    35
cac gtt anc aaa att ggt tca gca tct acc atg ggc tac ggg      285
His Val Xaa Lys Ile Gly Ser Ala Ser Thr Met Gly Tyr Gly
          40                    45                    50

```

<210> 459

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 15..311

<221> sig\_peptide

<222> 15..86

<223> Von Heijne matrix

score 4.59999990463257

seq QGMLLAILEXCGA/IP

<400> 459

```

tcctcaagtt cttc atg gtc aag tcc gtc atc ttt ctt tcc ttc tgg caa      50
          Met Val Lys Ser Val Ile Phe Leu Ser Phe Trp Gln
                    -20                    -15
ggc atg ctc ctg gcc atc ctg gag rag tgt ggg gcc atc ccc aaa atc      98
Gly Met Leu Leu Ala Ile Leu Glu Xaa Cys Gly Ala Ile Pro Lys Ile
          -10                    -5                    1
cac tcg gcc cgc gtg tcg gtg ggc gag ggc acc gtg gct gcc ggc tac      146
His Ser Ala Arg Val Ser Val Gly Glu Gly Thr Val Ala Ala Gly Tyr
5                    10                    15                    20
cag gac ttc atc atc tgt gtg gag atg ttc ttt gca gcc ctg gcc ctg      194
Gln Asp Phe Ile Ile Cys Val Glu Met Phe Phe Ala Ala Leu Ala Leu
          25                    30                    35
cgg cac gcc ttc acc tac aag gtc tat gct gac aag agg ctg gac gca      242
Arg His Ala Phe Thr Tyr Lys Val Tyr Ala Asp Lys Arg Leu Asp Ala
          40                    45                    50
caa gtg cca aca tac ggc cct tac ggc cgc tgt gcc ccc atg aag agc      290

```

311

```
<210> 460
<211> 425
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 161..424
```

```
<221> sig_peptide
<222> 161..418
<223> Von Heijne matrix
      score 4.59999990463257
      seq AAAALCILILLXA/MY
```

<400>	460	
agggccggggt	gatgcgcagg caatttatca tcttgatctc ccactgagtc agggagctct	60
cctgtcacca	gtattgattt cagaggatgg actaaatttc ctaggatttc cattaagaat	120
taagaaaaaaa	gctctaagca cgcagggtag ccagacagac atg gat atg aga tgg	175
	Met Asp Met Arg Trp	
	-85	
cac tgt gaa aac tcg cag acc aca gat gac atc ctt gtg gcc tca gca		223
His Cys Glu Asn Ser Gln Thr Thr Asp Asp Ile Leu Val Ala Ser Ala		
-80	-75 -70	
gag tgt ccc agc gat gat gag gac att gac ccc tgt gag ccg agc tca		271
Glu Cys Pro Ser Asp Asp Glu Asp Ile Asp Pro Cys Glu Pro Ser Ser		
-65	-60 -55 -50	
ggg ggg tta gcc aac cca acc cga gca ggc ggc aga gag ccg tat cca		319
Gly Gly Leu Ala Asn Pro Thr Arg Ala Gly Gly Arg Glu Pro Tyr Pro		
-45	-40 -35	
ggc tca gca gaa gtg atc cgg gag tcc agc agc acc acg ggt atg gtc		367
Gly Ser Ala Glu Val Ile Arg Glu Ser Ser Ser Thr Thr Gly Met Val		
-30	-25 -20	
gtt ggg ata gta gcc gct gcc gcc ctg tgc atc ctt atc ctc ctc wat		415
Val Gly Ile Val Ala Ala Ala Ala Leu Cys Ile Leu Ile Leu Leu Xaa		
-15	-10 -5	
gcc atg tac a		425
Ala Met Tyr		
1		

```
<210> 461
<211> 420
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 45..419
```

```
<221> sig_peptide
<222> 45..104
<223> Von Heijne matrix
      score 4.59999990463257
      seq PTLTLTCIGSVVS/SD
```

<400> 461  
 aaaaagctgt gggctcagaa qcagaattct ggggtgtctc cacc atg qcc tgg acy 56

250

Met Ala Trp Thr  
-20

```

cct ctc tgg ccc act ctc ctc act ctt tgc ata ggt tct gtg gtt tct      104
Pro Leu Trp Pro Thr Leu Leu Thr Leu Cys Ile Gly Ser Val Val Ser
      -15                      -10                      -5
tct gac ctg act cag gac cct gct gtg tct gtg gcc ttg gga cag aga      152
Ser Asp Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Arg
1                      5                      10                      15
gtc agg atc aca tgc cag gga gac aac ctc gaa gag tat ttt gca agc      200
Val Arg Ile Thr Cys Gln Gly Asp Asn Leu Glu Glu Tyr Phe Ala Ser
      20                      25                      30
tgg tac cga cag agg ccc gga cag gcc cct gtc ctt gtc atc tat ggt      248
Trp Tyr Arg Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly
      35                      40                      45
aaa aac aac cgg ccc tca ggg att cca gsc cgr ktc tct ggc tcc aag      296
Lys Asn Asn Arg Pro Ser Gly Ile Pro Xaa Arg Xaa Ser Gly Ser Lys
      50                      55                      60
tca ggc aat aca gct tta ttg acc atc gyc ggg gct cag gcg gag gat      344
Ser Gly Asn Thr Ala Leu Leu Thr Ile Xaa Gly Ala Gln Ala Glu Asp
65                      70                      75                      80
gab gct gac tat tac tgt agt kat cgc gac cat act gat aat cgg tgg      392
Xaa Ala Asp Tyr Tyr Cys Ser Xaa Arg Asp His Thr Asp Asn Arg Trp
      85                      90                      95
gtg ttc ggc ggg ggg acc agg ctg aca g      420
Val Phe Gly Gly Thr Arg Leu Thr
      100                      105

```

&lt;210&gt; 462

&lt;211&gt; 257

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 46..255

&lt;221&gt; sig\_peptide

&lt;222&gt; 46..105

&lt;223&gt; Von Heijne matrix

score 4.59999990463257

seq XILTCLIFRNSEG/FQ

&lt;400&gt; 462

```

tttttttttt tccccaagcg aaswtgaaca gttgctaagt ggaaa atg gag gct gaa      57
Met Glu Ala Glu
      -20
ttt tac atg gkg att ctt acc tgc ttg atc ttc agg aac tca gaa ggg      105
Phe Tyr Met Xaa Ile Leu Thr Cys Leu Ile Phe Arg Asn Ser Glu Gly
      -15                      -10                      -5
ttt cag att gyc cat gtc cag aaa caa cag tgt ctt ttc aaa aat gag      153
Phe Gln Ile Xaa His Val Gln Lys Gln Gln Cys Leu Phe Lys Asn Glu
1                      5                      10                      15
aaa gtg gtc gtg ggc tca tgc aac agg acc atc cag aac cag cag tgg      201
Lys Val Val Val Gly Ser Cys Asn Arg Thr Ile Gln Asn Gln Gln Trp
      20                      25                      30
atg tgg act gag gat gaa aag ctc ctt cat gtt aaa tct gca ctg tgc      249
Met Trp Thr Glu Asp Glu Lys Leu Leu His Val Lys Ser Ala Leu Cys
      35                      40                      45
ttg gcc at      257
Leu Ala
      50

```

&lt;210&gt; 463

```
<220>  
<221> CDS  
<222> 61..117
```

```
<221> sig_peptide
<222> 61..111
<223> Von Heijne matrix
      score 4.59999990463257
      seq ACALCVWLCKVSC/SI
```

```

<400> 463
aataggaaga caaaagacaa aaaaaaatcc accaccacca aaatatccct ttgtacatgt      60
atg tgc gtg tgc gcg tgt gct ttg tgt gtg tgg ttg tgt gtt aaa tca      108
Met Cys Val Cys Ala Cys Ala Leu Cys Val Trp Leu Cys Val Lys Ser
          -15                -10                -5

tgc agt att      117
Cys Ser Ile
      1

```

```
<210> 464
<211> 142
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 39..140
```

```
<221> sig_peptide
<222> 39..101
<223> Von Heijne matrix
      score 4.59999990463257
      seq FIYLLAFCMPSLE/KC
```

```

<400> 464
cttattgtgg attgtgggtt taattttgta tttccctg atg att agt gat gtt cag      56
                                   Met Ile Ser Asp Val Gln
                                   -20
cac ctt ttc ata tac ttg tta gcc ttt tgt atg cct tcc ttg gag aaa      104
His Leu Phe Ile Tyr Leu Leu Ala Phe Cys Met Pro Ser Leu Glu Lys
-15          -10          -5          1
tgt cta tac ggg tct ttg gcc cac ttt ttt ttt tt      142
Cys Leu Tyr Gly Ser Leu Ala His Phe Phe Phe ,
          5          10

```

```
<210> 465
<211> 300
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 216..299
```

```
<221> sig_peptide
<222> 216..260
<223> Von Heijne matrix
      score 4.59999990463257
      seq LFRVLFSXTCALX/OD
```

<400> 465  
 agttacttct ttgctagggt gaggaagggt tggaagcgcc tcctgcagcc acgaatatcc 60  
 tccagtgcct gagagaaaac ggcctaatacg aaacgtccg cggcatacat ccattcttaa 120  
 aacttgagtg gctgcttttc tgggtggaaa agagcgggtat cagacaggggt gagcagtcgg 180  
 ggaacggatg aacaaagact tgcaccgtgg ccctg atg cct ttg ttc cga gtt 233  
 Met Pro Leu Phe Arg Val  
 -15 -10  
 cta ttc agt tgw act tgt gcg ttg twa cag gac ttt aga atg cag ccc 281  
 Leu Phe Ser Xaa Thr Cys Ala Leu Xaa Gln Asp Phe Arg Met Gln Pro  
 -5 1 5  
 tgc ccc cca acc ccc aag g 300  
 Cys Pro Pro Thr Pro Lys  
 10

<210> 466  
 <211> 235  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 146..235  
 <221> sig\_peptide  
 <222> 146..217  
 <223> Von Heijne matrix  
 score 4.59999990463257  
 seq LLFYVLLFRNLYT/HT

<400> 466  
 tttatatctt taattgcaag gataaaagaa ggggtgcatc tcaaaggcca tgataaatat 60  
 aaaggataga aaagttacgt tgatgggtgtg cccctcgata tctagaagat agcatagtc 120  
 atgcattctc agaaagatcc tatcc atg tgg tat gta gag atg tgg gtt tct 172  
 Met Trp Tyr Val Glu Met Trp Val Ser  
 -20  
 ttt ttt cta ctt ttt tat gtg ctt ctt ttt aga aac tta tac aca cac 220  
 Phe Phe Leu Leu Phe Tyr Val Leu Leu Phe Arg Asn Leu Tyr Thr His  
 -15 -10 -5 1  
 aca cac cac act ggg 235  
 Thr His His Thr Gly  
 5

<210> 467  
 <211> 220  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 58..219  
 <221> sig\_peptide  
 <222> 58..147  
 <223> Von Heijne matrix  
 score 4.59999990463257  
 seq VLVVSFVVGGLGC/NX

<221> misc\_feature  
 <222> 218  
 <223> n=a, g, c or t

<400> 467  
 accacaactc ccagggtgct ccgcgtcctc gccgctgtcg ccgccgcgga gacaaag 57  
 atg gct gcg aga gtc ggc gcc ttc ctc aag aat gcc tgg gac aag gag 105  
 Met Ala Ala Arg Val Gly Ala Phe Leu Lys Asn Ala Trp Asp Lys Glu  
 -30 -25 -20 -15  
 cca gtg ctg gtc gtg tcc ttc gtc gtc ggg ggc ctc ggc tgt aat dct 153  
 Pro Val Leu Val Val Ser Phe Val Val Gly Gly Leu Gly Cys Asn Xaa  
 -10 -5 1  
 gcc ccc att gag ccc cta ctt caa gta ctc cgt cat gat caa caa ggc 201  
 Ala Pro Ile Glu Pro Leu Leu Gln Val Leu Arg His Asp Gln Gln Gly  
 5 10 15  
 cac gcc cta caa cta cna c 220  
 His Ala Leu Gln Leu Xaa  
 20

<210> 468  
 <211> 462  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 154..462  
 <221> sig\_peptide  
 <222> 154..222  
 <223> Von Heijne matrix  
 score 4.59999990463257  
 seq WTCVAPVYPACSG/RR

<400> 468  
 gactgcagcc gcgagctcct ggaggcggcg ggatggaggc ggccggccgag cctggaaacc 60  
 tggccggcgt caggcacatc atcctgggtcc tctcaggaaa ggggggctgt gggaaaagca 120  
 ccattctccac ggagctggcc ctggcactgc gcc atg cag gca aga agg tgg gaa 174  
 Met Gln Ala Arg Arg Trp Glu  
 -20  
 tcc tgg atg tgg acc tgt gtg gcc cca gta tac ccc gca tgc tcg ggg 222  
 Ser Trp Met Trp Thr Cys Val Ala Pro Val Tyr Pro Ala Cys Ser Gly  
 -15 -10 -5  
 cgc agg gca rdr gct gtk sac cag tgs grr ccg cgg ctg ggc amc sgt 270  
 Arg Arg Ala Xaa Ala Val Xaa Gln Xaa Xaa Pro Arg Leu Gly Xaa Xaa  
 1 5 10 15  
 ctt cct gga ccg gga bca gag cat ctc gct cat gtc tgt ggg ctt cct 318  
 Leu Pro Gly Pro Gly Xaa Glu His Leu Ala His Val Cys Gly Leu Pro  
 20 25 30  
 gct gga gaa gcc gga cga ggc cgt ggt gtg gag agg ccc caa gaa aaa 366  
 Ala Gly Glu Ala Gly Arg Gly Arg Gly Val Glu Arg Pro Gln Glu Lys  
 35 40 45  
 cgc gct gat aaa gca gtw kgt gtc cga cgt ggc ctg ggg gga gct gga 414  
 Arg Ala Asp Lys Ala Val Xaa Val Arg Arg Gly Leu Gly Gly Ala Gly  
 50 55 60  
 cta cct ggt ggt gac acg ccc cgg gga cct ccg atg agc aca tgg cca 462  
 Leu Pro Gly Gly Asp Thr Pro Arg Gly Pro Pro Met Ser Thr Trp Pro  
 65 70 75 80

<210> 469  
 <211> 438  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 391..438

<221> sig\_peptide

<222> 391..432

<223> Von Heijne matrix

score 4.59999990463257

seq FLFFFGNSPCCGA/TG

<400> 469

tatagtttca gttatgacat gagcacaac atcatgattt ctgttctttt taatgcactc	60
agactggcta agaatatggt ctgtgttggt gaatattcca tatgtatttg aaaataatat	120
atactctgct cttgttaggt tctagaaatg tcaattacct caaattctct gagagtgcag	180
ctcagttctt ctatatcctt actggtttct gcctacttgc tctgtcagtt actgagcaaa	240
aagtagcaaa gtctgcagct gtaatacatt tgtttatttc tctcattttt gttagtattt	300
gcttcatgta ctttgaagct rtgttgtag catgcataca cataggatga ttatggcttc	360
ttggaaaatt gacccttta gcattatgta atg ttc ctc ttt ttc ttt ggt aac	414
Met Phe Leu Phe Phe Phe Gly Asn	

-10

agt cca tgt tgt gga gcc aca ggg

Ser Pro Cys Cys Gly Ala Thr Gly

-5

1

438

<210> 470

<211> 131

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 11..130

<221> sig\_peptide

<222> 11..85

<223> Von Heijne matrix

score 4.59999990463257

seq SLSLSLSASLIIS/PS

<400> 470

atcttttcac atg ggc ctc tcc cac cat cggttc tca gcc cca tct tct	49
Met Gly Leu Ser His His Arg Val Ser Ala Pro Ser Ser	
-25 -20 -15	
ctc tct ctc tct ctc tcg gcc tcc ctc att att tct ccc tct ccc tcc	97
Leu Ser Leu Ser Leu Ser Ala Ser Leu Ile Ile Ser Pro Ser Pro Ser	
-10 -5 1	
gcc tct cca tct ctc ctt sct ccc cct bcc cgg g	131
Ala Ser Pro Ser Leu Leu Xaa Pro Pro Xaa Arg	
5 10 15	

<210> 471

<211> 211

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 115..210

<221> sig\_peptide

<222> 115..183

<223> Von Heijne matrix

score 4.5

seq LSMLLRLVSNRP/PV

<400> 471

255

```

tggcgcgatc ttggctcacc gcaccttccg cctccccggg tgcagcgctt ctccctgctc   60
agcctcccga ttagcgggga tgacagggag tcacccccac gcctgggcttg gctg atg   117
                                     Met
ttt gtg ttt tta gta ggc acg ccg tgt ctc tcc atg ttg ctc agg ctg   165
Phe Val Phe Leu Val Gly Thr Pro Cys Leu Ser Met Leu Leu Arg Leu
      -20                -15                -10
gtc tcc aac tcc cga cct cct gtg atg cgc cca cct cgg cct ggg g   211
Val Ser Asn Ser Arg Pro Pro Val Met Arg Pro Pro Arg Pro Gly
      -5                1                5

```

&lt;210&gt; 472

&lt;211&gt; 150

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 25..150

&lt;221&gt; sig\_peptide

&lt;222&gt; 25..123

&lt;223&gt; Von Heijne matrix

score 4.5

seq VTITILFLIVSMA/LK

&lt;400&gt; 472

```

ctttattgag ggatacttta ctct atg aaa ttc act cat ttt aag tgt aca   51
                                     Met Lys Phe Thr His Phe Lys Cys Thr
                                     -30                -25
att cgg tta tta tta cta tat tta cag aat cct gta acc atc aca att   99
Ile Arg Leu Leu Leu Tyr Leu Gln Asn Pro Val Thr Ile Thr Ile
      -20                -15                -10
tta ttt tta atc gtt tcc atg gcc ctg aaa ata aac cac ata ccc aag   147
Leu Phe Leu Ile Val Ser Met Ala Leu Lys Ile Asn His Ile Pro Lys
      -5                1                5
ggg   150
Gly

```

&lt;210&gt; 473

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 227..352

&lt;221&gt; sig\_peptide

&lt;222&gt; 227..268

&lt;223&gt; Von Heijne matrix

score 4.5

seq SCMSLFPCCPAQS/KN

&lt;400&gt; 473

```

tatttgatta aaaaagactc ttcttgtttt ctgttttgtc tgagttttca ttatacccac   60
ttctcaacta ccccatccca mgggtagaag tttttaaaat ttgcatattt aamattcatt   120
ttcgamttat ctgaaattaa tcaatatctc tactgtagtc ttggataatg ccaagagttt   180
aaaatgctat aatccaaaca cctgtttgga ctcaatatgt catttt atg tct tgt   235
                                     Met Ser Cys
atg tca ctt ttc ccc tgt tgc cct gct cag agt aag aat tat atg tta   283
Met Ser Leu Phe Pro Cys Cys Pro Ala Gln Ser Lys Asn Tyr Met Leu
      -10                -5                1                5
tta tta ttc att att tta ctt cca act caa ttt tta tat tca aaa tta   331

```

256

Leu Leu Phe Ile Ile Leu Leu Pro Thr Gln Phe Leu Tyr Ser Lys Leu  
 10 15 20  
 gtt aca att tgc tgt tgt ttt 352  
 Val Thr Ile Cys Cys Cys Phe  
 25

<210> 474  
 <211> 141  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 64..141

<221> sig\_peptide  
 <222> 64..105  
 <223> Von Heijne matrix  
 score 4.5  
 seq LVCCTINSSFALG/IS

<221> misc\_feature  
 <222> 38  
 <223> n=a, g, c or t

<400> 474  
 tactttaagt tctagggtac gtctgcacaa cgtsrggnnt tgatacatag gtatatatgt 60  
 gcc atg ttg gtt tgc tgc acc atc aac tca tca ttt gca tta ggt att 108  
 Met Leu Val Cys Cys Thr Ile Asn Ser Ser Phe Ala Leu Gly Ile  
 -10 -5 1  
 tct cgt aat gct atc cct ctg cca gcc cct ggg 141  
 Ser Arg Asn Ala Ile Pro Leu Pro Ala Pro Gly  
 5 10

<210> 475  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 92..298

<221> sig\_peptide  
 <222> 92..250  
 <223> Von Heijne matrix  
 score 4.5  
 seq ALYVICQFILIRS/GV

<400> 475  
 cagattaaga gatggagaaa ggtgtagggm tgattctttt tttggtgaga cctcgcataa 60  
 ctatcataaa tttgacagtg agtatgagag a atg gga cgt ggt cct ggc ccc 112  
 Met Gly Arg Gly Pro Gly Pro  
 -50  
 tta caa gag aga tct ctc ttt gag ama aag aga ggc gct cct cca agt 160  
 Leu Gln Glu Arg Ser Leu Phe Glu Xaa Lys Arg Gly Ala Pro Pro Ser  
 -45 -40 -35  
 agc aat att gaa gac ttc cat gga ctc tta ccg aag gtt atc ccc atc 208  
 Ser Asn Ile Glu Asp Phe His Gly Leu Leu Pro Lys Val Ile Pro Ile  
 -30 -25 -20 -15  
 tgt gct cta tat gtg att tgc cag ttc att cta ata agg agt gga gtc 256  
 Cys Ala Leu Tyr Val Ile Cys Gln Phe Ile Leu Ile Arg Ser Gly Val

```

          -10          -5          1
aac ata tca atg gag caa gtc aca gtc gtc gat gcc agt ctg gg      300
Asn Ile Ser Met Glu Gln Val Thr Val Val Asp Ala Ser Leu
          5          10          15

```

<210> 476  
 <211> 232  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 112..231

<221> sig\_peptide  
 <222> 112..150  
 <223> Von Heijne matrix  
 score 4.5  
 seq MLYCVVVVHSVCC/AV

```

<400> 476
tttttaggggg gtttggttcg tttttgaact gtatacagat gaaattatac agaatgcttt      60
tttttggtta tatggccttt ttcactctgt agtgtatttg tgagattcat c atg ttg      117
                                     Met Leu
tat tgt gta gtt gtg gtt cat tct gtt tgc tgt gca gta tac tat ttt      165
Tyr Cys Val Val Val Val His Ser Val Cys Cys Ala Val Tyr Tyr Phe
      -10          -5          1          5
gtg att att cat aca ata gaa cat att aca tat tta tgt atc cat tct      213
Val Ile Ile His Thr Ile Glu His Ile Thr Tyr Leu Cys Ile His Ser
          10          15          20
acc att cta ctg tgt gtg g      232
Thr Ile Leu Leu Cys Val
          25

```

<210> 477  
 <211> 236  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 124..234

<221> sig\_peptide  
 <222> 124..201  
 <223> Von Heijne matrix  
 score 4.5  
 seq VFXSLFLIQLLIS/FS

<221> misc\_feature  
 <222> 171  
 <223> n=a, g, c or t

```

<400> 477
aagtggcagc btcagcaccc agggctgtgg taggtcacag tctctgggyk ggtctcagtg      60
tccaacactg tagctgggtgc ctgccagggt cccagtgggt ggggtcacca ggtctgaaga      120
gag atg tgc tgg ytg cgg gya tgg ggc cag atc ctc ctg cca gtt ttc      168
Met Cys Trp Leu Arg Xaa Trp Gly Gln Ile Leu Leu Pro Val Phe
      -25          -20          -15
cbn tcc ctc ttt ctc atc caa ttg ctt atc agc ttc tca gag aat ggt      216
Xaa Ser Leu Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly
      -10          -5          1          5

```

ttt atc cac agc ccc atg gg  
 Phe Ile His Ser Pro Met  
 10

236

<210> 478  
 <211> 201  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 138..200

<221> sig\_peptide  
 <222> 138..179  
 <223> Von Heijne matrix  
 score 4.5  
 seq CGLXILCGPWLHA/AP

<400> 478  
 tctacatcac aggtkktca gtgaaatatg tggtaagatg tacaaataag atgtgccccca 60  
 ccaccagaat gatcagttct gtgaggacac gtccgtgact gtaccctctt tcagaagtgc 120  
 taterattaa tgtgggtt atg tgt ggc ctg akk atc ctc tgt ggg cct tgg 170  
 Met Cys Gly Leu Xaa Ile Leu Cys Gly Pro Trp  
 -10 -5  
 ctc cat gca gca cct cca tcc ccg ccg cgg g 201  
 Leu His Ala Ala Pro Pro Ser Pro Pro Arg  
 1 5

<210> 479  
 <211> 151  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 25..150

<221> sig\_peptide  
 <222> 25..123  
 <223> Von Heijne matrix  
 score 4.5  
 seq SISLLMLXXYWS/CW

<400> 479  
 acatagcatt ttatgkacta gaaa atg ttc cat gga agg gtt atg gcc atg 51  
 Met Phe His Gly Arg Val Met Ala Met  
 -30 -25  
 ggt kat tta acc aaa cat tta aat cta aac att tct atc tca ctg ttg 99  
 Gly Xaa Leu Thr Lys His Leu Asn Leu Asn Ile Ser Ile Ser Leu Leu  
 -20 -15 -10  
 ctt atg ctg wwd gwa tat tgg tct tgt tgg ata aaa tca ccc ccg scc 147  
 Leu Met Leu Xaa Tyr Trp Ser Cys Trp Ile Lys Ser Pro Pro Xaa  
 -5 1 5  
 atg g 151  
 Met

<210> 480  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 116..511

<221> sig\_peptide  
<222> 116..499  
<223> Von Heijne matrix  
score 4.5  
seq LALHHLSSGHSSG/WT

<221> misc\_feature  
<222> 150  
<223> n=a, g, c or t

```

<400> 480
gctcgcatca tggcggctga gtgggcttct cgtttctggc tttgggctac gctgctgatt    60
cctgcggccg cgggtctacga agaccaagtg ggcaagtttg attggagaca gcaat atg    118
                                         Met
ttg gga agg tca agt ttg ctc cst tgg aaa tnt tcc cct gga tcc aag    166
Leu Gly Arg Ser Ser Leu Leu Xaa Trp Lys Xaa Ser Pro Gly Ser Lys
      -125                      -120                      -115
aag ttg gtt gta gcc aca gag aag aat gtg att gca gca tta aat tcc    214
Lys Leu Val Val Ala Thr Glu Lys Asn Val Ile Ala Ala Leu Asn Ser
      -110                      -105                      -100
cga act ggg gag atc ttg tgg cgc cat gtt gac aag ggc acg gca gaa    262
Arg Thr Gly Glu Ile Leu Trp Arg His Val Asp Lys Gly Thr Ala Glu
      -95                      -90                      -85                      -80
ggg gct gtg gat gcc atg ctg ctg cac gga cag gat gtg atc act gtg    310
Gly Ala Val Asp Ala Met Leu Leu His Gly Gln Asp Val Ile Thr Val
      -75                      -70                      -65
tcc aat gga ggc cga atc atg cgt tcc tgg gag act aac atc ggg ggc    358
Ser Asn Gly Gly Arg Ile Met Arg Ser Trp Glu Thr Asn Ile Gly Gly
      -60                      -55                      -50
ctg aac tgg gag ata acc ctg gac agt ggc agt ttc cag gca ctt ggg    406
Leu Asn Trp Glu Ile Thr Leu Asp Ser Gly Ser Phe Gln Ala Leu Gly
      -45                      -40                      -35
ctg gtt ggc ctg cag gag tct gta agg tac atc gca gtc ctg aag aag    454
Leu Val Gly Leu Gln Glu Ser Val Arg Tyr Ile Ala Val Leu Lys Lys
      -30                      -25                      -20
act aca ctt gcc ctc cat cac ctc tcc agt ggg cac tca agt ggg tgg    502
Thr Thr Leu Ala Leu His His Leu Ser Ser Gly His Ser Ser Gly Trp
      -15                      -10                      -5                      1
aca tct cca    511
Thr Ser Pro

```

<210> 481  
<211> 429  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 212..427

<221> sig\_peptide  
<222> 212..382  
<223> Von Heijne matrix  
score 4.5  
seq IWVRFNFLASSQA/CS

```

<400> 481
aggagagggga atttgtttta aaagagagaa agacattgag actgtgtaaa ggggatgttg    60
caacctttta aaatctgtga tctcagacca aattatacaa tataatctca gtaggtgcca    120

```

```

gtagtaggga aaagtgtcag ccctcgtgtc tggcactaag taccacccac cccaacccca 180
gtgatggggag cctctaaatg actgagattt a atg tct act acc tat ttg aat 232
                               Met Ser Thr Thr Tyr Leu Asn
                               -55
gag gac ttg aag aag aaa ttc agt gca gtk ata gag cag gtg ctt ttt 280
Glu Asp Leu Lys Lys Lys Phe Ser Ala Val Ile Glu Gln Val Leu Phe
-50                               -45                               -40                               -35
gca cac tta tcc cca cta cat gtg tgg ctc cag ctc agg tct ctc tgt 328
Ala His Leu Ser Pro Leu His Val Trp Leu Gln Leu Arg Ser Leu Cys
                               -30                               -25                               -20
gag trt ttg acc tgc atc tgg gtt aga ttc aat ttt tta gcc tca agc 376
Glu Xaa Leu Thr Cys Ile Trp Val Arg Phe Asn Phe Leu Ala Ser Ser
                               -15                               -10                               -5
caa gca tgc tcc aaa tgc aac tcc tcg ttt ctc atc atg tca tcc tct 424
Gln Ala Cys Ser Lys Cys Asn Ser Ser Phe Leu Ile Met Ser Ser Ser
                               1                               5                               10
tca cc 429
Ser
15

```

<210> 482  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 145..384

<221> sig\_peptide  
 <222> 145..261  
 <223> Von Heijne matrix  
 score 4.5  
 seq LIILDLLVPVIGL/IT

```

<400> 482
tacacgtaca gctcagcctt tctgttagct gcaacttcag tgttggtgaa ttattatgct 60
tctttgcaca ttgacttcta tggcgcctac aacacgtcag cttgtggaat tgagctgctt 120
cctcgaaaag gtccctcgct gtgg atg gca ctt atc gtt cta cag cta aca 171
                               Met Ala Leu Ile Val Leu Gln Leu Thr
                               -35
ttt gga att gga tac gtt aca cta ctc cag att cat tcc atc tat tca 219
Phe Gly Ile Gly Tyr Val Thr Leu Leu Gln Ile His Ser Ile Tyr Ser
-30                               -25                               -20                               -15
caa tta att att ttg gat ctc ttg gtt cct gta ata ggc tta atc aca 267
Gln Leu Ile Ile Leu Asp Leu Leu Val Pro Val Ile Gly Leu Ile Thr
                               -10                               -5                               1
gag cta cca tta cac atc aga gag act tta ctg ttt act tct tcc ttg 315
Glu Leu Pro Leu His Ile Arg Glu Thr Leu Leu Phe Thr Ser Ser Leu
                               5                               10                               15
att ctc aca tta aat aca gtg ttt gtc ctg gca gtg aaa ctg aar tgg 363
Ile Leu Thr Leu Asn Thr Val Phe Val Leu Ala Val Lys Leu Lys Trp
                               20                               25                               30
ttt tat tat tcc aca cga tat g 385
Phe Tyr Tyr Ser Thr Arg Tyr
35                               40

```

<210> 483  
 <211> 202  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 39..200

<221> sig\_peptide  
<222> 39..110  
<223> Von Heijne matrix  
score 4.5  
seq XVAXFLLTFYVIS/QV

<400> 483  
catattaatg aaaagtgcc taaactgaaa aaccaaac atg agg gta gca ggt gct 56  
Met Arg Val Ala Gly Ala  
-20  
gca aar ttg gtg gta rct gtg gca rtg ttt tta ctg aca ttt tat gtt 104  
Ala Lys Leu Val Val Xaa Val Ala Xaa Phe Leu Leu Thr Phe Tyr Val  
-15 -10 -5  
att tct caa gta ttt gaa ata aaa atg gat gca agt tta gga aat cta 152  
Ile Ser Gln Val Phe Glu Ile Lys Met Asp Ala Ser Leu Gly Asn Leu  
1 5 10  
ttt gca aga tca gca ttg gac aca gct gca cgt tct aca aag cct ccg 200  
Phe Ala Arg Ser Ala Leu Asp Thr Ala Ala Arg Ser Thr Lys Pro Pro  
15 20 25 30  
gg 202

<210> 484  
<211> 310  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 148..309  
<221> sig\_peptide  
<222> 148..192  
<223> Von Heijne matrix  
score 4.5  
seq TLVFLSTRQVLQC/QP

<400> 484  
gcggggctgg aggcggtggc tgcggttgcg ggaccggcac tatgctgggc cttcctacca 60  
cttatgtgtg gcttgtagt ggcctagggc ctctcctccc tgctgaagtc cctcctctgc 120  
aggtggccgt ctgcccggcc cagcacc atg cac acg ctt gtg ttc ttg agc aca 174  
Met His Thr Leu Val Phe Leu Ser Thr  
-15 -10  
cgg cag gtg ctg cag tgc cag cca gct gcc tgc cag gcc ctg ccc ctg 222  
Arg Gln Val Leu Gln Cys Gln Pro Ala Ala Cys Gln Ala Leu Pro Leu  
-5 1 5 10  
ctg cca cgc gaa ctc ttc ccc ctg ctg ttc aag gtg gcc ttc atg ghc 270  
Leu Pro Arg Glu Leu Phe Pro Leu Leu Phe Lys Val Ala Phe Met Xaa  
15 20 25  
aag aag aca gtg gta ctg cgc gak ttg gta cac acg cgg g 310  
Lys Lys Thr Val Val Leu Arg Xaa Leu Val His Thr Arg  
30 35

<210> 485  
<211> 420  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 372..419

```

<221> sig_peptide
<222> 372..413
<223> Von Heijne matrix
      score 4.5
      seq TVVISCLVGECS/WK

<400> 485
agccggtggc agcacagcca ggacagccat ttcctcagca gccttcggta aaggcaacag      60
attctgacgg taactgtgta tcagttggaa ttactgcact aactttgagg gccataactca    120
aggactccaa taataaccaa gtcaatggcc ttagtggaata tacaacaatt ccgttttagca    180
gctgttgggc caactacaca gaccttactc cccttagaac aggaaaaaat tataagattg     240
aatttatact ggataatggt gttggggtag aatccagaac ttccagcctg ctggcagagt     300
ctgtctctag cagtggcagc agcagcagca gcmacagcaa agcatcaact gtgggtacat     360
atgcccagat a atg act gtm gta att agc tgt ctg gtt gga gaa tgt ggc      410
              Met Thr Val Val Ile Ser Cys Leu Val Gly Glu Cys Gly
              -10                               -5

tct tgg aaa t                                     420
Ser Trp Lys
  1

<210> 486
<211> 226
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..225

<221> sig_peptide
<222> 10..150
<223> Von Heijne matrix
      score 4.5
      seq PIFGLLVPSQIFS/SL

<400> 486
caaccatac atg tgc aca ctc aca gac aca cac act cac gtc caa gtg cac      51
              Met Cys Thr Leu Thr Asp Thr His Thr His Val Gln Val His
              -45                               -40                               -35

aag tca aaa cct tgc cag ctc ctc tcc cct cct cca cca rsc cat ggt      99
Lys Ser Lys Pro Cys Gln Leu Leu Ser Pro Pro Pro Pro Xaa His Gly
              -30                               -25                               -20

cct ctt ctt ctc cct atc ttt ggc ctt ctt gtg ccc tct cag att ttc     147
Pro Leu Leu Leu Pro Ile Phe Gly Leu Leu Val Pro Ser Gln Ile Phe
              -15                               -10                               -5

agc tct ctt ctc aat tct cta cat ctg ggc ctg cct tcc ttc cca aag     195
Ser Ser Leu Leu Asn Ser Leu His Leu Gly Leu Pro Ser Phe Pro Lys
  1              5              10              15

atg cca ctc atg att ttc ctc ccc cgc tgg g      226
Met Pro Leu Met Ile Phe Leu Pro Arg Trp
              20              25

<210> 487
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 221..454

<221> sig_peptide

```

&lt;222&gt; 221..409

&lt;223&gt; Von Heijne matrix

score 4.5

seq QILXSTLAMKIHS/QQ

&lt;400&gt; 487

```

agaaaatgga ggcgaatctg tatttccagt taactgctca gaagagagat gctgaagagc    60
tgtagtcgtg catccttctc accctccggt agaaagcctc ctctcatcct cagaagacta    120
ctgtcagagg atgtaggvat ggacatcccc tttgaagagg gcgtgctgag tcccagtgt    180
gcagacatga ggcctgaacc tcctaattct ctggatctta atg aca ctc atc ctc    235
                                   Met Thr Leu Ile Leu
                                   -60
gga gaa tca agc tca cag ccc caa ata tca atc ttt ctc tgg acc aaa    283
Gly Glu Ser Ser Ser Gln Pro Gln Ile Ser Ile Phe Leu Trp Thr Lys
      -55                    -50                    -45
gtg aag gat cta ttc tct ctg atg ata act tgg aca gtc cag atg aaa    331
Val Lys Asp Leu Phe Ser Leu Met Ile Thr Trp Thr Val Gln Met Lys
      -40                    -35                    -30
ttg aca tca atg tgg atg aac ttg ata ccc ccg atg aag cag att ctt    379
Leu Thr Ser Met Trp Met Asn Leu Ile Pro Pro Met Lys Gln Ile Leu
      -25                    -20                    -15
tdg agt aca ctg gcc atg aag atc cac agc caa caa aga ttc tgg cca    427
Xaa Ser Thr Leu Ala Met Lys Ile His Ser Gln Gln Arg Phe Trp Pro
      -10                    -5                    1                    5
aga gtc aga gtc tat tcc aga ata tac    454
Arg Val Arg Val Tyr Ser Arg Ile Tyr
      10                    15

```

&lt;210&gt; 488

&lt;211&gt; 329

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 253..327

&lt;221&gt; sig\_peptide

&lt;222&gt; 253..309

&lt;223&gt; Von Heijne matrix

score 4.5

seq VLFLNLFQKIEE/EE

&lt;400&gt; 488

```

cggctaagt gatgcctcca gctttgttct ttttgettag gattgctttg gctatttggg    60
ctcctttttg ggtccatatt aattttaaaa cagttttttc tggttttgtg aaggatgtca    120
ttggtagttt ataggaatag cahtgaatct gtagattgct ttgggcagta tggccatttt    180
aacaatatta attcttccta tctatgaata tggaatgttt ttccatgtgt ttgtgtcatc    240
tctttatacc tg atg tat aaa gaa aag ctg gta tta ttc cta ctc aat ctg    291
                                   Met Tyr Lys Glu Lys Leu Val Leu Phe Leu Leu Asn Leu
                                   -15                    -10
ttc caa aaa att gag gag gag gaa ctc ttc cct aat ga    329
Phe Gln Lys Ile Glu Glu Glu Glu Leu Phe Pro Asn
      -5                    1                    5

```

&lt;210&gt; 489

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 149..412



<211> 348  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 247..348

<221> sig\_peptide  
 <222> 247..333  
 <223> Von Heijne matrix  
       score 4.5  
       seq ILLILQLLKXSLK/KC

<221> misc\_feature  
 <222> 323..324  
 <223> n=a, g, c or t

<400> 491  
 ttatgtttaa aagggtcacia gtctagaata actgaattgg gaattggaaa taccttaatt       60  
 ctataatttg tatctaaaat taggttttcc cttttaagtt gttaattttc tatggkttgt       120  
 gctgcatgct ttcactttta ttagtactta cagccaaaga gatgggcaaa tgtctagaaa       180  
 aattaatggt ttgattcagg aatttgtgcc tagtgatggc ctccaataga gaattttcca       240  
 gagaga atg aag act cag ttt cta agt tgg ggc aaa ttt agt ttt tgt       288  
       Met Lys Thr Gln Phe Leu Ser Trp Gly Lys Phe Ser Phe Cys  
                       -25                       -20  
 ttt ggt att ctt ctt ata tta cag cta tta aaa bnn tct ctt aaa aaa       336  
 Phe Gly Ile Leu Leu Ile Leu Gln Leu Leu Lys Xaa Ser Leu Lys Lys  
 -15                       -10                       -5                       1  
 tgc cgg cac ggg       348  
 Cys Arg His Gly  
                       5

<210> 492  
 <211> 126  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 5..124

<221> sig\_peptide  
 <222> 5..79  
 <223> Von Heijne matrix  
       score 4.5  
       seq LRFILPSSWDCRC/AP

<400> 492  
 ctac atg ctt cct gct gtg gct gtc tgg gaa ccc gtg gtc ctc cgc ttc       49  
       Met Leu Pro Ala Val Ala Val Ser Glu Pro Val Val Leu Arg Phe  
       -25                       -20                       -15  
 att ctg ccg agt tcc tgg gat tgc agg tgc gcg ccg cca ctc ctg act       97  
 Ile Leu Pro Ser Ser Trp Asp Cys Arg Cys Ala Pro Pro Leu Leu Thr  
 -10                       -5                       1                       5  
 ggt ttt tgt att ttt tgg ktg gag acg gg       126  
 Gly Phe Cys Ile Phe Trp Xaa Glu Thr  
                       10                       15

<210> 493  
 <211> 300  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 119..298

<221> sig\_peptide

<222> 119..217

<223> Von Heijne matrix

score 4.40000009536743

seq WLLMVAPRLPAGA/RD

<400> 493

```

acactgcctg cctggtgcag cccatgtgac gggtcgagct ccggggccctg ctgtccctgg      60
ccgggctatc ccagtggcct caggcacctt ctccagacct acccagaaaag atgcccgg      118
atg gat cct gca gct ccg tgg ctt ttc tgg gaa gca gcg gcc cct gct      166
Met Asp Pro Ala Ala Pro Trp Leu Phe Trp Glu Ala Ala Ala Pro Ala
          -30          -25          -20
ctc aag aga ccc tgg ctc ctg atg gtg gcc cca agg ttg cca gct ggt      214
Leu Lys Arg Pro Trp Leu Leu Met Val Ala Pro Arg Leu Pro Ala Gly
          -15          -10          -5
gct agg gac tca gga cag ttt ccc aga aaa ggc caa gcg ggc agc ccc      262
Ala Arg Asp Ser Gly Gln Phe Pro Arg Lys Gly Gln Ala Gly Ser Pro
          1          5          10          15
tcc agg ggc cgg gtg agg aag ctg ggg ggt gcg gtg gg      300
Ser Arg Gly Arg Val Arg Lys Leu Gly Gly Ala Val
          20          25

```

<210> 494

<211> 295

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 182..295

<221> sig\_peptide

<222> 182..274

<223> Von Heijne matrix

score 4.40000009536743

seq SRLXALLSPYAFT/LX

<400> 494

```

tttatacaca cacacacaca cacactcata ttcattacat gtgtgtactt tctggttgct      60
tcagtaggac ttttctaggc ttctttggac tatgtgtgat attttacttc agggactgaa      120
tttcacaact gcctactatg caactttgtg attttcttga aagcacaakt actatatata      180
a atg aaa atg tcc acc ccc tcc ccg ctt tct aaa aaa gtg ctc aga aac      229
Met Lys Met Ser Thr Pro Ser Pro Leu Ser Lys Lys Val Leu Arg Asn
          -30          -25          -20
cag gtc tca aga ttg rtt gcg ttg ctt tcc cca tac gct ttc act ctg      277
Gln Val Ser Arg Leu Xaa Ala Leu Leu Ser Pro Tyr Ala Phe Thr Leu
          -15          -10          -5          1
sct cgt ctt gcc tca ggg      295
Xaa Arg Leu Ala Ser Gly
          5

```

<210> 495

<211> 244

<212> DNA

<213> Homo sapiens

<220>

<221> CDS  
 <222> 70..243

<221> sig\_peptide  
 <222> 70..114  
 <223> Von Heijne matrix  
 score 4.40000009536743  
 seq RFLLLYATQQGQA/KA

<400> 495  
 ggaagtcgcg ttgtgcaggt tcgtgcccggt ctggcgcggtg gtggtttcac tggtacatgc 60  
 cttgaagtgt atg agg agg ttt ctg tta cta tat gct aca cag cag gga cag 111  
 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln  
 -15 -10 -5  
 gca aag gcc atc gca gaa gaa atg tgt rag caa gct gtg gta cat gga 159  
 Ala Lys Ala Ile Ala Glu Glu Met Cys Xaa Gln Ala Val Val His Gly  
 1 5 10 15  
 ttt tct gca gat ctt cac tgt att agt gaa tcc gat aag gtc tgc gtg 207  
 Phe Ser Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Val Ser Val  
 20 25 30  
 att cag aat aca cct act ttt gca acg ggg ggg cgg g 244  
 Ile Gln Asn Thr Pro Thr Phe Ala Thr Gly Gly Arg  
 35 40

<210> 496  
 <211> 215  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 91..213  
 <221> sig\_peptide  
 <222> 91..171  
 <223> Von Heijne matrix  
 score 4.40000009536743  
 seq FVNLLNLCFAYTFA/LY

<400> 496  
 atttaagtcc agagagcaag gtgattgcag tttctttgtt cggtttgctt attttttact 60  
 gcttattttct gtgtgcataa attcagcgac atg cta ata gac ata tgg tca atg 114  
 Met Leu Ile Asp Ile Trp Ser Met  
 -25 -20  
 gtg ctt aga gaa aat ctg ttt gta aac ctg aat ctc tgt ttt gcc tac 162  
 Val Leu Arg Glu Asn Leu Phe Val Asn Leu Asn Leu Cys Phe Ala Tyr  
 -15 -10 -5  
 aca ttt gca ttg tat tcc tgc cct gct cca act cgt tgt cct aga cca 210  
 Thr Phe Ala Leu Tyr Ser Cys Pro Ala Pro Thr Arg Cys Pro Arg Pro  
 1 5 10  
 tcc ag 215  
 Ser

<210> 497  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 36..254

<221> sig\_peptide

&lt;222&gt; 36..89

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq WFPLSCSPSLPLS/IP

&lt;400&gt; 497

```

cttttgggggt tcgctgtttc ttccctctct gctgg atg ctg tct tgc ccc tgg      53
                                   Met Leu Ser Cys Pro Trp
                                   -15
ttt ccc cta tcc tgt tct ccc tcc ttg cct ctg agc atc cca gac tgc      101
Phe Pro Leu Ser Cys Ser Pro Ser Leu Pro Leu Ser Ile Pro Asp Cys
      -10                -5                1
ctg cct gcc ttc ctc tgg ccg ctg ggg ata ccc tgg cct gat gga gag      149
Leu Pro Ala Phe Leu Trp Pro Leu Gly Ile Pro Trp Pro Asp Gly Glu
5                10                15                20
ggg cta aga cct tcc cgt ctt ctc cgg aca cgg gaa aac att acc cct      197
Gly Leu Arg Pro Ser Arg Leu Leu Arg Thr Arg Glu Asn Ile Thr Pro
      25                30                35
ctc tct tta ttc gct atg ctg agt ggc agg gag ggt gcc ccg ctc ctg      245
Leu Ser Leu Phe Ala Met Leu Ser Gly Arg Glu Gly Ala Pro Leu Leu
      40                45                50
gtc ccc ctg g      255
Val Pro Leu
      55

```

&lt;210&gt; 498

&lt;211&gt; 82

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 23..82

&lt;221&gt; sig\_peptide

&lt;222&gt; 23..61

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq MVVVSFLASSLP/AE

&lt;400&gt; 498

```

ctttttcgtc tgggctgcca ac atg gta gtt gtt tcg ttt ctt gcc tcc tct      52
                                   Met Val Val Val Ser Phe Leu Ala Ser Ser
                                   -10                -5
tcc ttg ccg gcg gag acc cct aag caa ggg      82
Ser Leu Pro Ala Glu Thr Pro Lys Gln Gly
      1                5

```

&lt;210&gt; 499

&lt;211&gt; 474

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 39..473

&lt;221&gt; sig\_peptide

&lt;222&gt; 39..359

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq IILFVVITSRRG/SP

&lt;400&gt; 499

```

ttcctggacc gcgctggaag ccctggcggc ggcgggccc atg ggg csc ttg gcg ctg      56
                               Met Gly Xaa Leu Ala Leu
                               -105
cyc gcc tgg ctg cag ccc agg tat agg aag aat gcg tat ctt ttc atc      104
Xaa Ala Trp Leu Gln Pro Arg Tyr Arg Lys Asn Ala Tyr Leu Phe Ile
-100                               -95                               -90
tat tac tta atc cag ttc tgt ggc cas tct tgg ata ttt gca aat atg      152
Tyr Tyr Leu Ile Gln Phe Cys Gly Xaa Ser Trp Ile Phe Ala Asn Met
-85                               -80                               -75                               -70
aca gtc aga ttc ttt tca ttt gga aaa gat tca atg gtt gac act ttt      200
Thr Val Arg Phe Phe Ser Phe Gly Lys Asp Ser Met Val Asp Thr Phe
                               -65                               -60                               -55
tat gct att gga ctt gtg atg cga ctt tgc caa tcc gta tct ctc ctg      248
Tyr Ala Ile Gly Leu Val Met Arg Leu Cys Gln Ser Val Ser Leu Leu
                               -50                               -45                               -40
gaa ctg ctg cac ata tat gtt ggc att gag tca aac cat ctt ctc cca      296
Glu Leu Leu His Ile Tyr Val Gly Ile Glu Ser Asn His Leu Leu Pro
-35                               -30                               -25
agg ttt ttg cag ctc aca gaa aga ata atc atc ctt ttt gtg gtg atc      344
Arg Phe Leu Gln Leu Thr Glu Arg Ile Ile Ile Leu Phe Val Val Ile
-20                               -15                               -10
acc agt cga aga gga agt cca acg aga aat atg tgg tgt gtg tgt tat      392
Thr Ser Arg Arg Gly Ser Pro Thr Arg Asn Met Trp Cys Val Cys Tyr
-5                               1                               5                               10
tcg tct ttg gat cta tgg ata tgg tta rgt aca ctt ata gca tgc tda      440
Ser Ser Leu Asp Leu Trp Ile Trp Leu Xaa Thr Leu Ile Ala Xaa Xaa
15                               20                               25
tca gtc ata gga ata tcc tat gct gtc ttg aca t.      474
Ser Val Ile Gly Ile Ser Tyr Ala Val Leu Thr
30                               35

```

&lt;210&gt; 500

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 177..239

&lt;221&gt; sig\_peptide

&lt;222&gt; 177..230

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq SLTLTALLVPSRV/QP

&lt;400&gt; 500

```

cttcactcat ggggagagca tttctacctg acaccctccc atttctgttt tccttaccca      60
gatctacctt ctgagatatc atccttcttc agggagataa ggaaaaaaag ccacagggtc      120
ccggagagcc aggggaatgg tgagtgttct ctgtctccat tactggctgt aacagg atg      179
                               Met
gac aca ttc cct tct ctt acc ctg act gcc tta ttg gtg cct agt aga      227
Asp Thr Phe Pro Ser Leu Thr Leu Thr Ala Leu Leu Val Pro Ser Arg
-15                               -10                               -5
gtt cag ccc cag gg      241
Val Gln Pro Gln
1

```

&lt;210&gt; 501

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 178..429

&lt;221&gt; sig\_peptide

&lt;222&gt; 178..237

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq LRYVASAVFGVIG/SQ

&lt;221&gt; misc\_feature

&lt;222&gt; 17

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 501

```

gaggtgagtc ctggrntgc gtggttgggg cggagagcat tatctgcggc tccgattttg      60
cagattcttg ctgagcggtt cgtgatgtca gcagcagccg agacgggcgt gttaaaggcc      120
ggttgctagg gctgggggaa ctcagattgc ttcacctgtg gtatcagaca tcacaac      177
atg ggg ctc acc aag cag tac cta cgc tat gtt gct agt gcg gtc ttt      225
Met Gly Leu Thr Lys Gln Tyr Leu Arg Tyr Val Ala Ser Ala Val Phe
-20          -15          -10          -5
ggc gtt atc ggc agc caa aaa ggt aat att gtc ttt gtg aca ctt cgt      273
Gly Val Ile Gly Ser Gln Lys Gly Asn Ile Val Phe Val Thr Leu Arg
          1          5          10
ggt gag aaa gga cgt tat gtg gca gta cca gct tgt gaa cac gtt ttc      321
Gly Glu Lys Gly Arg Tyr Val Ala Val Pro Ala Cys Glu His Val Phe
          15          20          25
atc wgg gac tta agg aaa gga gag aag att ctt atc ctt cag ggg ctt      369
Ile Xaa Asp Leu Arg Lys Gly Glu Lys Ile Leu Ile Leu Gln Gly Leu
          30          35          40
aaa caa gaa gtt act tgc tta tgc ccc tcc cca gat ggg cta cac tta      417
Lys Gln Glu Val Thr Cys Leu Cys Pro Ser Pro Asp Gly Leu His Leu
45          50          55          60
gct gtt ggg tat g      430
Ala Val Gly Tyr

```

&lt;210&gt; 502

&lt;211&gt; 413

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 333..413

&lt;221&gt; sig\_peptide

&lt;222&gt; 333..404

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq VFFSVLYVQQGLS/SQ

&lt;221&gt; misc\_feature

&lt;222&gt; 7,359

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 502

```

agggasnggc agtgatcacg caagccggag cggcgggctg acgttggaag agctgccagg      60
tagctgaaag caggcagcca ggcagccgag acacttccca gcgattccag cctgggctcc      120
gcagaagcct cgctgaatcc cagccagctg gttctaacct tccagaatcg caatcccttc      180
tccccacagc cagccctcgc cgagcaagca gcaggatggt tgcagtgtcg cgcccagggc      240

```

271

```

tctgagactg agcctgccat ccactcgcac gcctttcttt cagggtttt eggctgttg 300
ctacactgat gtgaccccc tccctttttg ga atg atg ggg atc ttt ttg gtg 353
                               Met Met Gly Ile Phe Leu Val
                               -20
tat gtn gga ttt gtt ttc ttt tcc gtt tta tat gta caa caa ggg ctt 401
Tyr Val Gly Phe Val Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu
      -15                -10                -5
tct tct caa gca 413
Ser Ser Gln Ala
      1

```

<210> 503  
 <211> 167  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 26..166

<221> sig\_peptide  
 <222> 26..91  
 <223> Von Heijne matrix  
         score 4.40000009536743  
         seq WVLDPALLLTCLT/FP

```

<400> 503
gaatcggaca acttaaagtc tcgat atg agc ctc gga ttg cat tcg aac tcc 52
                               Met Ser Leu Gly Leu His Ser Asn Ser
                               -20                -15
tgg gtt cta gac cca gct ctg cta cta act tgt ctg acc ttc ccc att 100
Trp Val Leu Asp Pro Ala Leu Leu Leu Thr Cys Leu Thr Phe Pro Ile
      -10                -5                1
tat aaa ctg ttg tgg gtg aga ggt ggg acw agg wga act ctr wgr gcv 148
Tyr Lys Leu Leu Trp Val Arg Gly Gly Thr Arg Xaa Thr Leu Xaa Ala
      5                10                15
ctg cac tcg gcg cgg acg g 167
Leu His Ser Ala Arg Thr
20                25

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<210> 504  
 <211> 420  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 217..420

<221> sig\_peptide  
 <222> 217..396  
 <223> Von Heijne matrix  
         score 4.40000009536743  
         seq MWVXCXFCFVLFC/FE

<221> misc\_feature  
 <222> 47..48,368..369,373  
 <223> n=a, g, c or t

```

<400> 504
ggktccgctc cctggggcgc acgtcagtcg ggaggcggaa gcgcagnnga ggcggaagg 60
ttgtagtgcc gcgagttgag ctctctttgc ctaagtggtc gcgccccctt taagagcagc 120

```

```

gattgtaagg agagggcggtc cgggtgtcct cgggtcccag gtgattgtga agtgctgacc 180
aattgccact ggacatactt gaaacaaaat aggaata atg gca gca aac tct tca 234
                                     Met Ala Ala Asn Ser Ser
                                     -60 -55
gga caa ggt ttt caa aac aaa aat aga gtt gca atc ttg gca gaa ctg 282
Gly Gln Gly Phe Gln Asn Lys Asn Arg Val Ala Ile Leu Ala Glu Leu
                                     -50 -45 -40
aca aag aga aaa gaa aac tac tta tgc aga acc agt ctt caa caa atc 330
Thr Lys Arg Lys Glu Asn Tyr Leu Cys Arg Thr Ser Leu Gln Gln Ile
                                     -35 -30 -25
atc ctg gar cta ggt att gac act ata atg tgg gtt tnn tgt ntg ttt 378
Ile Leu Glu Leu Gly Ile Asp Thr Ile Met Trp Val Xaa Cys Xaa Phe
                                     -20 -15 -10
tgt ttt gtt ttg ttt tgt ttt gag acg gag tct cgc cct gtc 420
Cys Phe Val Leu Phe Cys Phe Glu Thr Glu Ser Arg Pro Val
                                     -5 1 5

```

&lt;210&gt; 505

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 43..456

&lt;221&gt; sig\_peptide

&lt;222&gt; 43..147

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq PAPLLFLPPAAPG/GE

&lt;221&gt; misc\_feature

&lt;222&gt; 416..417

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 505

```

gtagtcggat agttggcggg tgggtgagtg gaagcggtcg cc atg tcc gcg ggg 54
                                     Met Ser Ala Gly
                                     -35
agc gcg aca cat cct gga gct ggc ggg cgc cgc agc aaa tgg gac caa 102
Ser Ala Thr His Pro Gly Ala Gly Gly Arg Arg Ser Lys Trp Asp Gln
                                     -30 -25 -20
cca gct cca gcc cca ctt ctc ttc ctc ccg cca gcg gcc cca ggt ggg 150
Pro Ala Pro Ala Pro Leu Phe Leu Pro Pro Ala Ala Pro Gly Gly
                                     -15 -10 -5 1
gag gtc acc agc agt ggg gga agt cct ggg gsc acc aca gct gct cct 198
Glu Val Thr Ser Ser Gly Gly Ser Pro Gly Xaa Thr Thr Ala Ala Pro
                                     5 10 15
tca gga gcc ttg gat gct gct gct gct gtg gct gcc aag att aat gcc 246
Ser Gly Ala Leu Asp Ala Ala Ala Val Ala Ala Lys Ile Asn Ala
                                     20 25 30
atg ctc atg gca aaa ggg aag ctg aaa cca act cag rat gct tct gag 294
Met Leu Met Ala Lys Gly Lys Leu Lys Pro Thr Gln Xaa Ala Ser Glu
                                     35 40 45
aag ctt cag gct cct ggc aaa ggc cta act agc aat aaa agc aag gat 342
Lys Leu Gln Ala Pro Gly Lys Gly Leu Thr Ser Asn Lys Ser Lys Asp
                                     50 55 60 65
gac ctg gtg gta gct gaa gta gaa att aat gat gtg cct ctc aca tgt 390
Asp Leu Val Val Ala Glu Val Glu Ile Asn Asp Val Pro Leu Thr Cys
                                     70 75 80
agg aac ttg ctg act cga gga cag ann caa gac gag atc agc cga ctt 438

```

273

Arg Asn Leu Leu Thr Arg Gly Gln Xaa Gln Asp Glu Ile Ser Arg Leu  
                   85                                  90                                  95  
 agt ggg gct gca gta tca a  
 Ser Gly Ala Ala Val Ser  
                   100

457

<210> 506  
 <211> 315  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 141..314

<221> sig\_peptide  
 <222> 141..203  
 <223> Von Heijne matrix  
           score 4.40000009536743  
           seq IRAVCLSGGSCWG/GV

<400> 506  
 ctctttctgt cttgattttt ctgtgtgtct ctctgcgtct tgtctatttg tttctctctt 60  
 ttcttctctg tggccctccc ctttgtctct tcctttctgt tttctcctgt agttcctcct 120  
 cttctctccc ctgattgctc atg agt ccc ctt gat cag gct gta ata cgt gct 173  
                   Met Ser Pro Leu Asp Gln Ala Val Ile Arg Ala  
                   -20                                  -15  
 gtg tgt ctc agt gga ggt tcc tgc tgg gga gga gtc cgt tgt ctt gtg 221  
 Val Cys Leu Ser Gly Gly Ser Cys Trp Gly Gly Val Arg Cys Leu Val  
 -10                  -5                                  1                                  5  
 cgt ggg ggc ccg aac ata ggc cct gca gcc cag ctg ctt ggg ggc att 269  
 Arg Gly Gly Pro Asn Ile Gly Pro Ala Ala Gln Leu Leu Gly Gly Ile  
                   10                                  15                                  20  
 cca ctc tgc tgg cca cca gct gtg act gca ggt gaa gtg aaa ctg c 315  
 Pro Leu Cys Trp Pro Pro Ala Val Thr Ala Gly Glu Val Lys Leu  
                   25                                  30                                  35

<210> 507  
 <211> 208  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 152..208

<221> sig\_peptide  
 <222> 152..196  
 <223> Von Heijne matrix  
           score 4.40000009536743  
           seq SFHFIXFLPFPWA/EX

<221> misc\_feature  
 <222> 201..202  
 <223> n=a, g, c or t

<400> 507  
 agaatcgcg aggcgcaatt gtgccctggt tcgcccaagat gtcggtccca aagtataagc 60  
 cgtcgagcct gcgcactctg cctgagaccc tcgaccagc ccggctcctg tcctcctgta 120  
 ttctctgcagt ccttttaagg aagaaaaagt a atg aac tca ttt cat ttt att 172  
                   Met Asn Ser Phe His Phe Ile  
                   -15                                  -10

274

tss ttc ctc cct ttc ccc tgg gct gaa wnn gcg cag 208  
 Xaa Phe Leu Pro Phe Pro Trp Ala Glu Xaa Ala Gln  
 -5 1

<210> 508  
 <211> 169  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 65..169

<221> sig\_peptide  
 <222> 65..151  
 <223> Von Heijne matrix  
 score 4.40000009536743  
 seq LLSTHTWTDALA/FS.

<400> 508  
 atacagacac ccagrsagga ccctgaacac acagacaggc acagggaccc ctgtgcccac 60  
 aggg atg ggc tgg cac tca cat agt tcc caa ggc gtg caw gca atg cct 109  
 Met Gly Trp His Ser His Ser Ser Gln Gly Val Xaa Ala Met Pro  
 -25 -20 -15  
 ctg ctg ctg tcc aca cac acc tgg aca gac aca gcc ctg gca ttc agc 157  
 Leu Leu Leu Ser Thr His Thr Trp Thr Asp Thr Ala Leu Ala Phe Ser  
 -10 -5 1  
 aca cac aca cac 169  
 Thr His Thr His  
 5

<210> 509  
 <211> 118  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 12..116

<221> sig\_peptide  
 <222> 12..77  
 <223> Von Heijne matrix  
 score 4.40000009536743  
 seq WFLRSWTPQTAG/RV

<400> 509  
 caattcaagt c atg crg gct gtg aga aac gcg ggg tcg tgg ttc ctg cgg 50  
 Met Xaa Ala Val Arg Asn Ala Gly Ser Trp Phe Leu Arg  
 -20 -15 -10  
 tcc tgg act tgg ccc cag aca gcc ggc agg gtc gtg gcc aga rsg ccg 98  
 Ser Trp Thr Trp Pro Gln Thr Ala Gly Arg Val Val Ala Arg Xaa Pro  
 -5 1 5  
 gcc ggg acc atc tgc aca gg 118  
 Ala Gly Thr Ile Cys Thr  
 10

<210> 510  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<220>

&lt;221&gt; CDS

&lt;222&gt; 334..402

&lt;221&gt; sig\_peptide

&lt;222&gt; 334..378

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq ALFILVSISLFYA/LF

&lt;400&gt; 510

```

cctcctcagc ctcctcagta ccattctggt accaccattg gtcctgcatt ctgagtttgc      60
cacctggcac gtgcccttca aatgtctcca ctgcgtcttt gcctttccct tttctgttgc      120
gtgccatcat tccgattccg attttaacag caacctgctg atttcctgcc atagtttcct      180
actttccatt ctgagccctt ttaatccact tataacaatat aactactccc tgaattattt      240
ggtcatacca cttgtatctg ccgaaccctt attcctcccc tggggtagct tttccactaa      300
acacacacag ggaaatgcc aacaaatagc tct atg tgt gcc ttg ttc att ctt      354
                                Met Cys Ala Leu Phe Ile Leu
                                -15                                -10
ggt tcc att tct ttg ttt tat gca ctt ttt atc tct cca tcc ata caa      402
Val Ser Ile Ser Leu Phe Tyr Ala Leu Phe Ile Ser Pro Ser Ile Gln
-5                                1                                5

```

&lt;210&gt; 511

&lt;211&gt; 343

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 159..341

&lt;221&gt; sig\_peptide

&lt;222&gt; 159..317

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq NLVLYFLVHLLFS/LS

&lt;400&gt; 511

```

cagaggcttt tatttgcata aatgtcggac cgtcttagct ctcttgtaga aggaactttt      60
tgccatatta tagtggctca ccttacctcc tggaaatgcat tctggcctca agtctgtacc      120
tagcattgat agaggaagcc cagcctgggtg tgcacagc atg tac ctg gtg tgc aca      176
                                Met Tyr Leu Val Cys Thr
                                -50
aca tgc acc tgg tgt gta ttt tct gaa atg ttt gtt cat gga tta aac      224
Thr Cys Thr Trp Cys Val Phe Ser Glu Met Phe Val His Gly Leu Asn
-45                                -40                                -35
atc act cag ctg ctg agc cag ctg gat tac ttt ttc cat tcc aat      272
Ile Thr Gln Leu Val Leu Ser Gln Leu Asp Tyr Phe Phe His Ser Asn
-30                                -25                                -20
ctg aca aac ttg gtc ttg tat ttc tta gtc cat tta ctt ttt tcc ctt      320
Leu Thr Asn Leu Val Leu Tyr Phe Leu Val His Leu Leu Phe Ser Leu
-15                                -10                                -5                                1
agc ctg ttt atg ccg ctg acg gg      343
Ser Leu Phe Met Pro Leu Thr
5

```

&lt;210&gt; 512

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

<222> 7..420

```
<221> sig_peptide
```

<222> 7..240

## <223> Von Heijne matrix

score 4.40000009536743

seq FWWLGSLXVTWL/IH

<221> misc feature

<222> 93,  $\overline{100}$ , 137..138

<223> n=a, q, c or t

<400> 512

taagtg atg aag ctg aaa tta tac cta tgt ata tta ggt ccc tgg ggc	48
Met Lys Leu Lys Leu Tyr Leu Cys Ile Leu Gly Pro Trp Gly	
-75 -70 -65	
tgc aak rkc aaa gta cca cta att ggg ttt ctt aaa aga ata aan hta	96
Cys Xaa Xaa Lys Val Pro Leu Ile Gly Phe Leu Lys Arg Ile Xaa Xaa	
-60 -55 -50	
tat nwt ctc aca gtt ctg aaa cct agd agt ctg ara tca ann tca gca	144
Tyr Xaa Leu Thr Val Leu Lys Pro Xaa Ser Leu Xaa Ser Xaa Ser Ala	
-45 -40 -35	
ggg ttg gtt cct tct gag gac tct aaa aaa gaa tct gtt tca tgc ctc	192
Gly Leu Val Pro Ser Glu Asp Ser Lys Lys Glu Ser Val Ser Cys Leu	
-30 -25 -20	
tct cct agg ttc tgg tgg tgg ctg gga agc ctg akt gtt act tgg ctt	240
Ser Pro Arg Phe Trp Trp Trp Leu Gly Ser Leu Xaa Val Thr Trp Leu	
-15 -10 -5	
ata cat gca tca ctc cag tct ctg tct cct ttt tct cat gcc att ttc	288
Ile His Ala Ser Leu Gln Ser Leu Ser Pro Phe Ser His Ala Ile Phe	
1 5 10 15	
tca tgt gtc tct gtg ttt tcc ttt gct tat aag gat acc agt cat att	336
Ser Cys Val Ser Val Phe Ser Phe Ala Tyr Lys Asp Thr Ser His Ile	
20 25 30	
gaa tta ggg cct gct cta ata acc tca tct caa tta cct ctg caa gga	384
Glu Leu Gly Pro Ala Leu Ile Thr Ser Ser Gln Leu Pro Leu Gln Gly	
35 40 45	
acc aat ttc caa ata atg tca cac tca cat gta gca	420
Thr Asn Phe Gln Ile Met Ser His Ser His Val Ala	
50 55 60	

<210> 513

<211> 324

<212> DNA

<213> Homo sapiens

**<220>**

<221> CDS

<222> 219..323

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<221> sig_peptide
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<222> 219..317

### <223> Von Heijne matrix

score 4.40000009536743

seq LKLLFLILILIAG/YR

<400> 513

aaaaacattct	gaatagttta	tttgtcttga	cggaaagtaa	aaagaacaaa	cttgttttat	60
acaaaatcag	atgctccaaa	tggtcagttg	atgatgatac	caatcaaaga	aaactaagga	120
ggaagaaaaa	gaaaacagga	aagagaggag	gcaacaggaa	aatcggcctt	cgctcttcag	180
tctacgcttg	aaattgccag	ggatggataa	atctgaag	atg aat gaa aaa aag aaa		236
			Met	Asn	Glu Lys Lys Lys	

-30

cta	ctg	gga	acg	gaa	cag	aaa	caa	aaa	aaa	agg	atg	gga	aat	ctg	aag	284
Leu	Leu	Gly	Thr	Glu	Gln	Lys	Gln	Lys	Lys	Arg	Met	Gly	Asn	Leu	Lys	
		-25				-20				-15						
ctg	cta	ttt	ctt	att	ctg	atc	tta	ata	gca	gga	tac	agg	g			324
Leu	Leu	Phe	Leu	Ile	Leu	Ile	Leu	Ile	Ala	Gly	Tyr	Arg				
		-10				-5				1						

&lt;210&gt; 514

&lt;211&gt; 303

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 212..301

&lt;221&gt; sig\_peptide

&lt;222&gt; 212..292

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq SALMLPLGCAVRT/RM

&lt;400&gt; 514

tttccctcac	tctctgcctc	ccccatcgca	ccccacagga	gggtttccct	cactctctgc	60
ctcccccatc	gcaaccacaca	ggaggggttc	cctcactctg	cctcctccaw	cgcaccccca	120
kggaggtggt	ttccctcact	ggttctgttg	gtggcggtgg	cagcaatccg	agtcacatgg	180
caccagagta	tgtcacgggt	ggcggatctg	a atg ggg	ctg cag agc	ctc aca	232
			Met Gly	Leu Gln	Ser Leu Thr	

-25

ctt	cca	gtg	tct	tgc	agc	cct	tct	gcc	ctg	atg	ctt	ccc	ttg	gga	tgt	280
Leu	Pro	Val	Ser	Cys	Ser	Pro	Ser	Ala	Leu	Met	Leu	Pro	Leu	Gly	Cys	
-20			-15			-10			-5							
gct	gtc	cgc	acg	cgc	atg	ctt	ga									303
Ala	Val	Arg	Thr	Arg	Met	Leu										

1

&lt;210&gt; 515

&lt;211&gt; 455

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 342..455

&lt;221&gt; sig\_peptide

&lt;222&gt; 342..434

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq LTTLESLAGSVXS/EQ

&lt;400&gt; 515

tcatatctgg	waatggcaaa	cagggatgaa	aatcgattat	gttttgagaga	ctccttttgg	60
acatgtatca	gtgtgttgat	ttgcacaaac	caataaaaagc	cctacatttt	ttggaaatgg	120
atccctagat	ttcaagcatg	tataatcact	caaagtggat	atgatcacag	gcattcttct	180
cttgagctca	gcaaaactat	gcctaccaac	accgaagaga	agtcaaagat	ttttatgaaa	240
aaaaattgca	gatgatgttg	gtgagataat	aggatatgag	caatgaaccc	ttgggtgggg	300
ttccagggca	cttaaattgc	ctcgtgtctt	gagtccttaa	g atg gac	tca aac aaa	356
				Met Asp	Ser Asn Lys	

-30

aaa	tta	gta	tta	tca	ata	aca	ggt	aat	act	gtg	tgg	att	cta	aca	aca	404
Lys	Leu	Val	Leu	Ser	Ile	Thr	Gly	Asn	Thr	Val	Trp	Ile	Leu	Thr	Thr	

```

      -25              -20              -15
tta gaa tca tta gct ggc agt gtc aam tct gaa caa gat ttg tca gct      452
Leu Glu Ser Leu Ala Gly Ser Val Xaa Ser Glu Gln Asp Leu Ser Ala
-10              -5              1              5
tat
Tyr

```

```

<210> 516
<211> 360
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 196..360

```

```

<221> sig_peptide
<222> 196..336
<223> Von Heijne matrix
      score 4.40000009536743
      seq SFXXCLFLXLXXS/EM

```

```

<221> misc_feature
<222> 330..332
<223> n=a, g, c or t

```

```

<400> 516
aagagcgttg ggcagatata gtctgtagat atttttgaaa cgtctttggg tttgtcccat      60
ttggggtttg ctcagcttct tgaatctgta gggtttgggg atcccccamc ctgcaaattt      120
ggtgatattt ttgctcttat ttctkcaagt gaacttgaaa tcccaccctg ttggttttct      180
ccttctaaga ctctg atg acg tgt atg tta gcc tgt agg tgt agt ctc amg      231
      Met Thr Cys Met Leu Ala Cys Arg Cys Ser Leu Xaa
      -45              -40
ggg ccc caa gat ttt cgt ttc tgc tct gtc ttt tct ctg ttg ctc aag      279
Gly Pro Gln Asp Phe Arg Phe Cys Ser Val Phe Ser Leu Leu Leu Lys
-35              -30              -25              -20
ttg ggt aat ttc tat ttt tct ttt wct dtc tgt ctw ttt ctw dta ctd      327
Leu Gly Asn Phe Tyr Phe Ser Phe Xaa Xaa Cys Leu Phe Leu Xaa Leu
      -15              -10              -5
wyn nnt tct gag atg gag tcm cac tct ttc agc      360
Xaa Xaa Ser Glu Met Glu Ser His Ser Phe Ser
      1              5

```

```

<210> 517
<211> 453
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 113..451

```

```

<221> sig_peptide
<222> 113..307
<223> Von Heijne matrix
      score 4.40000009536743
      seq FIEAALLIHGSAC/VY

```

```

<400> 517
attttccttg gcgggaacag caaaatggcg ccagaactag tggcgggctg aggacgccgt      60
accctcggga aggcagccct gcggtcctt tgccgcccgt tccctcccgg ac atg gag      118
      Met Glu

```

```

                                     -65
gac gtg gag gcg cgc ttc gcc cac ctc ttg cag ccc atc cgc gac ctc      166
Asp Val Glu Ala Arg Phe Ala His Leu Leu Gln Pro Ile Arg Asp Leu
                                     -60
acc aag aac tgg gag gtg gac gtg gcg gcc cag ctg ggc gag tat ctg      214
Thr Lys Asn Trp Glu Val Asp Val Ala Ala Gln Leu Gly Glu Tyr Leu
                                     -45
gag gag ctg gat cag atc tgc att tct ttt gac gaa ggc aag acc aca      262
Glu Glu Leu Asp Gln Ile Cys Ile Ser Phe Asp Glu Gly Lys Thr Thr
                                     -30
atg aac ttc att gag gca gcg ttg ttg atc cat ggc tct gcc tgc gtc      310
Met Asn Phe Ile Glu Ala Ala Leu Leu Ile His Gly Ser Ala Cys Val
                                     -15
tac agt aag aag gtg gaa tac ctc tac tca ctc gtc tac cag gcc ctt      358
Tyr Ser Lys Lys Val Glu Tyr Leu Tyr Ser Leu Val Tyr Gln Ala Leu
                                     5
gat ttc atc tct gga aag agg cgg gcc aag cag ctc tct tcg gtg cag      406
Asp Phe Ile Ser Gly Lys Arg Arg Ala Lys Gln Leu Ser Ser Val Gln
                                     20
gag gac agg gcc aat ggg gtt gca gct ccg ggg tcc cca gga ggc ag      453
Glu Asp Arg Ala Asn Gly Val Ala Ala Pro Gly Ser Pro Gly Gly
                                     35
                                     40
                                     45

```

<210> 518  
 <211> 245  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 185..244

<221> sig\_peptide  
 <222> 185..229  
 <223> Von Heijne matrix  
 score 4.40000009536743  
 seq VSYLILTLHVQT/AV

```

<400> 518
agttttcttc agaacagagg ctgagctcga agcgccgggc agtacagtga gggagagccg      60
aggggaaccag cgcggtgcct agcggaactc cagggctgga atcccgagac acaagtgcac      120
ctgctagctg ttagcacttg gcagacggag ttctcctcta gggtagttct aactttgggt      180
aata atg ttt gtc agc tac ctg ata tta aca ttg ctc cac gtt caa aca      229
Met Phe Val Ser Tyr Leu Ile Leu Thr Leu Leu His Val Gln Thr
-15 -10 -5
gca gtg tta gca aga c      245
Ala Val Leu Ala Arg
1 5

```

<210> 519  
 <211> 275  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 96..275

<221> sig\_peptide  
 <222> 96..170  
 <223> Von Heijne matrix  
 score 4.40000009536743  
 seq IFLLYFKFWGTCA/ER

<400> 519  
 ttgtttttta gaaaaatgaa taattttcttt ttatatatt ctgttacatt ttttccccac 60  
 ttaatagaac gtccagaaaa tctttgcatc tcaga atg cct gaa gct gcc ttg 113  
 Met Pro Glu Ala Ala Leu  
 -25 -20  
 ttc ttg ttt ttt tta ttc att ttt tta tta tac ttt aag ttc tgg ggt 161  
 Phe Leu Phe Phe Leu Phe Ile Phe Leu Leu Tyr Phe Lys Phe Trp Gly  
 -15 -10 -5  
 aca tgt gca gaa cgt gca ggt ttg tta cat agg tat act cgt gcc atg 209  
 Thr Cys Ala Glu Arg Ala Gly Leu Leu His Arg Tyr Thr Arg Ala Met  
 1 5 10  
 gag gtt tgc tgc acc cat caa cca tca tct aca tta ggt att tct cct 257  
 Glu Val Cys Cys Thr His Gln Pro Ser Ser Thr Leu Gly Ile Ser Pro  
 15 20 25  
 aat gct ctc ctt ccc cta 275  
 Asn Ala Leu Leu Pro Leu  
 30 35

<210> 520  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 91..180

<221> sig\_peptide  
 <222> 91..159  
 <223> Von Heijne matrix  
 score 4.40000009536743  
 seq LCMHLSIHPXXCA/CI

<400> 520  
 gtctgagcgg cacagacgag atctcgatcg aaggcgagat ggcggaactg ctagatcttc 60  
 acgaggctgg gggcgaagat ttcgccatgg atg agg atg ggg acg aga gca tcc 114  
 Met Arg Met Gly Thr Arg Ala Ser  
 -20  
 ccg cct ctg tgc atg cat ctg tcc atc cat ccc cky mtc tgt gca tgc 162  
 Pro Pro Leu Cys Met His Leu Ser Ile His Pro Xaa Xaa Cys Ala Cys  
 -15 -10 -5 1  
 atc tgt cca tcc atc cag gg 182  
 Ile Cys Pro Ser Ile Gln  
 5

<210> 521  
 <211> 218  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 104..217

<221> sig\_peptide  
 <222> 104..211  
 <223> Von Heijne matrix  
 score 4.40000009536743  
 seq XVCVCVCVCVCVC/VC

<221> misc\_feature  
 <222> 145,151,174

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 521

```

atttatgtag gcaggtggat gccaaactgcc agtgcagggg ggcataagtt agcggttccaa      60
agttaagcta tgggtgcattc caaatccatt cacacttagg aga atg tac cca aga      115
                               Met Tyr Pro Arg
                               -35
gtg tgg gga tgt ttt caa tta ctg cat ttn ctt can bga aca aga acs      163
Val Trp Gly Cys Phe Gln Leu Leu His Xaa Leu Xaa Xaa Thr Arg Thr
      -30                -25                -20
aca ggt aag tnw gtg tgt gtg tgt gtg tgt gtg tgt gtg tgt gtg tgt      211
Thr Gly Lys Xaa Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys
      -15                -10                -5
gtg tgt g
Val Cys
1

```

&lt;210&gt; 522

&lt;211&gt; 313

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 12..311

&lt;221&gt; sig\_peptide

&lt;222&gt; 12..53

&lt;223&gt; Von Heijne matrix

score 4.40000009536743

seq AAVVLAATRLLRG/SG

&lt;400&gt; 522

```

ggagacgcaa g atg gcg gct gtg gtg ctg gcg gcg acg cgg ttg ctg cgg      50
                Met Ala Ala Val Val Leu Ala Ala Thr Arg Leu Leu Arg
                        -10                -5
ggc tcg ggt tct tgg ggc tgt tcg cgg ctg agg ttt gga cct cct gcg      98
Gly Ser Gly Ser Trp Gly Cys Ser Arg Leu Arg Phe Gly Pro Pro Ala
      1                5                10                15
tac aga cgg ttt agt agt ggt ggt gcc tat ccc aac atc ccc ctc tct      146
Tyr Arg Arg Phe Ser Ser Gly Gly Ala Tyr Pro Asn Ile Pro Leu Ser
                        20                25                30
tct ccc tta cct gga gta ccc aag cct gtt ttt gct aca gtt gat gga      194
Ser Pro Leu Pro Gly Val Pro Lys Pro Val Phe Ala Thr Val Asp Gly
                        35                40                45
cag gaa aag ttt gaa acc aaa gta acc aca ttg gat aat ggg ctt cgc      242
Gln Glu Lys Phe Glu Thr Lys Val Thr Thr Leu Asp Asn Gly Leu Arg
                        50                55                60
gtg gca tct cag aat aag ttt gga cag ttt tgt aca gta gga att ctt      290
Val Ala Ser Gln Asn Lys Phe Gly Gln Phe Cys Thr Val Gly Ile Leu
                        65                70                75
atc aat tca gga tcg aga tat ga      313
Ile Asn Ser Gly Ser Arg Tyr
80                85

```

&lt;210&gt; 523

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

<222> 324..500

<221> sig\_peptide

<222> 324..398

<223> Von Heijne matrix

score 4.30000019073486

seq ALYLSTLNLYFANS/LY

<221> misc\_feature

<222> 284,469..470,472

<223> n=a, g, c or t

<400> 523

```

gtctaggctc ttcaagttag gattcatatc tatgacatgt gctgtacagt gcttctactg      60
tgaggtagtc tcccagacag aaaccacatg ggccttcagg catagatggc cagtaaataa      120
ttactttaca gtggtgtcat ttcttaggag acmcagagtr agaccttaag tgagatctta      180
cctacctcct cccatccaat ctatccatac aaggttggac cttaaagcagc cttgagctta      240
ataatgatgt gtgttagaac aaggatactg agattagact aagntgggtc ttttaagtcag      300
ccgtctctga caaagggcac aca atg tac tgt ctg arg tgt gtg gag aaa ata      353
                               Met Tyr Cys Leu Xaa Cys Val Glu Lys Ile
                               -25                               -20

gca aaa gct ctt tat ctc agc ctt aat tta tat ttt gca aat tca ctt      401
Ala Lys Ala Leu Tyr Leu Ser Leu Asn Leu Tyr Phe Ala Asn Ser Leu
-15                               -10                               -5                               1
tat tat atg tgt gtg tgt tca tac ata tac ttt tat tta tkt att tat      449
Tyr Tyr Met Cys Val Cys Ser Tyr Ile Tyr Phe Tyr Leu Xaa Ile Tyr
                               5                               10                               15

kkt tat kkt tta ata aaa ann dng tct tat tat gtt gcc cag act ggt      497
Xaa Tyr Xaa Leu Ile Lys Xaa Xaa Ser Tyr Tyr Val Ala Gln Thr Gly
                               20                               25                               30

ctc aa      502
Leu

```

<210> 524

<211> 118

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 11..118

<221> sig\_peptide

<222> 11..97

<223> Von Heijne matrix

score 4.30000019073486

seq SAVFLTAVFSSHS/WL

<400> 524

```

atctttgttg atg tgt cag ctc cgc agg ggt ttg ggg aaa cgg ccg ctg      49
                               Met Cys Gln Leu Arg Arg Gly Leu Gly Lys Arg Pro Leu
                               -25                               -20

agt gag gcg tcg gct gtg ttt ctc acc gcg gtc ttt tcc tcc cac tct      97
Ser Glu Ala Ser Ala Val Phe Leu Thr Ala Val Phe Ser Ser His Ser
-15                               -10                               -5

tgg ctg gtt gga ccc cgc tat      118
Trp Leu Val Gly Pro Arg Tyr
1                               5

<210> 525
<211> 276
<212> DNA

```



<210> 527  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 316..426

<221> sig\_peptide  
 <222> 316..408  
 <223> Von Heijne matrix  
 score 4.30000019073486  
 seq VCSSLRSXRPCWC/DG

<400> 527  
 catttcctaa tctctgcatt ttccagcaag taagtggtag tgacttggtg ctttcaagta 60  
 tgttttgtct aaaattcata gatgctgaac tgtgtatatt tgttgtcaag tttgaaaggt 120  
 acttgggttt ttgggggtgt taggaggttag ggtggatggt actattaaat acatttagac 180  
 tttttaaaat aagtgttaact gatcatttcc aacaaatatt tactatgtcc atacttgtgc 240  
 tccaaaagac aattctgtct tcctcttgag atacatgtct cgggggccct gtaggtctgg 300  
 tctgagaggg tcccc atg ggt ggc tgt gtc wgc tgg cgc ttt ctt gga cac 351  
 Met Gly Gly Cys Val Xaa Trp Arg Phe Leu Gly His  
 -30 -25 -20  
 tcc tct gct ctc agg act gtg tgt agc agt ctg cgc tca gya agg cca 399  
 Ser Ser Ala Leu Arg Thr Val Cys Ser Ser Leu Arg Ser Xaa Arg Pro  
 -15 -10 -5  
 tgt tgg tgt gat ggg ctt cgg ctc aga tg 428  
 Cys Trp Cys Asp Gly Leu Arg Leu Arg  
 1 5

<210> 528  
 <211> 400  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 83..400

<221> sig\_peptide  
 <222> 83..235  
 <223> Von Heijne matrix  
 score 4.30000019073486  
 seq STCLLRALSSELC/AP

<400> 528  
 gacacggaag tagctccgaa caggaagagg acgaaaaaaaa taaccgtccg cgacgccgag 60  
 acaaacgga cccgcaacca cc atg aac agc aaa ggt caa tat cca aca cag 112  
 Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln  
 -50 -45  
 cca acc tac cct gtg cag cct cct ggg aat tcc agt ata ccc tca gac 160  
 Pro Thr Tyr Pro Val Gln Pro Pro Gly Asn Ser Ser Ile Pro Ser Asp  
 -40 -35 -30  
 ctt gca tct tcc tca ggc tcc acc cta tac cga tgc tcc acc tgc cta 208  
 Leu Ala Ser Ser Ser Gly Ser Thr Leu Tyr Arg Cys Ser Thr Cys Leu  
 -25 -20 -15 -10  
 ctc aga gct cta tcg tcc gag ctt tgt gca ccc agg ggc tgc cac agt 256  
 Leu Arg Ala Leu Ser Ser Glu Leu Cys Ala Pro Arg Gly Cys His Ser  
 -5 1 5  
 ccc cac cat gtc agc cgc att tcc tgg acc ctc tct gta tct tcc cat 304  
 Pro His His Val Ser Arg Ile Ser Trp Thr Leu Ser Val Ser Ser His

285

10	15	20	
ggc cca gtc tgt ggc tgt tgg gcc ttt agg ttc cac aat ccc cat ggc	352		
Gly Pro Val Cys Gly Cys Trp Ala Phe Arg Phe His Asn Pro His Gly			
25	30	35	
tta tta tcc agt cgg tcc cat cta tcc amc tgg ctc cac agt gct ggt	400		
Leu Leu Ser Ser Arg Ser His Leu Ser Xaa Trp Leu His Ser Ala Gly			
40	45	50	55

&lt;210&gt; 529

&lt;211&gt; 244

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 68..244

&lt;221&gt; sig\_peptide

&lt;222&gt; 68..133

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq LFFETGSPSVAQS/GV

&lt;400&gt; 529

cttacagagt taataagcat caaagaactt actgaaggac tttataaatt aaataccatt	60
atgtaga atg gtg gtg gtt agt gcc ttt att tat tta ttt ttt gag aca	109
Met Val Val Val Ser Ala Phe Ile Tyr Leu Phe Phe Glu Thr	
-20 -15 -10	
ggg tct ccc tct gtc gcc cag tct gga gtg cag tgg tgt gat ctc ggc	157
Gly Ser Pro Ser Val Ala Gln Ser Gly Val Gln Trp Cys Asp Leu Gly	
-5 1 5	
tta ctg cag cct ccg cct cct gga ttc aag cga ttc tct tgc ctc agc	205
Leu Leu Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser	
10 15 20	
ctc cta ggt agb drg gat tgc aga cgt gcg cca ccc ggg	244
Leu Leu Gly Xaa Xaa Asp Cys Arg Arg Ala Pro Pro Gly	
25 30 35	

&lt;210&gt; 530

&lt;211&gt; 434

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 124..432

&lt;221&gt; sig\_peptide

&lt;222&gt; 124..195

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq LXFLGMFLSGMVA/QI

&lt;400&gt; 530

ggsctttgga ttggawagag gagctgggca ggaggcaggg caaggagaaa gctgttcggg	60
ggctctgtct ggattttggt tgcctcctcc aatgttcctc tacctctact acaaggatgg	120
gtc atg ttt gtg tct gka aca rcg ttt ttc ttt kcg ctc ckc ttt ctg	168
Met Phe Val Ser Xaa Thr Xaa Phe Phe Phe Xaa Leu Xaa Phe Leu	
-20 -15 -10	
ggc atg ttc ctc tct ggc atg gtg gct caa att gat gct aac tgg aac	216
Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala Asn Trp Asn	
-5 1 5	
ttc ctg gat ttt gcc tac cat ttt aca gta ttt gtc ttc tat ttt gga	264

286

```

Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe Tyr Phe Gly
      10      15      20
gcc ttt tta ttg gaa gca gca gcc aca tcc ctg cat gat ttg cat tgc      312
Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp Leu His Cys
      25      30      35
aat aca acc ata acc rgg cag cca ctc ctg agt gat aac cag tat aac      360
Asn Thr Thr Ile Thr Xaa Gln Pro Leu Leu Ser Asp Asn Gln Tyr Asn
      40      45      50      55
ata aac gta gca gcc tca att ttt gcc ttt atg acg aca gct tgt tat      408
Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr Ala Cys Tyr
      60      65      70
ggg tgc agt ttg ggt ctg gct tta cg      434
Gly Cys Ser Leu Gly Leu Ala Leu
      75

```

&lt;210&gt; 531

&lt;211&gt; 406

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 284..406

&lt;221&gt; sig\_peptide

&lt;222&gt; 284..361

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq AXYL LVGLFPLKC/HX

&lt;221&gt; misc\_feature

&lt;222&gt; 384

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 531

```

taatatatgt magaatagca gggaccatgt cttctgttca atatkgtatc ctgagcacct      60
agtatTTaag taggtatttc agtaaataat gtaacatata taataaataa tattaatatt      120
tggtgactaa atgaatttag gtctggacct tgatggctta atgtctttct aaaaatctac      180
ttccatatct aagcctttct tgactacttt cgcttttttc tgtgaactta aaagtcttta      240
ttcattgttt gccggatgct aaacatttac aaaagtaatc ctt atg tca tct gaa      295
                               Met Ser Ser Glu
                               -25
att ttc taw ktt dtk cak att gck tat gct tda tat ttg cta gtt ggt      343
Ile Phe Xaa Xaa Xaa Xaa Ile Ala Tyr Ala Xaa Tyr Leu Leu Val Gly
      -20      -15      -10
ctt ttc cct cta aaa tgc cac wag agt hat ttt tct aag tna caa atc      391
Leu Phe Pro Leu Lys Cys His Xaa Ser Xaa Phe Ser Lys Xaa Gln Ile
      -5      1      5      10
tca tca ttt gtg gaa      406
Ser Ser Phe Val Glu
      15

```

&lt;210&gt; 532

&lt;211&gt; 212

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 23..211

&lt;221&gt; sig\_peptide

287

&lt;222&gt; 23..76

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq LTVTLGRLASACS/HS

&lt;400&gt; 532

```

gtttccggcc gaggtgcgg cc atg gca gca tct tcc ctg acg gtc acc tta      52
                        Met Ala Ala Ser Ser Leu Thr Val Thr Leu
                        -15                                -10
ggg cgg ctg gcg tcc gcg tgc agc cac agc atc ctg aga cct tcg ggg      100
Gly Arg Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly
                        -5                                5
ccc gga gca gcc tcc ctt tgg tct gct tct cga agg ttc aat tca cag      148
Pro Gly Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln
                        10                                15                                20
agc act tca tat cta cca gga tat gtt cvt aaa aca tcc ctg agt tca      196
Ser Thr Ser Tyr Leu Pro Gly Tyr Val Xaa Lys Thr Ser Leu Ser Ser
25                                30                                35                                40
cca cct tgg ccg agg g
Pro Pro Trp Pro Arg
                        45

```

&lt;210&gt; 533

&lt;211&gt; 149

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 76..147

&lt;221&gt; sig\_peptide

&lt;222&gt; 76..129

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq CICSCLFSSQYLX/XS

&lt;400&gt; 533

```

tataggtgat tataatcaag tgtaggttc ctgaattttg acatcctttt agaacttggg      60
tctggaattc cagaa atg tta att gct gct tgt att tgt tct tgt ttg ttt      111
                        Met Leu Ile Ala Ala Cys Ile Cys Ser Cys Leu Phe
                        -15                                -10
ttt agc cag tat ttg gsy ytt tct aat cca gcc gcg gg                      149
Phe Ser Gln Tyr Leu Xaa Xaa Ser Asn Pro Ala Ala
-5                                1                                5

```

&lt;210&gt; 534

&lt;211&gt; 145

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 56..145

&lt;221&gt; sig\_peptide

&lt;222&gt; 56..103

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq WVLSYMWQSASLG/FS

&lt;400&gt; 534

```

tgggctactc atggywagat aagacttaca cttctgaaag aggccttaga gtttc atg      58

```

288

```

                                Met
aag tgc tgg gtt ctc agc tac atg tgg cag agt gca tct ctg ggt ttt      106
Lys Cys Trp Val Leu Ser Tyr Met Trp Gln Ser Ala Ser Leu Gly Phe
-15                               -10                               -5                               1
agt aac agg att aaa tct mac ttg aga cct cca gca ggc      145
Ser Asn Arg Ile Lys Ser Xaa Leu Arg Pro Pro Ala Gly
                    5                               10

```

<210> 535  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 81..383

<221> sig\_peptide  
 <222> 81..287  
 <223> Von Heijne matrix  
       score 4.30000019073486  
       seq GIRLSCVLSHLQA/WD

```

<400> 535
aaatcctcag cagatTTTTg ttcaagagct gcttccagat tggcttctag ctgccagtgt      60
gaccttgggc agaaccttca atg tct gtg ggg ctg tgt ttt ctt atc tgg caa      113
                                Met Ser Val Gly Leu Cys Phe Leu Ile Trp Gln
                                -65                               -60
atg gga att atg cts ttg cct cgg gaa tgt tgg aag gtc aaa gac agt      161
Met Gly Ile Met Leu Leu Pro Arg Glu Cys Trp Lys Val Lys Asp Ser
                                -55                               -50                               -45
aag aag tac aaa agc tgc aga gaa tca gta ctg cct gca caa gca tgt      209
Lys Lys Tyr Lys Ser Cys Arg Glu Ser Val Leu Pro Ala Gln Ala Cys
                                -40                               -35                               -30
aca gga gag tcc cct gtc tta tct gga gtc agg gtt ctg ggg atc cgc      257
Thr Gly Glu Ser Pro Val Leu Ser Gly Val Arg Val Leu Gly Ile Arg
                                -25                               -20                               -15
ctc tcg tgc gtg tta tcc cat ctc caa gcc tgg gac tcc tgg gac aat      305
Leu Ser Cys Val Leu Ser His Leu Gln Ala Trp Asp Ser Trp Asp Asn
-10                               -5                               1                               5
cag aag gtg tgc tac ctg ggt gca ccc tgc ttt ggg aaa agg ctg agt      353
Gln Lys Val Cys Tyr Leu Gly Ala Pro Cys Phe Gly Lys Arg Leu Ser
                    10                               15                               20
cca acc acc tgg ctc act ttt tgg gtg gga c      384
Pro Thr Thr Trp Leu Thr Phe Trp Val Gly
                    25                               30

```

<210> 536  
 <211> 207  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 78..206

<221> sig\_peptide  
 <222> 78..119  
 <223> Von Heijne matrix  
       score 4.30000019073486  
       seq FAFLAGCSGSLW/SR

<400> 536

289

```

aactttatccc agatatacta tatgccaaac aatgtttgtc accagggata ccacaacaga      60
aaacaaatac actaaaa atg ttc gct ttc ctg gcc ggg tgc agt ggc tca      110
                Met Phe Ala Phe Leu Ala Gly Cys Ser Gly Ser
                        -10                                -5
tgc ctg tgg tcc cgg cac ttc ggg aga ctg cgg cgg gcg gct ccc ttg      158
Cys Leu Trp Ser Arg His Phe Gly Arg Leu Arg Arg Ala Ala Pro Leu
                1                5                10
agc cca gag ttt gag acc ggc ctg ggt aac atg gtg gaa ccc caa tgg g      207
Ser Pro Glu Phe Glu Thr Gly Leu Gly Asn Met Val Glu Pro Gln Trp
        15                20                25

```

&lt;210&gt; 537

&lt;211&gt; 394

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 268..393

&lt;221&gt; sig\_peptide

&lt;222&gt; 268..318

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq FLFVPHLISCNWC/EP

&lt;400&gt; 537

```

ttagcaaadc acagatgaag gtctcattac tatatgcaga gggtagccata agttacaadc      60
cctttgtgcc tctggctgct ccaacatcac agatgccatc ctgaatgctc taggtcagaa      120
ctgcccacgg cttaggtaaa catttcttgt ttagctcaaa aaaatcatag aacaaaagtt      180
tccttcaccc atatttcttc cttggaactt tggaatttta aggtaggcac tgcagacgct      240
ttgaaatttt aaggtagtcc ctttttag atg ccc acc tac ttc ctt ttt gta cct      294
                Met Pro Thr Tyr Phe Leu Phe Val Pro
                        -15                                -10
cat ttg att tca tgt aat tgg tgt gaa cca agg ggt aac aat ccc caa      342
His Leu Ile Ser Cys Asn Trp Cys Glu Pro Arg Gly Asn Asn Pro Gln
                -5                1                5
att cca cta ctt gct atc cat act aga aaa aag aat caa cat ttt att      390
Ile Pro Leu Leu Ala Ile His Thr Arg Lys Lys Asn Gln His Phe Ile
        10                15                20
act t      394
Thr
25

```

&lt;210&gt; 538

&lt;211&gt; 415

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 237..413

&lt;221&gt; sig\_peptide

&lt;222&gt; 237..317

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq LTSVSLXXXXXXG/SV

&lt;221&gt; misc\_feature

&lt;222&gt; 308..309,375

&lt;223&gt; n=a, g, c or t

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<400> 538
gaatcctcgc aaagaattgg caatgtcggt gcctttctct gccggaaggc tggcwactac      60
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ctctttgaac caaatgtct ccaaaaacaa gattctaatt tatacttaat atttcccca      180
gaagcccaat cattaaagcc acctttccag gaacagaagt gtttttgaca ctgtga atg      239
                                         Met

ctt tgg acc agt ttc cag aat cct ctt cag gta gtg ctt ctc acc agc      287
Leu Trp Thr Ser Phe Gln Asn Pro Leu Gln Val Val Leu Leu Thr Ser
-25 -20 -15

gtt tcc ctt ttd aww wtg gbn ndc mta ggt tca gtc cga atc awk cta      335
Val Ser Leu Xaa Xaa Xaa Xaa Xaa Gly Ser Val Arg Ile Xaa Leu
-10 -5 1 5

tct cac tgg tca agc tca gcc ttc ttc ttc ctd att cw b nck kyw hwt      383
Ser His Trp Ser Ser Ser Ala Phe Phe Phe Leu Ile Xaa Xaa Xaa Xaa
10 15 20

ctt tca cat gtg aca aaa caa atg cat ttg aa      415
Leu Ser His Val Thr Lys Gln Met His Leu
25 30

<210> 539
<211> 160
<212> DNA
<213> Homo sapiens

<220>
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<222> 66..158

<221> sig_peptide
<222> 66..107
<223> Von Heijne matrix
score 4.30000019073486
seq LTCLCGCFIVLLV/CV

<400> 539
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ttatt atg ctg act tgt ttg tgt ggt tgc ttt ata gtg tta ctt gtc tgt      110
Met Leu Thr Cys Leu Cys Gly Cys Phe Ile Val Leu Leu Val Cys
-10 -5 1

gta ctt aaa tgt gtt ttt gta gtg gct agt aat ggc ctt ttc ttt cct      158
Val Leu Lys Cys Val Phe Val Val Ala Ser Asn Gly Leu Phe Phe Pro
5 10 15

tt      160

<210> 540
<211> 327
<212> DNA
<213> Homo sapiens

<220>
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<222> 207..326

<221> sig_peptide
<222> 207..293
<223> Von Heijne matrix
score 4.30000019073486
seq HLSILAFVAIAFG/VL

<400> 540
catttttttc atgtgttttt ttggctgcat aaatgtcttc ttttgagaag tgtctgttca      60
tgteccctgc ccactttttg atgggggtgt ttgttttttt cttgtaaatt tgtttgagtt      120

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291

cattgtagat tctggatatt agccctttgt cagatgagta gggtgcgaaa attttctccc 180  
 atgttgtagg ttgcctgttc actctg atg gta gtt tct ttt gct gtg cag aag 233  
 Met Val Val Ser Phe Ala Val Gln Lys

-25

ctc ttt agt tta att aga tcc cat ttg tca att ttg gct ttt gtt gcc 281  
 Leu Phe Ser Leu Ile Arg Ser His Leu Ser Ile Leu Ala Phe Val Ala  
 -20 -15 -10 -5  
 att gct ttt ggt gtt ttg gac atg aag tcc ttg ccc acg cca ggg g 327  
 Ile Ala Phe Gly Val Leu Asp Met Lys Ser Leu Pro Thr Pro Gly  
 1 5 10

&lt;210&gt; 541

&lt;211&gt; 396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 84..395

&lt;221&gt; sig\_peptide

&lt;222&gt; 84..278

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq FFSRLGATSVXRA/CT

&lt;221&gt; misc\_feature

&lt;222&gt; 271,328,344..345,347

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 541

cttctgcact cacagccgaa ggaaagcagc aggttggggc ttcttggtggc caacttcaga 60  
 gcctgtcacc aggaaaggta agc atg gga gga agg aag atg gcg aca gat gaa 113  
 Met Gly Gly Arg Lys Met Ala Thr Asp Glu

-65

-60

gaa aat gtc tat ggt tta gaa gag aac gct cag tcc cgg cag gag tcc 161  
 Glu Asn Val Tyr Gly Leu Glu Glu Asn Ala Gln Ser Arg Gln Glu Ser  
 -55 -50 -45 -40

acg cgg agg ctc atc ctt gtt ggg aga aca ggg gcc ggg aag agc gcc 209  
 Thr Arg Arg Leu Ile Leu Val Gly Arg Thr Gly Ala Gly Lys Ser Ala  
 -35 -30 -25

act ggg aac agc atc ctg ggc cag aga cgg ttc ttc tcc agg ctg ggg 257  
 Thr Gly Asn Ser Ile Leu Gly Gln Arg Arg Phe Phe Ser Arg Leu Gly  
 -20 -15 -10

gcc acg tct gtg anc agg gcc tgc acc acg grh agc cgc agg tgg gac 305  
 Ala Thr Ser Val Xaa Arg Ala Cys Thr Thr Xaa Ser Arg Arg Trp Asp  
 -5 1 5

aag tgc cac gtg gaa gtc gtr gnd ctm gga cat vwk can nmh ggg aag 353  
 Lys Cys His Val Glu Val Val Xaa Leu Gly His Xaa Xaa Xaa Gly Lys  
 10 15 20 25

tgt cca aga cag atc ctg gct gtg agg aga gag gtc act gct a 396  
 Cys Pro Arg Gln Ile Leu Ala Val Arg Arg Glu Val Thr Ala  
 30 35

&lt;210&gt; 542

&lt;211&gt; 247

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 8..247

<221> sig\_peptide  
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 <223> Von Heijne matrix  
 score 4.30000019073486  
 seq ALALTXTLTPAPG/EH

<221> misc\_feature  
 <222> 78,182,194  
 <223> n=a, g, c or t

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 Met Gln Leu Gln Val Leu Gly Arg Pro Gln Gly Ala Pro Gln  
 -30 -25 -20  
 ctg gct ccc cag gcc ttg gct cta act bnk acc ctc ctc cca gcc cca 97  
 Leu Ala Pro Gln Ala Leu Ala Leu Thr Xaa Thr Leu Leu Pro Ala Pro  
 -15 -10 -5  
 gga gaa cac gat tck ccr atg stc att ggc cag ttt ccc cwa aac cct 145  
 Gly Glu His Asp Ser Pro Met Xaa Ile Gly Gln Phe Pro Xaa Asn Pro  
 1 5 10 15  
 ccc tcc gag cac ccg ggc gcc agt ccc agg cgg wmr ngg acg ggc tgg 193  
 Pro Ser Glu His Pro Gly Ala Ser Pro Arg Arg Xaa Xaa Thr Gly Trp  
 20 25 30  
 nra ccc caa agc tgg gac cgg agg gtg agc ccg gca gag gca gag aca 241  
 Xaa Pro Gln Ser Trp Asp Arg Arg Val Ser Pro Ala Glu Ala Glu Thr  
 35 40 45  
 cgc agg 247  
 Arg Arg

<210> 543  
 <211> 221  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 87..221

<221> sig\_peptide  
 <222> 87..209  
 <223> Von Heijne matrix  
 score 4.30000019073486  
 seq HLFTLGFCLSLCP/HP

<221> misc\_feature  
 <222> 154  
 <223> n=a, g, c or t

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 ataccgagta gtgaaactgc caggtc atg gga gta tac acg tgt cca att ttt 113  
 Met Gly Val Tyr Thr Cys Pro Ile Phe  
 -40 -35  
 gtg cat tac tac gag aac cat gga cca acc ccw agt ttc cnt gcc ttt 161  
 Val His Tyr Tyr Glu Asn His Gly Pro Thr Pro Ser Phe Xaa Ala Phe  
 -30 -25 -20  
 att tcc ttt cat cta ttt act ttg ggc ttt ctt tgt tcc cta tgc ccc 209  
 Ile Ser Phe His Leu Phe Thr Leu Gly Phe Leu Cys Ser Leu Cys Pro  
 -15 -10 -5  
 cac ccc cac ggg 221

His Pro His Gly

1

&lt;210&gt; 544

&lt;211&gt; 375

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 307..375

&lt;221&gt; sig\_peptide

&lt;222&gt; 307..354

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq SVSCSSSLWVSLS/KD

&lt;221&gt; misc\_feature

&lt;222&gt; 302

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 544

tcaatggaag aaggagwaaa aagagaagag gaaaatggga ccaatactgc tgatcatgtt 60

cgaaattcca gttgggcaaaa aaacggctcc taccaaggtg ctcttcataa cgctcttgaa 120

gaagccacag aacaaaacat acgagctggt acccaggcag ttttgcaggt ggatcacttt 180

atggctatatt ttaaaaaataa aataatcatt aaatatttct gtccagtatt tcagtataca 240

gtatactttt cacaatataa aaatagaagc ttaatactgg gcattcatac tttttaaaga 300

gnatga atg aag aaa tcg gtt tcc tgc tgt agt tct cta tgg gta agt 348

Met Lys Lys Ser Val Ser Cys Cys Ser Ser Leu Trp Val Ser

-15 -10 -5

ctt agt aaa gac gag aat gct gaa atg 375

Leu Ser Lys Asp Glu Asn Ala Glu Met

1 5

&lt;210&gt; 545

&lt;211&gt; 376

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 260..376

&lt;221&gt; sig\_peptide

&lt;222&gt; 260..349

&lt;223&gt; Von Heijne matrix

score 4.30000019073486

seq TVLLSGSPRAVVS/AV

&lt;400&gt; 545

tagtggacag cccaagctgc ttctcttaga atggctgtgg cttcacaagt gatgagaaga 60

gcatgcgctt gatttcagat cccattaca agctcataat gaatgagtca caggagaaaag 120

gtgrgacttg gggccctttc gtgcctgatg ggaagctcct gmaccccg gaggccctc 180

cagactgtcc ttgcccacct ggctgcactg gcctctttat gccaacccag tgaggacagg 240

ttctgaggga cctggacag atg ctg ctg ccc cta gcc atg gct gga cga tgt 292

Met Leu Leu Pro Leu Ala Met Ala Gly Arg Cys

-30 -25 -20

tat aca gcc aag cac agc acw gtg ctg ctc tca gga agc cca agg gct 340

Tyr Thr Ala Lys His Ser Thr Val Leu Leu Ser Gly Ser Pro Arg Ala

-15 -10 -5

gtg gtc agt gca gtg gtg atg gtg ggc aca ggg tgc 376

294

Val Val Ser Ala Val Val Met Val Gly Thr Gly Cys  
 1 5

<210> 546  
 <211> 109  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 30..107

<221> sig\_peptide  
 <222> 30..86  
 <223> Von Heijne matrix  
 score 4.30000019073486  
 seq LRAFLLSVPLGKG/SA

<400> 546  
 cccacagcct tccctggtgt gcctgcagt atg cca tcc tgc tgc tac ctt agg 53  
 Met Pro Ser Cys Cys Tyr Leu Arg  
 -15  
 gct ttt ctg ctc tct gtc cct ctg ggg aaa ggc tca gcc ctt aag gat 101  
 Ala Phe Leu Leu Ser Val Pro Leu Gly Lys Gly Ser Ala Leu Lys Asp  
 -10 -5 1 5  
 ccc gtg ct 109  
 Pro Val

<210> 547  
 <211> 306  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 3..305

<221> sig\_peptide  
 <222> 3..74  
 <223> Von Heijne matrix  
 score 4.19999980926514  
 seq LLLSSLWIVCLH/LD

<400> 547  
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 Met Val Ala Asp Lys Glu Val Gln Thr Arg Thr Leu Leu Leu Ser  
 -20 -15 -10  
 tca cta tgg ata gtc tgt tgc ctc cat cta gat tct ctt att tca rrr 95  
 Ser Leu Trp Ile Val Cys Cys Leu His Leu Asp Ser Leu Ile Ser Xaa  
 -5 1 5  
 aaa tat cct ctc cat gca att agg aga tat tta tcg acg ctg aga aac 143  
 Lys Tyr Pro Leu His Ala Ile Arg Arg Tyr Leu Ser Thr Leu Arg Asn  
 10 15 20  
 caa aga gcc gaa gaa cag gtt gca cgt ttt caa aaa ata cct aat ggt 191  
 Gln Arg Ala Glu Glu Gln Val Ala Arg Phe Gln Lys Ile Pro Asn Gly  
 25 30 35  
 gaa aat gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa 239  
 Glu Asn Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu  
 40 45 50 55  
 tta cca gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat 287  
 Leu Pro Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn  
 60 65 70  
 ggt cta aaa caa tgt gaa g 306

Gly Leu Lys Gln Cys Glu  
75

<210> 548  
<211> 148  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 89..148

<221> sig\_peptide  
<222> 89..130  
<223> Von Heijne matrix  
score 4.19999980926514  
seq HICLFFSFSXXFX/LF

<400> 548  
aggatagctg aaaggagttc atctaactgg agtcccacta gaagtaagaa acccctattg 60  
tttatttttt aataatgtaa tttttatt atg cat att tgt ctt ttt ttt tct 112  
Met His Ile Cys Leu Phe Phe Ser  
-10  
ttt tct ttw wct ttt tkt ctt ttc ttt ttt ttt ttt 148  
Phe Ser Xaa Xaa Phe Xaa Leu Phe Phe Phe Phe Phe  
-5 1 5

<210> 549  
<211> 374  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 240..374

<221> sig\_peptide  
<222> 240..296  
<223> Von Heijne matrix  
score 4.19999980926514  
seq ILARLCRMQTCWC/LS

<400> 549  
tacattcggc ccggccatgg cagcggcgcc cctgaaagtg tgcacgtgg gctcggggaa 60  
ctggggttca gctgttgcaa aarkrattgg taataatgtc aagaaacttc agaaatttgc 120  
ctccacagtc aagatgtggg tcttttraar aaamcrgkkr akkggcagra aactgacaga 180  
catcataaat aatgaccatg aaaatgtaaa atatcttcct ggacacaagc tgccagaaa 239  
atg tgg ttg cca tgt caa atc tta gcg agg ctg tgc agg atg cag acc 287  
Met Trp Leu Pro Cys Gln Ile Leu Ala Arg Leu Cys Arg Met Gln Thr  
-15 -10 -5  
tgc tgg tgt ttg tca ttc ccc acc agt tca ttc aca gaa tct gtg atg 335  
Cys Trp Cys Leu Ser Phe Pro Thr Ser Ser Phe Thr Glu Ser Val Met  
1 5 10  
aga tca ctg gga gag tgc cca aga aag cgc tgg ggg ggg 374  
Arg Ser Leu Gly Glu Cys Pro Arg Lys Arg Trp Gly Gly  
15 20 25

<210> 550  
<211> 476  
<212> DNA  
<213> Homo sapiens

<220>

&lt;221&gt; CDS

&lt;222&gt; 147..476

&lt;221&gt; sig\_peptide

&lt;222&gt; 147..398

&lt;223&gt; Von Heijne matrix

score 4.19999980926514

seq VTILVSLALAFLA/CI

&lt;400&gt; 550

agacacacgc gaggcgctgt cctttcagca ccacaagctc gggctgagga gggaggactc 60

ctggccgtcc tctcckctt caaattggct tgaatctgct ctgaccccc acgagtgcag 120

cacagtctgg gaagaaaggc gtaagg atg gwg aag ctg arc agt aac ccc agc 173

Met Xaa Lys Leu Xaa Ser Asn Pro Ser

-80

gag aag gga acc aag ccg cct tca gtt gag gat ggc ttc cag acc gtc 221

Glu Lys Gly Thr Lys Pro Pro Ser Val Glu Asp Gly Phe Gln Thr Val

-75 -70 -65 -60

cct ctc atc act ccc ttg gag gtt aat cac tta cag ctg cct gct cca 269

Pro Leu Ile Thr Pro Leu Glu Val Asn His Leu Gln Leu Pro Ala Pro

-55 -50 -45

gaa aag gtg att gtg aag aca aga acg gaa tat cag ccg gaa cag aag 317

Glu Lys Val Ile Val Lys Thr Arg Thr Glu Tyr Gln Pro Glu Gln Lys

-40 -35 -30

aac aaa ggg aag ttc cgg gtg cca aaa atc gct gaa ttt acg gtc acc 365

Asn Lys Gly Lys Phe Arg Val Pro Lys Ile Ala Glu Phe Thr Val Thr

-25 -20 -15

atc ctt gtc agc ctg gcc cta gct ttc ctt gcg tgc atc gtg ttc ctg 413

Ile Leu Val Ser Leu Ala Leu Ala Phe Leu Ala Cys Ile Val Phe Leu

-10 -5 1 5

gtg gtt tac aaa gcc ttc acc tat gat cac agc tgc cca gag gat tcg 461

Val Val Tyr Lys Ala Phe Thr Tyr Asp His Ser Cys Pro Glu Asp Ser

10 15 20

tct atr agc acc ggg 476

Ser Xaa Ser Thr Gly

25

&lt;210&gt; 551

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 77..229

&lt;221&gt; sig\_peptide

&lt;222&gt; 77..139

&lt;223&gt; Von Heijne matrix

score 4.19999980926514

seq EVLSLLFXCIYWG/QY

&lt;400&gt; 551

catcctcatc ttcttctct cttgttactt tggatatttg ctgaaaggtc gtcagttgct 60

ccacacaact tataaa atg ttc ats gcc gca gca gga gta gag gtc ctg agc 112

Met Phe Xaa Ala Ala Ala Gly Val Glu Val Leu Ser

-20 -15 -10

ctc cta ttt tkc tgc atc tac tgg ggt caa tat gcc acc gat ggc att 160

Leu Leu Phe Xaa Cys Ile Tyr Trp Gly Gln Tyr Ala Thr Asp Gly Ile

-5 1 5

ggc aac gag agt gtg aag atc ttg gcc aag ctg ctc ttc tcc tcc agc 208

Gly Asn Glu Ser Val Lys Ile Leu Ala Lys Leu Leu Phe Ser Ser Ser

10 15 20

231

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<210> 552
<211> 229
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 125..229
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<221> sig_peptide
<222> 125..202
<223> Von Heijne matrix
      score 4.19999980926514
      seq FLSFLSFFFFSFF/LF
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<400> 552
agtttcactc cgaaagtsct tcttacagag caactccaag gatgggctga aaagcacata      60
gagaaaatgg aacagtgcga agttggaagg tccgtgcggg tggcagcgcc agtgtgggga      120
tgag atg ctc aca gga cgg ttt tta ggc ggc tca caa ggg ttt ttt ctt      169
      Met Leu Thr Gly Arg Phe Leu Gly Gly Ser Gln Gly Phe Phe Leu
          -25              -20              -15

tct ttt ctt tct ttc ttt ttt tcc ttt ttc ctt ttc ctt yct ttt      217
Ser Phe Leu Ser Phe Phe Phe Phe Ser Phe Phe Leu Phe Leu Xaa Phe
      -10              -5              1              5

ttt ttt ttt ttt
Phe Phe Phe Phe

```

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<210> 553
<211> 232
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 110..232
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<221> sig_peptide
<222> 110..193
<223> Von Heijne matrix
      score 4.19999980926514
      seq FVFMSKLLLSFS/FL
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<400> 553
acgatcagat ctgakraaaa ttgagccccc aaaagcagtt atcagactat ttgaaataaaa      60
gatttatatt cacctttaat aacaatgtac cattaataac acatattac atg ttt att      118
                                     Met Phe Ile

tkr taw rak atg aaa cag wcr ttt cat att ata gac ttt gtt ttc atg      166
Xaa Xaa Xaa Met Lys Gln Xaa Phe His Ile Ile Asp Phe Val Phe Met
-25                               -20                               -10
agt aaa ctt tta tta ttt tca ttt tca ttt tta ara aaa gcr cgc atg      214
Ser Lys Leu Leu Leu Phe Ser Phe Ser Phe Leu Xaa Lys Ala Arg Met
                               -5                               1                               5

awt aca gca gca cct ggg      232
Xaa Thr Ala Ala Pro Gly
      10

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<210> 554  
<211> 141  
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 31..141

<221> sig\_peptide

<222> 31..84

<223> Von Heijne matrix

score 4.19999980926514

seq HILTAVLPLVSHQ/QN

<400> 554

ttacattcct	cacttctagt	ggtttgatta	atg gtc	aca cca	gta cac	atc ctg	54
			Met Val Thr	Pro Val His	Ile Leu		
						-15	
aca gcc	gtg ctt	cca ctt	gtg tct	cac cag	caa aac	cat ctg	102
Thr Ala	Val Leu	Pro Leu	Val Ser	His Gln	Gln Asn	His Leu	
						Gly Gly	
-10		-5		1		5	
agg ttt	gca tct	ctg gga	tcc tca	ggc att	agg cac	ggg	141
Arg Phe	Ala Ser	Leu Gly	Ser Ser	Gly Ile	Arg His	Gly	
	10		15				

<210> 555

<211> 376

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 319..375

<221> sig\_peptide

<222> 319..363

<223> Von Heijne matrix

score 4.19999980926514

seq ILHLATLLNLFIS/SN

<221> misc\_feature

<222> 144..145,202,276..277

<223> n=a, g, c or t

<400> 555

ttctatttct	gtgaagaatg	tcacagaatg	cagtcacat	attgcataga	atctgtagat	60
tgcatgggt	agcatggaca	ttttaacaat	attgattcct	ccaattcatg	aacatgaaat	120
atctttccat	tttttgaggt	ctanncaatc	tcttttatca	gtgtktccta	attctgatta	180
tagagatcct	tcacatcttt	gnttcaagtt	gattcctacg	tatttcactt	tatttggtggc	240
tggtgtaaat	gggattactt	tttgcatctc	tttchnnsaa	ttgttcagtc	agcatacagg	300
aatgatactg	atttttgt	atg ttg	att tta	cat ctt	gca act	351
		Met Leu	Ile Leu	His Leu	Ala Thr	
		-15		-10	-5	
ttg ttt	atc agt	tct aac	agt ttt	g		376
Leu Phe	Ile Ser	Ser Asn	Ser Phe			
	1					

<210> 556

<211> 279

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 199..279

<221> sig\_peptide

<222> 199..243

<223> Von Heijne matrix

score 4.19999980926514

seq LASFGPFRSSCFA/AR

<400> 556

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cccttggttac tgctacccat cctacctgca ccctgctttt tccctcttgs cacgcttttt    60
ttctctctccc tcttaccccc accctgtaca aaatgcataa aggatggaaa aactactgca    120
gccagaagtc tttgaatgag gcatcaatgg atgaatattt aggcagctta gggctgtttc    180
gaaagctgac tgccaagg atg cct ctt gcc tct ttc ggg cca ttt cgg agc    231
```

Met Pro Leu Ala Ser Phe Gly Pro Phe Arg Ser

-15 -10 -5

```
agt tgt ttt gca gcc agg tcc atc att tgg aaa tca gga agg caa ggg    279
```

Ser Cys Phe Ala Ala Arg Ser Ile Ile Trp Lys Ser Gly Arg Gln Gly

1 5 10

<210> 557

<211> 340

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 233..340

<221> sig\_peptide

<222> 233..325

<223> Von Heijne matrix

score 4.19999980926514

seq FLLSFLSFRSPLC/HH

<400> 557

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caaagaaatt agtggctaaa cgtagagaaa ttaagatgaa ggaactggca catggagcca    60
ctgtgtacta taaagtattt ttattggtat ttagtcttgc tgttattggt gctaagtatt    120
gtattgaata attaccagct gttgttagtt atttgaaatt aggtgcctaa agcaacctct    180
catcttcgag aaagtcacat ttcttgaaac tttttaaaaa cttgcttgaa ac atg gag    238
```

Met Glu

-30

```
act tgg aat ggg acg tct atc ata gta gca cat ctg ara tcc ttc tca    286
```

Thr Trp Asn Gly Thr Ser Ile Ile Val Ala His Leu Xaa Ser Phe Ser

-25 -20 -15

```
ttc ctg ctg tca ttt ctg tcc ttt cgc agt cca ctt tgt cac cac ccc    334
```

Phe Leu Leu Ser Phe Leu Ser Phe Arg Ser Pro Leu Cys His His Pro

-10 -5 1

```
ctc ggg    340
```

Leu Gly

5

<210> 558

<211> 365

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 288..365

<221> sig\_peptide

<222> 288..329

<223> Von Heijne matrix

score 4.19999980926514

seq QFLSLIFASCSST/TP

```

<400> 558
acatttgcaa ccttggccat ctgtccagaa cctgctccca cctcaggccc aggccaaccg      60
tgactgctg caatgggctc tgagctggag acggcgatgg agaccctcat caacgtgttc      120
cacgcccact cgggcaaaga gggggacaag tacaagctga gcaagaagga gctgaaagag      180
ctgctgcaga cggagctctc tggcttcctg gatgtgaaag agcttatgct gtaggcaaca      240
gaagccctca agacttttga ggaggcctag aagagtccca taattca atg cag ttc      296
                                   Met Gln Phe
ctc tcg ctc atc ttt gcc tcc tgc tcc tca acc acc ccc tta cct ctg      344
Leu Ser Leu Ile Phe Ala Ser Cys Ser Ser Thr Thr Pro Leu Pro Leu
   -10               -5               1               5
amt cag tgc tgt acc ctt ccc      365
Xaa Gln Cys Cys Thr Leu Pro
              10

```

```

<210> 559
<211> 354
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 103..354

<221> sig_peptide
<222> 103..261
<223> Von Heijne matrix
      score 4.19999980926514
      seq VLALVCHSASISV/FP

```

```

<400> 559
aatattataa tgaggctctg caggggcttg aacttaggtc cctgtaaggg agctactgtt      60
ccctggtatg acccactcta gctgagctgt gcagagactg ag atg gtc acc tca      114
                                   Met Val Thr Ser
                                   -50
aag agc agg gga ccc ckt gtc cag act ctg ggg cat gct ggc aac ctg      162
Lys Ser Arg Gly Pro Xaa Val Gln Thr Leu Gly His Ala Gly Asn Leu
      -45               -40               -35
agg agt ctg cgg gag tgg cct gat ctg tgc tgc ttg agg ctt ttt gtc      210
Arg Ser Leu Arg Glu Trp Pro Asp Leu Cys Cys Leu Arg Leu Phe Val
      -30               -25               -20
cca gat cac act gta ctt gct ctg gtg tgc cac agc gca tcc atc tct      258
Pro Asp His Thr Val Leu Ala Leu Val Cys His Ser Ala Ser Ile Ser
      -15               -10               -5
gtc ttc cct tct cag gtc acc tgc aga ctc cca agg aca ggg tca cat      306
Val Phe Pro Ser Gln Val Thr Cys Arg Leu Pro Arg Thr Gly Ser His
      1               5               10               15
ccc atc tgc gtc atc tct caa ggt gcc ttt cac gat cct cac cca aat      354
Pro Ile Cys Val Ile Ser Gln Gly Ala Phe His Asp Pro His Pro Asn
      20               25               30

```

```

<210> 560
<211> 328
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 168..326

<221> sig_peptide

```

<222> 168..248  
 <223> Von Heijne matrix  
 score 4.19999980926514  
 seq RLVVLFASPXVRP/AS

<221> misc\_feature  
 <222> 230  
 <223> n=a, g, c or t

<400> 560  
 attaagggac aataatggcc gctttcaagg tgtggatttt ggctccttga gcctgtctga 60  
 gcgaggggtg gcagcgccgg cgccccagaa tccgggacag aaagggctbc aagagtcgcg 120  
 cttggtgmga gaaatcccag atcctgtgat gggggacacc agtgagg atg cct cga 176  
 Met Pro Arg  
 -25  
 tcc atc gat ksg aag gca ctg atc tgg act gtc agg ttg gtg gtc tta 224  
 Ser Ile Asp Xaa Lys Ala Leu Ile Trp Thr Val Arg Leu Val Val Leu  
 -20 -15 -10  
 ttt gcn agt cca awa gtg cgg cca gcg agc agc atg tct tca agg ctc 272  
 Phe Ala Ser Pro Xaa Val Arg Pro Ala Ser Ser Met Ser Ser Arg Leu  
 -5 1 5  
 ctg ctc ccc gsc ctt cat tac tcg gac tgg act tgc tgg ctt cct gaa 320  
 Leu Leu Pro Xaa Leu His Tyr Ser Asp Trp Thr Cys Trp Leu Pro Glu  
 10 15 20  
 cgg aga ga 328  
 Arg Arg  
 25

<210> 561  
 <211> 341  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 69..341

<221> sig\_peptide  
 <222> 69..230  
 <223> Von Heijne matrix  
 score 4.19999980926514  
 seq TVVFLTLLSVVIL/IF

<221> misc\_feature  
 <222> 270..272,321..322  
 <223> n=a, g, c or t

<400> 561  
 ccttcaccag cagcccgctc gactggaaag atctgcctct tctccaagaa actcaaccac 60  
 tagtgaca atg acc agc ctc ctg act act cct tct cca aga gaa gaa ctg 110  
 Met Thr Ser Leu Leu Thr Thr Pro Ser Pro Arg Glu Glu Leu  
 -50 -45  
 atg acc acc cca att tta cag ccc act gag gcc ctg tcc cca gaa gat 158  
 Met Thr Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp  
 -40 -35 -30 -25  
 gga gcc agc aca gca ctc att gca gtt gtt atc acc gtt gtc ttc ctc 206  
 Gly Ala Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu  
 -20 -15 -10  
 acc ctg ctc tcg gtc gtg atc ttg atc ttc ttt tac ctg tac aag aac 254  
 Thr Leu Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn  
 -5 1 5

302

```

aaa ggc agc tac gtm nnn tat gaa cct aca gaa ggt gag ccc agt gcc      302
Lys Gly Ser Tyr Val Xaa Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala
  10                      15                      20
atc gtc cag atg gag adw nnc ttg gcc aag ggc agc gag                  341
Ile Val Gln Met Glu Xaa Xaa Leu Ala Lys Gly Ser Glu
  25                      30                      35

```

&lt;210&gt; 562

&lt;211&gt; 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 334..483

&lt;221&gt; sig\_peptide

&lt;222&gt; 334..387

&lt;223&gt; Von Heijne matrix

score 4.19999980926514

seq LIYLVSSFLALNQ/AS

&lt;400&gt; 562

```

gttagttggg cagggctgaa gtgtatgtgg tgaggaaaag aggctcctac tgtagacagc      60
cttgttctac agatcctccc agaaatctct gggccaggtg gaaccaggg tcagagaggg      120
atgggagaga ggtttaattt tccatgataa ataaaaatct ataaaataat aaacaagaga      180
aaagagattg gaaacagcca gggtggagca gtgagtgtgt aaggaaacct ggctgccctc      240
tccagattcc ccaggctctc agagaagatc agcagaaagt ctgcaagass ctaagaacca      300
tcagccctca gctgcacctc ctccctcca agg atg aca aag gcg sgv ctc atc      354
                                Met Thr Lys Ala Xaa Leu Ile
                                -15

```

```

tat ttg gtc agc agc ttt ctt gcc cta aat cag gcc agc ctc atc agt      402
Tyr Leu Val Ser Ser Phe Leu Ala Leu Asn Gln Ala Ser Leu Ile Ser
  -10                      -5                      1                      5

```

```

cgc tgt gac ttg gcc cag gtg ctg cag ctg gag gac ttg gat ggg ttt      450
Arg Cys Asp Leu Ala Gln Val Leu Gln Leu Glu Asp Leu Asp Gly Phe
          10                      15                      20

```

```

gag ggt tac tcc ctg agt gac tgg ctg tgc tgg c                        484
Glu Gly Tyr Ser Leu Ser Asp Trp Leu Cys Trp
          25                      30

```

&lt;210&gt; 563

&lt;211&gt; 229

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 122..229

&lt;221&gt; sig\_peptide

&lt;222&gt; 122..190

&lt;223&gt; Von Heijne matrix

score 4.19999980926514

seq QLILLGIFRGIRH/QI

&lt;400&gt; 563

```

gaaaggcctc gaaggcagcg tctactcga ccaccaaggc aagacaagcc acctckattt      60
agacggctaa gagagaggga ggctgcttca aaatcaaatg aggtggtagc agtgcccaca      120
a atg gca cag tta ata atg tgg ctc aag aac cag tta ata ctc ttg ggg      169
  Met Ala Gln Leu Ile Met Trp Leu Lys Asn Gln Leu Ile Leu Leu Gly
          -20                      -15                      -10
ata ttt cgg gga ata aga cac cag att tat cta atc aga act ctt cag      217

```

303

Ile Phe Arg Gly Ile Arg His Gln Ile Tyr Leu Ile Arg Thr Leu Gln

-5

1

5

atc agg caa tgg

229

Ile Arg Gln Trp

10

&lt;210&gt; 564

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 80..352

&lt;221&gt; sig\_peptide

&lt;222&gt; 80..169

&lt;223&gt; Von Heijne matrix

score 4.19999980926514

seq LAXTLTLTCSVSG/VS

&lt;400&gt; 564

actttctgag agtcctggac ctctgtgca agaacatgaa acatctgtgg ttcttccttc 60

tcctgggtggc aggtcccag atg ggt cct gtc cca ggt gca gct gca gga gtm 112

Met Gly Pro Val Pro Gly Ala Ala Ala Gly Val

-30 -25 -20

rgg ccc ayg amt ggc gaa ctt gcg grg acc ctg tcc ctc acc tgc agt 160

Xaa Pro Xaa Xaa Gly Glu Leu Ala Xaa Thr Leu Ser Leu Thr Cys Ser

-15 -10 -5

gtc tct ggt gtc tcc atc act agt tat tac tgg agc tgg atc cgc car 208

Val Ser Gly Val Ser Ile Thr Ser Tyr Tyr Trp Ser Trp Ile Arg Gln

1 5 10

gcc cca ggg aag ggg ccg gag tgg atc ggg cdk atc gat cat agc ggg 256

Ala Pro Gly Lys Gly Pro Glu Trp Ile Gly Xaa Ile Asp His Ser Gly

15 20 25

gat acc gac tac aat ccc tcc ctc cag agt cga gtc acc ctc tca gtg 304

Asp Thr Asp Tyr Asn Pro Ser Leu Gln Ser Arg Val Thr Leu Ser Val

30 35 40 45

gac acg tcg aag aac cag ttc tca ctg agg ttg ctt tct gtg agc gca 352

Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu Leu Ser Val Ser Ala

50 55 60

&lt;210&gt; 565

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 85..201

&lt;221&gt; sig\_peptide

&lt;222&gt; 85..192

&lt;223&gt; Von Heijne matrix

score 4.19999980926514

seq LPLFLCPLGMVET/SF

&lt;400&gt; 565

agttctgcgc tgtgagccgg ggcacaaaga gccctctgca ctacgcgcgc agaccgcgga 60

ccagttggag gcactctgtcc accc atg tgg ttc cag aca cgt tca tgt ggc 111

Met Trp Phe Gln Thr Arg Ser Cys Gly

-35 -30

cac cat gac ccc gtc ggc atc aca ggg gta acc aag gtg atc ctc cct 159

304

His His Asp Pro Val Gly Ile Thr Gly Val Thr Lys Val Ile Leu Pro  
 -25 -20 -15  
 ctc ttc ctg tgt cca ctg ggg atg gta gag acc agc ttc ggg 201  
 Leu Phe Leu Cys Pro Leu Gly Met Val Glu Thr Ser Phe Gly  
 -10 -5 1

<210> 566  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 87..422

<221> sig\_peptide  
 <222> 87..413  
 <223> Von Heijne matrix  
 score 4.19999980926514  
 seq LVFLLMYLFPRQL/LI

<400> 566  
 ctctcccgct tctctcgctg tgaagatggc gctctccagg gtcttcaaag cttcaccttt 60  
 ctccaaaggc agatgtgaag aacttg atg tct tat gtg gta acc aag aca aaa 113  
 Met Ser Tyr Val Val Thr Lys Thr Lys  
 -105  
 gcg att aat ggg aaa tac cat cgt ttc ttg ggt cgt cat ttc ccc cgc 161  
 Ala Ile Asn Gly Lys Tyr His Arg Phe Leu Gly Arg His Phe Pro Arg  
 -100 -95 -90 -85  
 ttc tat gtc ctg tac aca atc ttc atg aaa gga ttg cag atg tta tgg 209  
 Phe Tyr Val Leu Tyr Thr Ile Phe Met Lys Gly Leu Gln Met Leu Trp  
 -80 -75 -70  
 gct gat gcc aaa aag gct aga aga ata aag aca aat atg tgg aag cac 257  
 Ala Asp Ala Lys Lys Ala Arg Arg Ile Lys Thr Asn Met Trp Lys His  
 -65 -60 -55  
 aat ata aag ttt cat caa ctt cca tac cgg gag atg gag cat ttg aga 305  
 Asn Ile Lys Phe His Gln Leu Pro Tyr Arg Glu Met Glu His Leu Arg  
 -50 -45 -40  
 cag ttc cgc caa gac gtc acc aag tgt ctt ttc cta ggt att att tcc 353  
 Gln Phe Arg Gln Asp Val Thr Lys Cys Leu Phe Leu Gly Ile Ile Ser  
 -35 -30 -25  
 att cca cct ttt gcc aac tac ctg gtc ttc ttg cta atg tac ctg ttt 401  
 Ile Pro Pro Phe Ala Asn Tyr Leu Val Phe Leu Leu Met Tyr Leu Phe  
 -20 -15 -10 -5  
 ccc agg caa cta ctg atc agg 422  
 Pro Arg Gln Leu Leu Ile Arg  
 1

<210> 567  
 <211> 218  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 48..218

<221> sig\_peptide  
 <222> 48..104  
 <223> Von Heijne matrix  
 score 4.19999980926514  
 seq LSLPSFLCTCCQF/FP

```
<210> 568
<211> 246
<212> DNA
<213> Homo sapiens
```

```
<221> sig_peptide
<222> 2..238
<223> Von Heijne matrix
      score 4.1999980926514
      seq LLLVSLLEHLSHV/HE
```

```
<210> 569
<211> 142
<212> DNA
<213> Homo sapiens
```

```
<221> sig_peptide
<222> 78..128
<223> Von Heijne matrix
      score 4.19999980926514
```

seq CFALCIILICVMS/CR

<400> 569  
 cacattagtt ttgaaactag ctctaatttc tectaccagg aggaatttct tccttcttgg 60  
 caatactgtg gtatttta atg gta ttt tac tgt ttt gca ctt tgt att ata 110  
                   Met Val Phe Tyr Cys Phe Ala Leu Cys Ile Ile  
                           -15                  -10  
 ctt att tgt gtt atg tct tgt cgc cac ctg gg 142  
 Leu Ile Cys Val Met Ser Cys Arg His Leu  
       -5                          1

<210> 570  
 <211> 207  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 12..206

<221> sig\_peptide  
 <222> 12..140  
 <223> Von Heijne matrix  
       score 4.09999990463257  
       seq VLITQLCLGKQS/EP

<400> 570  
 tcaatccttg a atg ctc tgg gag act gat ttg agt acc aat aaa act cca 50  
                   Met Leu Trp Glu Thr Asp Leu Ser Thr Asn Lys Thr Pro  
                           -40                  -35  
 gtc tcc tgc aca gct ggc tct gcg tgt gct ctt tct cta ttg caa ttc 98  
 Val Ser Cys Thr Ala Gly Ser Ala Cys Ala Leu Ser Leu Leu Gln Phe  
 -30                  -25                  -20                  -15  
 cct gtc ttg ata act cag ctc tgt cta ggc aaa ggg caa agt gaa ccc 146  
 Pro Val Leu Ile Thr Gln Leu Cys Leu Gly Lys Gly Gln Ser Glu Pro  
                   -10                  -5                  1  
 att ggg cca tta caa gat ttt gtg tct ttg gaa agc act tca cat ttt 194  
 Ile Gly Pro Leu Gln Asp Phe Val Ser Leu Glu Ser Thr Ser His Phe  
       5                          10                  15  
 tat tct ttt ttt t 207  
 Tyr Ser Phe Phe  
       20

<210> 571  
 <211> 373  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 276..371

<221> sig\_peptide  
 <222> 276..335  
 <223> Von Heijne matrix  
       score 4.09999990463257  
       seq LWCCSPSSRTSSS/LS

<221> misc\_feature  
 <222> 251  
 <223> n=a, g, c or t

<400> 571  
 attctgcagc caactttggt caccatctcc gcaatgcctt ggacgtcctg catagagagg 60  
 tgcccagagt cctgggtcaac ctctgtggact tcctgaaccc cactatsrtg cggcaggtgt 120  
 tcctgggrra cccagacaag tgcccagtg agcaggccag cgttttgtgt aactgcgttc 180  
 tgaccctgcg ggagaactcc caagagctag ccaggctggr ggccttcagc cgagcctacc 240  
 ggagcagcat nbcgagctgg tggggtcagg ccgct atg aca cgc agg agg act 293  
 Met Thr Arg Arg Arg Thr  
 -20 -15  
 tct ctg tgg tgc tgc agc cct tct tcc aga aca tcc agc tcc ctg tcc 341  
 Ser Leu Trp Cys Cys Ser Pro Ser Ser Arg Thr Ser Ser Ser Leu Ser  
 -10 -5 1  
 tgg cgg atg ggc tcc cag ata cgt cct tct tt 373  
 Trp Arg Met Gly Ser Gln Ile Arg Pro Ser  
 5 10

<210> 572  
 <211> 195  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 134..193

<221> sig\_peptide  
 <222> 134..187  
 <223> Von Heijne matrix  
 score 4.09999990463257  
 seq WCFHAVFFTVVCV/VR

<400> 572  
 gtgacaaagt accacagact ggggtggttga aacacagaaa tttattttct cacaatttcg 60  
 gaggtctctag aagtctgaga tcaagggtgtt ggcagggtttg gtttattcta aggcctttct 120  
 ctatggcttg tag atg gcc ttc tat ctc tgg tgt ttt cat gcg gtc ttt 169  
 Met Ala Phe Tyr Leu Trp Cys Phe His Ala Val Phe  
 -15 -10  
 ttc act gtg tgt gtg tgt gtg cgg gg 195  
 Phe Thr Val Cys Val Cys Val Arg  
 -5 1

<210> 573  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 173..352

<221> sig\_peptide  
 <222> 173..271  
 <223> Von Heijne matrix  
 score 4.09999990463257  
 seq PLIHLTLSGHSTC/FR

<400> 573  
 tcattcttgg gtgtttctcg cagaggggga tttggcaggg tcataggaca atagtggagg 60  
 gaaggtcagc agataaacia gtgaacaaag gtttctgggt ttcctaggca gargaccctt 120  
 gcggccttcc gcagtgtttg tgtccctggg tacttgagat tagggagtgg tg atg act 178  
 Met Thr  
 ctt aac gag cat gct gcc ttc aag cat ctg ttt aac aaa gca cat ctt 226  
 Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala His Leu  
 -30 -25 -20

308

```

gca cca ccc tta atc cat tta acb ctg agt gga cac agc aca tgt ttc      274
Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr Cys Phe
-15                      -10                      -5                      1
aga gag cac agg gtt ggg ggc aag gtc ata gat gaa cag cat ccc aag      322
Arg Glu His Arg Val Gly Gly Lys Val Ile Asp Glu Gln His Pro Lys
                    5                      10                      15
gca gaa gaa tct ttc tta gta cag gag ggg      352
Ala Glu Glu Ser Phe Leu Val Gln Glu Gly
                20                      25

```

<210> 574  
 <211> 121  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 35..121

<221> sig\_peptide  
 <222> 35..112  
 <223> Von Heijne matrix  
 score 4.09999990463257  
 seq SLASFLLLTFLPS/LP

```

<400> 574
accttctcttc tctccttcttt tcttccctc cttc atg tct ttc tct tcc tct ctc      55
                                Met Ser Phe Ser Ser Ser Leu
                                -25                      -20
cct cca tct ctc cct cct tcc ctc gct tcc ttc ctc ctt ttg acc ttc      103
Pro Pro Ser Leu Pro Pro Ser Leu Ala Ser Phe Leu Leu Leu Thr Phe
                    -15                      -10                      -5
ctt cct tcc ctc cct cgg      121
Leu Pro Ser Leu Pro Arg
                1

```

<210> 575  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 77..391

<221> sig\_peptide  
 <222> 77..214  
 <223> Von Heijne matrix  
 score 4.09999990463257  
 seq GCAPLRWVPQIRG/CP

<221> misc\_feature  
 <222> 31..32,314  
 <223> n=a, g, c or t

```

<400> 575
aaaaactgts sagacttttg ccggtccatt nncrctatct ctccccactc tgggtgtcct      60
acccaaggcg ctgtct atg cgt gcc cag ggc ctg tcc tgc gga tac cca gct      112
                                Met Arg Ala Gln Gly Leu Ser Cys Gly Tyr Pro Ala
                                -45                      -40                      -35
cgc ccc ttg cag ccc ttt tta gag cat ctc gcg ggc tct ggc atc acc      160
Arg Pro Leu Gln Pro Phe Leu Glu His Leu Ala Gly Ser Gly Ile Thr

```

309

```

          -30          -25          -20
aag cgc aca gcc ccg ggc tgc gct ccc cta agg tgg gtc cct cag atc      208
Lys Arg Thr Ala Pro Gly Cys Ala Pro Leu Arg Trp Val Pro Gln Ile
          -15          -10          -5
cgg ggc tgt cca tta acc agg ctg gcc caa aga ggc gca gac act cga      256
Arg Gly Cys Pro Leu Thr Arg Leu Ala Gln Arg Gly Ala Asp Thr Arg
          1          5          10
acc cgg gaa aac tta ttt tat tct cgg ttc ccg ggg ttg cag ctg cca      304
Thr Arg Glu Asn Leu Phe Tyr Ser Arg Phe Pro Gly Leu Gln Leu Pro
          15          20          25          30
gcg gct gak nac agt gcg tcc gct ttg tct ctc tgc act ccc cgc agc      352
Ala Ala Xaa Xaa Ser Ala Ser Ala Leu Ser Leu Cys Thr Pro Arg Ser
          35          40          45
ccc cct ctc ccg ctt cct ctc ccg att aac tcc ccc ggg      391
Pro Pro Leu Pro Leu Pro Leu Pro Ile Asn Ser Pro Gly
          50          55

```

&lt;210&gt; 576

&lt;211&gt; 288

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 133..288

&lt;221&gt; sig\_peptide

&lt;222&gt; 133..243

&lt;223&gt; Von Heijne matrix

score 4.09999990463257

seq SISFLPFQASIFG/KT

&lt;400&gt; 576

```

aaaggcacag cgcgggcgca ggcgcccaga ggcgacagga gacctcaggc ccagactcca      60
ctccccagct gtgaaaggac tgctggccag accccaagc tagcccgcca ggcctccata      120
gagctgcccc gc atg gct gca tcc agt acc agt cat ctt aaa aat aaa aca      171
          Met Ala Ala Ser Ser Thr Ser His Leu Lys Asn Lys Thr
          -35          -30          -25
aaa acc ttc ctt gcc ccc atg acc aac tgc cac tca att tcc ttt ctt      219
Lys Thr Phe Leu Ala Pro Met Thr Asn Cys His Ser Ile Ser Phe Leu
          -20          -15          -10
cct ttc caa gca agt att ttt gga aag act cgt ctg cag tca ctg agg      267
Pro Phe Gln Ala Ser Ile Phe Gly Lys Thr Arg Leu Gln Ser Leu Arg
          -5          1          5
cct tcc cac cct tac ccc cac      288
Pro Ser His Pro Tyr Pro His
          10          15

```

&lt;210&gt; 577

&lt;211&gt; 264

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 134..262

&lt;221&gt; sig\_peptide

&lt;222&gt; 134..250

&lt;223&gt; Von Heijne matrix

score 4.09999990463257

seq FXSCXCVSTLAYT/KG

310

```

<400> 577
attacacagt agagggagga agctaaagga agtctatgga caggtgaggg agggkgagac      60
tggggaattt tctgattgtt cagaggaatc ttgaagatga tggaaatatc agatgtgcta      120
aagtttccta gta atg ccc aag gat gct gac ctg gct ttc agt gct tca      169
          Met Pro Lys Asp Ala Asp Leu Ala Phe Ser Ala Ser
                    -35                      -30

ttg ttt gaa aga gca gag tcc ctt tat act ctg att tca aaa ttt ktt      217
Leu Phe Glu Arg Ala Glu Ser Leu Tyr Thr Leu Ile Ser Lys Phe Xaa
          -25                      -20                      -15

tct tgt dtk tgt gtg tct acc ttg gca tat act aaa gga agg ggg gg      264
Ser Cys Xaa Cys Val Ser Thr Leu Ala Tyr Thr Lys Gly Arg Gly
          -10                      -5                      1

```

```

<210> 578
<211> 205
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 115..204

<221> sig_peptide
<222> 115..198
<223> Von Heijne matrix
      score 4.09999990463257
      seq MPFLFLTLFHCLG/RR

```

```

<221> misc_feature
<222> 94
<223> n=a, g, c or t

```

```

<400> 578
tgtagaaata cagwtgatgt ttaatagtga tcttgatgcc tatacccttg caaactccac      60
ttcttagttc cagttacttt attgtasytt tttnttgyt ytttactgtg tgtg atg      117
                                Met
ttt gtg aat aga acc tgt ttt aat tct tcc ttt cca atc tgg atg cct      165
Phe Val Asn Arg Thr Cys Phe Asn Ser Ser Phe Pro Ile Trp Met Pro
          -25                      -20                      -15

ttt ctt ttt ctt aca tta ttc cac tgc tta gga cgt cgg g      205
Phe Leu Phe Leu Thr Leu Phe His Cys Leu Gly Arg Arg
          -10                      -5                      1

```

```

<210> 579
<211> 214
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 25..213

<221> sig_peptide
<222> 25..135
<223> Von Heijne matrix
      score 4.09999990463257
      seq HFLXAVSASSSXA/CL

```

```

<400> 579
gcctcctctw gcgctgtcct gtta atg gyg ggc agt agc cgc tgm vkg gga      51
          Met Xaa Gly Ser Ser Arg Xaa Xaa Gly
                    -35                      -30

```

311

```

ttg cag ata acc gct tcc cgc acg ggg aaa gtc tac cct gcc tgc cac      99
Leu Gln Ile Thr Ala Ser Arg Thr Gly Lys Val Tyr Pro Ala Cys His
      -25                      -20                      -15
ttt ctg skc gcc gtc agc gcc agt agc tcg cma gca tgt ctg tgg tac      147
Phe Leu Xaa Ala Val Ser Ala Ser Ser Ser Xaa Ala Cys Leu Trp Tyr
      -10                      -5                      1
cgc cca atm gct cgc aga ccg gct ggc ccc ggg ggg tca ctc agt tcg      195
Arg Pro Ile Ala Arg Arg Pro Ala Gly Pro Gly Gly Ser Leu Ser Ser
5                      10                      15                      20
gca caa gta cat cca gca g
Ala Gln Val His Pro Ala
      25

```

<210> 580  
 <211> 328  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 28..327  
  
 <221> sig\_peptide  
 <222> 28..105  
 <223> Von Heijne matrix  
 score 4.09999990463257  
 seq VTFWLLCRICTFG/FH

```

<400> 580
tgtttgatgat cagtatccaa aggcaaa atg att ttg ttt gac cat tta cat tgt      54
      Met Ile Leu Phe Asp His Leu His Cys
      -25                      -20
tca gca tca gga gtg act ttc tgg ttg ctt tgc agg atc tgt acg ttt      102
Ser Ala Ser Gly Val Thr Phe Trp Leu Leu Cys Arg Ile Cys Thr Phe
      -15                      -10                      -5
ggg ttt cat ggt ttt tct aaa tac aca gtt tca cgt gga aca cag cag      150
Gly Phe His Gly Phe Ser Lys Tyr Thr Val Ser Arg Gly Thr Gln Gln
1                      5                      10                      15
ggg gca gga avg tgv dgt gga tta cac cag aac tgg gaa cag tgg agg      198
Gly Ala Gly Xaa Xaa Xaa Gly Leu His Gln Asn Trp Glu Gln Trp Arg
      20                      25                      30
ggg ctt gtt ggg aag tct agt tct gcc gca gtt gtt ttc tgc ctt acs      246
Gly Leu Val Gly Lys Ser Ser Ser Ala Ala Val Val Phe Cys Leu Thr
      35                      40                      45
ttt gac ttg gtt acc agc ttt caa tta gca agt gca att gaa agt aca      294
Phe Asp Leu Val Thr Ser Phe Gln Leu Ala Ser Ala Ile Glu Ser Thr
      50                      55                      60
cat ttc cat gct ggg cgc gat ggc tca cac ctg t
His Phe His Ala Gly Arg Asp Gly Ser His Leu
      65                      70

```

<210> 581  
 <211> 356  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 264..356  
  
 <221> sig\_peptide  
 <222> 264..350  
 <223> Von Heijne matrix

score 4.09999990463257  
seq LLLFPASLRLLCV/HP

<221> misc\_feature  
<222> 146  
<223> n=a, g, c or t

<400> 581  
gtckcatttt gcctttgwaa tggaagtcac ttccaagtgt ctgttctcta ggttttcctt 60  
tttttctctt ttagaaattg gacacttcaa taaaatttgt aattacgtcc atctgwtga 120  
htattwgmatt tyratgksca tatctnstgc cagattgttaa actccgcgag tgcacatata 180  
agatccatta tggttctcat catatcccta gctcctagcg cagtgcgggg cacgtataag 240  
tgctcgaaaag ctcccacgtg gtg atg gag cta agc ttg ccc cct tcc atg tgt 293  
Met Glu Leu Ser Leu Pro Pro Ser Met Cys  
-25 -20  
gac tac cca amt ttc tgt ctc ctc ctc ttc ccg gcc tct ctc aga ctc 341  
Asp Tyr Pro Xaa Phe Cys Leu Leu Leu Phe Pro Ala Ser Leu Arg Leu  
-15 -10 -5  
ctc tgt gtg cat ccc 356  
Leu Cys Val His Pro  
1

<210> 582  
<211> 239  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 159..239

<221> sig\_peptide  
<222> 159..218  
<223> Von Heijne matrix  
score 4.09999990463257  
seq TVGCAGLAGSCR/IS

<400> 582  
agttcctggg ctcccgcgga gsatgagacg ttgtgaatta gatgtgagaa gagggacgct 60  
tggctctgca ccaccaagac cccacaggat cgatgcaccc acccctgctg atgaccatga 120  
ccatctaaar gggaaacatc atttgagggg ccctactc atg gat cag aag ccc ctc 176  
Met Asp Gln Lys Pro Leu  
-20 -15  
ttc act gtg ggg tgt gct ggg ttg gcg ggc agt tgc cgt gga atc agt 224  
Phe Thr Val Gly Cys Ala Gly Leu Ala Gly Ser Cys Arg Gly Ile Ser  
-10 -5 1  
ttc ctc agg acc cgc 239  
Phe Leu Arg Thr Arg  
5

<210> 583  
<211> 144  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 8..142

<221> sig\_peptide  
<222> 8..76  
<223> Von Heijne matrix

score 4.09999990463257  
seq FILLLLIQDLTMS/PT

```
<400> 583
ttttaaa atg tca gtt aat gmt att ttt att ttc tat ttt atc tta tta      49
      Met Ser Val Asn Xaa Ile Phe Ile Phe Tyr Phe Ile Leu Leu
            -20            -15            -10
tta ttg ata caa gat ctc act atg tca ccc act gct gga atg cag tgg      97
Leu Leu Ile Gln Asp Leu Thr Met Ser Pro Thr Ala Gly Met Gln Trp
            -5            1            5
cat aat cat ggc cca cca caa gcc ttg cct tgc cca ctg aga abc cc      144
His Asn His Gly Pro Pro Gln Ala Leu Pro Cys Pro Leu Arg Xaa
      10            15            20
```

<210> 584  
<211> 282  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 47..280  
  
<221> sig\_peptide  
<222> 47..181  
<223> Von Heijne matrix  
score 4.09999990463257  
seq ICLGSPLAECLLG/XX

<221> misc\_feature  
<222> 183,210  
<223> n=a, g, c or t

```
<400> 584
ccttgtttaa gccgtgatcg tgacctcacc atgtgtagac agtgag atg tca ttt      55
                        Met Ser Phe
                        -45
ctc aat gtg gac atc aca gat tgc ctg tat aac ccc agt gtg tgt ccc      103
Leu Asn Val Asp Ile Thr Asp Cys Leu Tyr Asn Pro Ser Val Cys Pro
      -40            -35            -30
gtg gct cag agc agt ctg acc tgt gac ttc ata gat ggt atc tgc ttg      151
Val Ala Gln Ser Ser Leu Thr Cys Asp Phe Ile Asp Gly Ile Cys Leu
      -25            -20            -15
ggg tgc cct ttg gct gag tgt ctg ctt ggt gna gwa wkw ksc att ttk      199
Gly Ser Pro Leu Ala Glu Cys Leu Leu Gly Xaa Xaa Xaa Xaa Ile Xaa
      -10            -5            1            5
ggr atc aat rns cym tgc ttt ccg tgt ggt gtg aag tgc gca ggt gtg      247
Gly Ile Asn Xaa Xaa Cys Phe Pro Cys Gly Val Lys Cys Ala Gly Val
      10            15            20
gtc ttg ggg ctg agc acc ctg tgg tat gtt gta gc      282
Val Leu Gly Leu Ser Thr Leu Trp Tyr Val Val
      25            30
```

<210> 585  
<211> 388  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 242..388

&lt;221&gt; sig\_peptide

&lt;222&gt; 242..352

&lt;223&gt; Von Heijne matrix

score 4.09999990463257

seq FTFLSPSFHSHVHL/SE

&lt;400&gt; 585

tgcattttta aaaatagcta gaagaaaaga actttaatat tcccaaaaca aataaaatat 60

aaatgtttga ggtgaggat atcccaatta ccttgatttg gttattattc attgtataca 120

gttttcaaaa tatcacatgt acccccaaaa tatgtaaaac tgttatatac aaataaataa 180

caaaactaaa aataacagct gtgcaaacat ttttaaaagg cttgctttaa atgggtttca 240

c atg aaa gta gga aag gac tct ctg gag tct tta cca tct tta tgt gag 289

Met Lys Val Gly Lys Asp Ser Leu Glu Ser Leu Pro Ser Leu Cys Glu

-35

-30

-25

aaa cac att ggt ccc agt ggt ctc ttt acc ttt ctt agt cca tcc ttt 337

Lys His Ile Gly Pro Ser Gly Leu Phe Thr Phe Leu Ser Pro Ser Phe

-20

-15

-10

cac tct gta cat ctt tct gaa ctc aat gaa tta tac act att gct gcc 385

His Ser Val His Leu Ser Glu Leu Asn Glu Leu Tyr Thr Ile Ala Ala

-5

1

5

10

ggg 388

Gly

&lt;210&gt; 586

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 346..435

&lt;221&gt; sig\_peptide

&lt;222&gt; 346..396

&lt;223&gt; Von Heijne matrix

score 4.09999990463257

seq VLISASLLRASQL/KI

&lt;221&gt; misc\_feature

&lt;222&gt; 170

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 586

tgtgctgtgt ggtaggaga aggaggatg ggagagagaa ggggaaggaa tgaggcatgg 60

agagagatca caaccatcgt ctcaatgaag cagcagcaca cacaggatg tgtggctcgcw 120

ccaagtccag gggagagagt ttaaaggcgg gatgatcata tgtgaagdhn tggcagcacc 180

aatatggcac tgtcaaagta aaagagaaat agatctgaac tggattttaa tgagaataat 240

agcaaatatt aacatttctt agatagtttg atattttattc tggaaagtatc gctaccaaca 300

tcaacatctg ggaaagcdag tgggcatcaa aatcctacct ggcta atg gaa agc aaa 357

Met Glu Ser Lys

-15

gtt tta atc agt gca tca ctc cta cgg gcc tct caa tta aaa ata aaa 405

Val Leu Ile Ser Ala Ser Leu Leu Arg Ala Ser Gln Leu Lys Ile Lys

-10

-5

1

tgr aac aaa atg aca aac ttc tta att ttg t 436

Xaa Asn Lys Met Thr Asn Phe Leu Ile Leu

5

10

&lt;210&gt; 587

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
 <221> CDS  
 <222> 24..377

<221> sig\_peptide  
 <222> 24..95  
 <223> Von Heijne matrix  
 score 4.09999990463257  
 seq RLPMLSLFRGSHX/XF

<400> 587  
 tcctgtcctg ggcgtacgtc aag atg gcg gcg tct gta tta aac acc gtg ctg 53  
 Met Ala Ala Ser Val Leu Asn Thr Val Leu  
 -20 -15  
 agg cgg ctt cct atg cta tct ctc ttc cga ggt tct cay vvg rbg ttc 101  
 Arg Arg Leu Pro Met Leu Ser Leu Phe Arg Gly Ser His Xaa Xaa Phe  
 -10 -5 1  
 agg ttc ccc tcc aga ctc ttt gca cca aag ctc cct ctg agg aag att 149  
 Arg Phe Pro Ser Arg Leu Phe Ala Pro Lys Leu Pro Leu Arg Lys Ile  
 5 10 15  
 ctt tgt cct cag ttc cca ttt ctc ctt ata agg atg agc cct gga aat 197  
 Leu Cys Pro Gln Phe Pro Phe Leu Leu Ile Arg Met Ser Pro Gly Asn  
 20 25 30  
 atc tgg aat cag aag aat acc agg agc gat atg gtt ctc gcc ccg tct 245  
 Ile Trp Asn Gln Lys Asn Thr Arg Ser Asp Met Val Leu Ala Pro Ser  
 35 40 45 50  
 ggg ctg act acc gcc gca acc aca agg gtg gtg tac ccc cac agc gga 293  
 Gly Leu Thr Thr Ala Ala Thr Thr Arg Val Val Tyr Pro His Ser Gly  
 55 60 65  
 ctc gga aga cat gta ttc gtc gga ata aag ttg ttg gga atc cct gcc 341  
 Leu Gly Arg His Val Phe Val Gly Ile Lys Leu Leu Gly Ile Pro Ala  
 70 75 80  
 cca tct gtc gag atc aca agt tgc atg ttg act tta g 378  
 Pro Ser Val Glu Ile Thr Ser Cys Met Leu Thr Leu  
 85 90

<210> 588  
 <211> 413  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 185..412

<221> sig\_peptide  
 <222> 185..238  
 <223> Von Heijne matrix  
 score 4.09999990463257  
 seq TLLTCLXLXGGEG/WK

<221> misc\_feature  
 <222> 218,224  
 <223> n=a, g, c or t

<400> 588  
 aggaggcgca gttactgata tagccaaggt gggacactac tggagggagc tagaagggat 60  
 cagccagcca tgcctccagt tcaggtactt ggcattgcta agctcagaac aggacttgcc 120  
 agtgtctaga tgaaaaagag gagagatctc aagagggata accaattggc tggcaaagta 180  
 acaa atg aaa agt aac ctg act cta ttg acc tgc tta ncc ctg nat ggg 229  
 Met Lys Ser Asn Leu Thr Leu Leu Thr Cys Leu Xaa Leu Xaa Gly

316

-15	-10	-5	
ggg gaa gga tgg aaa gga gca gct gtt tgc ttt gaa acg gtg gaa cag			277
Gly Glu Gly Trp Lys Gly Ala Ala Val Cys Phe Glu Thr Val Glu Gln			
1	5	10	
ttt tgc agc ctt aga aaa tgg cat gta aca tac cta rcc aaa gac agc			325
Phe Cys Ser Leu Arg Lys Trp His Val Thr Tyr Leu Xaa Lys Asp Ser			
15	20	25	
gga ctc tgt caa caa cag gag aag ctc tat acg aaa ttc ttg gtc tgc			373
Gly Leu Cys Gln Gln Gln Glu Lys Leu Tyr Thr Lys Phe Leu Val Cys			
30	35	40	45
ata aag gga gca tca aat gaa gaa att aag aaa acc tac a			413
Ile Lys Gly Ala Ser Asn Glu Glu Ile Lys Lys Thr Tyr			
50	55		

&lt;210&gt; 589

&lt;211&gt; 210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 138..209

&lt;221&gt; sig\_peptide

&lt;222&gt; 138..179

&lt;223&gt; Von Heijne matrix

score 4.09999990463257

seq LASPCVLVQGSX/SL

&lt;221&gt; misc\_feature

&lt;222&gt; 78,80,118

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 589

gaagataata ataataata ttataataat gatgatgatt ccaaggaaaa aacctacagc 60

gaatgttcca tttctacsn gcacgcagac actctcccta acactgataa cctgagcncc 120

cagcactgga cggaaga atg ctg gcg tct ccg tgt gta ctg gtt cag ggt 170

Met Leu Ala Ser Pro Cys Val Leu Val Gln Gly

-10

-5

tct ggs bcc agc ctt gtc agg acc ccc tgg tgt cca gag c 210

Ser Gly Xaa Ser Leu Val Arg Thr Pro Trp Cys Pro Glu

1

5

10

&lt;210&gt; 590

&lt;211&gt; 178

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 40..177

&lt;221&gt; sig\_peptide

&lt;222&gt; 40..96

&lt;223&gt; Von Heijne matrix

score 4.09999990463257

seq ILLLLITIIYSYL/ES

&lt;400&gt; 590

acaaggactg aaccagaagg aagaggacag agcaaagcc atg aac atc atc cta 54

Met Asn Ile Ile Leu

-15

317

```

gaa atc ctt ctg ctt ctg atc acc atc atc tac tcc tac ttg gag tcg      102
Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr Ser Tyr Leu Glu Ser
          -10                      -5                      1
ttg gtg aag ttt ttc att cct cag agg aga aaa tct gtg gct ggg gag      150
Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys Ser Val Ala Gly Glu
          5                      10                      15
att gtt ctc att act gga gct ggg cat g      178
Ile Val Leu Ile Thr Gly Ala Gly His
      20                      25

```

&lt;210&gt; 591

&lt;211&gt; 308

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 149..307

&lt;221&gt; sig\_peptide

&lt;222&gt; 149..265

&lt;223&gt; Von Heijne matrix

score 4.09999990463257

seq PSLIAGLFVGCCLA/GY

&lt;221&gt; misc\_feature

&lt;222&gt; 272

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 591

```

gcgagacggc tgggcgccga gtgggacagc gctgggtgcgg agactgcttc cggactccag      60
gtaccgcgct tggcggcagc tggccccaga cttctgtctt ttcaagmkgc aagtraargc      120
tcggggctgc rraattgcaa ccttgcca atg gac ctg atc ggt ttt ggt tat      172
                               Met Asp Leu Ile Gly Phe Gly Tyr
                               -35
gca gcc ctc gtg aca ttt gga agc att ttt gga tat aag cdg aga ggt      220
Ala Ala Leu Val Thr Phe Gly Ser Ile Phe Gly Tyr Lys Xaa Arg Gly
      -30                      -25                      -20
ggt gtt ccg tct ttg att gct ggt ctt ttt gtd gga tgt ttg gcc ggc      268
Gly Val Pro Ser Leu Ile Ala Gly Leu Phe Val Gly Cys Leu Ala Gly
      -15                      -10                      -5                      1
tat nsa gct tac cgt gtc tcc aat gac aaa cga gat gta a      308
Tyr Xaa Ala Tyr Arg Val Ser Asn Asp Lys Arg Asp Val
      5                      10

```

&lt;210&gt; 592

&lt;211&gt; 219

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 16..219

&lt;221&gt; sig\_peptide

&lt;222&gt; 16..72

&lt;223&gt; Von Heijne matrix

score 4.09999990463257

seq XTFLAAXRRLVTG/QT

&lt;400&gt; 592

```

acagttcatc cggaa atg gag ggg gtc gct ttv btc acc ttc ctc gct gcg      51

```

318

Met Glu Gly Val Ala Xaa Xaa Thr Phe Leu Ala Ala  
 -15 -10  
 sgg cgg cgg ttg gta acc ggt cag acc agc ccg aga ggg acc tgg tgc 99  
 Xaa Arg Arg Leu Val Thr Gly Gln Thr Ser Pro Arg Gly Thr Trp Cys  
 -5 1 5  
 ctg tac cca ggc ttc tgt cgc tct gtc gcc tgc gct atg ccc tgc tgt 147  
 Leu Tyr Pro Gly Phe Cys Arg Ser Val Ala Cys Ala Met Pro Cys Cys  
 10 15 20 25  
 agt cac agg agc tgt aga gag gac ccc ggt aca tct gaa agc cgg gaa 195  
 Ser His Arg Ser Cys Arg Glu Asp Pro Gly Thr Ser Glu Ser Arg Glu  
 30 35 40  
 atg gtg cgt gtg cgg gac cac ggg 219  
 Met Val Arg Val Arg Asp His Gly  
 45

<210> 593  
 <211> 215  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 105..215

<221> sig\_peptide  
 <222> 105..167  
 <223> Von Heijne matrix  
 score 4  
 seq IGLIGLTVPCGWG/SL

<400> 593  
 aggaacattt tttattttat ttttatagag ataggtctc tttctgtagc ccaagctgga 60  
 gtactgtctt agtctgtttt tatgctgctg ataacgacat accc atg act ggg caa 116  
 Met Thr Gly Gln  
 -20  
 ttt aca aaa gaa ata ggt tta att gga ctt aca gtt cca tgt ggc tgg 164  
 Phe Thr Lys Glu Ile Gly Leu Ile Gly Leu Thr Val Pro Cys Gly Trp  
 -15 -10 -5  
 gga agc ctc ata acc atg gca gaa ggc agg gag gag caa gtc acg tct 212  
 Gly Ser Leu Ile Thr Met Ala Glu Gly Arg Glu Glu Gln Val Thr Ser  
 1 5 10 15  
 ggg 215  
 Gly

<210> 594  
 <211> 161  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 89..160

<221> sig\_peptide  
 <222> 89..130  
 <223> Von Heijne matrix  
 score 4  
 seq HLGFIILSFHGLIA/NF

<400> 594  
 ctccatagtt ttaccttctc caggatgttg tatagatgga attgtacagt atgtagcctt 60  
 ttcacattgg cttctttcac taaataac atg cat tta gga ttc att ctt tct 112  
 Met His Leu Gly Phe Ile Leu Ser



320

Gln Pro Leu Pro Pro Gly Phe Lys Pro Xaa Ser Cys Leu Ser Leu Leu  
                           -15                          -10                          -5  
 agt aay tsa gat tac agg cat gca cca cca ttc ctg gct aat ttt kgw 380  
 Ser Asn Xaa Asp Tyr Arg His Ala Pro Pro Phe Leu Ala Asn Phe Xaa  
                   1                                  5                                  10  
 att ttt cat aga gat gga gtt tca cca 407  
 Ile Phe His Arg Asp Gly Val Ser Pro  
       15                                  20

&lt;210&gt; 597

&lt;211&gt; 274

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 90..272

&lt;221&gt; sig\_peptide

&lt;222&gt; 90..254

&lt;223&gt; Von Heijne matrix

score 4

seq LHQGLCLPQRVHC/SL

&lt;400&gt; 597

gctgaccgrg cgcacscgc ccccgsgcc atcttcccga ccgcgagccg tccaggtctc 60  
 agtgctrtgc cccccccaga gcctagagg atg ttt cat ggg atc cca gcc acg 113  
                                   Met Phe His Gly Ile Pro Ala Thr  
                                   -55                                  -50  
 ccg ggc ata gga gcc cct ggg aac aag ccg gag ctg tat gag gta cga 161  
 Pro Gly Ile Gly Ala Pro Gly Asn Lys Pro Glu Leu Tyr Glu Val Arg  
                   -45                                  -40                                  -35  
 caa cat ggc aga gct gtt tgc ggt ggt gaa gac aat gca agc cct gga 209  
 Gln His Gly Arg Ala Val Cys Gly Gly Glu Asp Asn Ala Ser Pro Gly  
                   -30                                  -25                                  -20  
 gaa ggc cta cat caa gga ctg tgt ctc ccc cag cga gta cac tgc agc 257  
 Glu Gly Leu His Gln Gly Leu Cys Leu Pro Gln Arg Val His Cys Ser  
                   -15                                  -10                                  -5                                  1  
 ctg ctc ccg gct cct gg 274  
 Leu Leu Pro Ala Pro  
                                   5

&lt;210&gt; 598

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 343..417

&lt;221&gt; sig\_peptide

&lt;222&gt; 343..408

&lt;223&gt; Von Heijne matrix

score 4

seq LFLSVLNFLFLLS/FS

&lt;400&gt; 598

gcattctagaa gtacaagttg atgattattg tccatttgat agagacactg gaagggtgtc 60  
 agtgtaaaca ctggccatgt gaagattgag cctgttgatg gtttcttttg tatcatagga 120  
 tgccacgtca ccaactaggg aattctgccc aatcagttga gccaaatagt gctgtcctat 180  
 tgtaaaattg tttaatctgt gtgcttgtgt gtgtgcttgt cagaatttgt gaatcataga 240  
 attgttttaa ctggaagaag accccaaga tcacttgctt caacccttc cttcctctct 300

321

```

tttccagaga ggttgcaatt tacttgagct gtgactagga tt atg cca cat tct      354
                                   Met Pro His Ser
                                   -20
ttt gta agt tgt aac cta ttt ttg tct gtr ttg aat ttc ctt ttt ttg      402
Phe Val Ser Cys Asn Leu Phe Leu Ser Val Leu Asn Phe Leu Phe Leu
                                   -15          -10          -5
cta agc ttt agc aca      417
Leu Ser Phe Ser Thr
1

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<210> 599  
 <211> 329  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 240..329

<221> sig\_peptide  
 <222> 240..317  
 <223> Von Heijne matrix  
 score 4  
 seq HLLLLSTLATIAG/NI

```

<400> 599
agaagactgg aactcagcaa gaaagtgatg aaaatgctct gagacataga aactctagac      60
ggcagcatag aaatggaaga aaaataccca gccagatcca gctcagagcc aagaaaatgt      120
acacaccaga tccccagcat tccaattat cacaaaaggt gccttaattt ctatctacaa      180
gacaacccta caatcctcac aggccctgag ctgagtatag aaagtcttct ggagtccat      239
atg gct gtt ttt ctc caa aag agg aaa cac aca atg aga cac cac cta      287
Met Ala Val Phe Leu Gln Lys Arg Lys His Thr Met Arg His His Leu
      -25          -20          -15
ctc ctc agt aca ctg gct act ata gca ggc aac att tac aga      329
Leu Leu Ser Thr Leu Ala Thr Ile Ala Gly Asn Ile Tyr Arg
-10          -5          1

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<210> 600  
 <211> 311  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 169..309

<221> sig\_peptide  
 <222> 169..246  
 <223> Von Heijne matrix  
 score 4  
 seq PVAEALLRAVFG/VV

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<400> 600
acagaggcgg caagactagg gtggaggaaa gctcaagggc catcgctggg tgcttcggtg      60
gcgggcagaa acgggactgg cagtgccac acgtgtgcgt tctccccgtc cgcccgaagg      120
agctacctgt gcaccctgcc tccggctctc ctgagcagag agatcctg atg gct gac      177
                                   Met Ala Asp
                                   -25
tca gaa gca ctc ccc tcc ctt gct ggg gac cca gtg gct gtg gaa gcc      225
Ser Glu Ala Leu Pro Ser Leu Ala Gly Asp Pro Val Ala Val Glu Ala
      -20          -15          -10
ttg ctc cgg gcc gtg ttt ggg gtt gtt gtg gat gag gcc att cag aaa      273
Leu Leu Arg Ala Val Phe Gly Val Val Val Asp Glu Ala Ile Gln Lys

```

322

-5 1 5  
 gga acc agt gtc tcc cag aag gtc tgc smg tgg aag ga 311  
 Gly Thr Ser Val Ser Gln Lys Val Cys Xaa Trp Lys  
 10 15 20

<210> 601  
 <211> 420  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 159..419

<221> sig\_peptide  
 <222> 159..266  
 <223> Von Heijne matrix  
 score 4  
 seq LAELPVSSPLCHA/VL

<221> misc\_feature  
 <222> 365..366  
 <223> n=a, g, c or t

<400> 601  
 ctaagccttt tctaccctct tctcaaagta gagccgaata tgattcagag gagagtctgg 60  
 gaagtgatga tgatgacaat gatgatgatg atgatgtttt agcatcagat ttccatctcc 120  
 aggaacattc taattcaaat tcatatagtt ggtccttg atg cgg ttg gcg atg gtg 176  
 Met Arg Leu Ala Met Val  
 -35  
 caa ttg gtg ctc aac aat ttg aag act ttt tat ccc ttc gca gat cat 224  
 Gln Leu Val Leu Asn Asn Leu Lys Thr Phe Tyr Pro Phe Ala Asp His  
 -30 -25 -20 -15  
 gat ctt gca gag ctt cca gtt agt tca cct ctt tgt cat gcg gtt cta 272  
 Asp Leu Ala Glu Leu Pro Val Ser Ser Pro Leu Cys His Ala Val Leu  
 -10 -5 1  
 aaa act ctt caa tgt tgg gaa caa gtt ctt ctc cga cga ctt gaa atc 320  
 Lys Thr Leu Gln Cys Trp Glu Gln Val Leu Leu Arg Arg Leu Glu Ile  
 5 10 15  
 cat ggt ggg cca cct caa aat tat atc gca agt cat acc gcc gan nag 368  
 His Gly Gly Pro Pro Gln Asn Tyr Ile Ala Ser His Thr Ala Xaa Xaa  
 20 25 30  
 agt ttg tct gca ggt cct gca att ctt cgc cac aaa gct tta ctg gaa 416  
 Ser Leu Ser Ala Gly Pro Ala Ile Leu Arg His Lys Ala Leu Leu Glu  
 35 40 45 50  
 cct a 420  
 Pro

<210> 602  
 <211> 463  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 311..463

<221> sig\_peptide  
 <222> 311..370  
 <223> Von Heijne matrix  
 score 4  
 seq LFILXYFXXYTLS/SG

<221> misc\_feature  
 <222> 353..354  
 <223> n=a, g, c or t

<400> 602  
 tggcaaaagac aaagagttga aacttatatg gcagaatcag agctcacaat ggtgctgggc 60  
 atttgggggtt ttgagtcttc tctgaagatc tttagacatct ttagctttat tctacaggcc 120  
 acggggaact actggatatt tgaaagaagg aatttatctg tctatcttct atttatctat 180  
 ctgtaatcta tcatctaate taggaaatga tagatctagg aagatgatag ctagataaat 240  
 atcagtcac ttcctatcat ctgggaaata gatttatatt gttttattat ttaattaat 300  
 taatttaaaa atg ttt aaa tta ttt tta ttt tta ttt att tta ttw tat 349  
 Met Phe Lys Leu Phe Leu Phe Leu Phe Ile Leu Xaa Tyr  
 -20 -15 -10  
 ttc nng vat tac act tta agt tct ggg ata tat gtg cag aat gtg cag 397  
 Phe Xaa Xaa Tyr Thr Leu Ser Ser Gly Ile Tyr Val Gln Asn Val Gln  
 -5 1 5  
 gtt tgt tac ata ggt ata cac atg cca tgg tgg ttt gct gca ccc atg 445  
 Val Cys Tyr Ile Gly Ile His Met Pro Trp Trp Phe Ala Ala Pro Met  
 10 15 20 25  
 aac ctg tca tct gca cta 463  
 Asn Leu Ser Ser Ala Leu  
 30

<210> 603  
 <211> 269  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 182..268

<221> sig\_peptide  
 <222> 182..244  
 <223> Von Heijne matrix  
 score 4  
 seq LIPLLSEILYALA/NI

<400> 603  
 tggttacaaa agtatcttga atttgataga gcttatgttg agaaataatt ttaaatcttt 60  
 taattccatt ttccatgaa ctttttgaag tccccgtata cataacttttt catggtgaga 120  
 acacttataa tctactgtca gcaattttca aatataaaat atattattaa ctgtagtcac 180  
 c atg ata tac agt aga tct ctt gaa ctt att cct ctt ttg tct gaa att 229  
 Met Ile Tyr Ser Arg Ser Leu Glu Leu Ile Pro Leu Leu Ser Glu Ile  
 -20 -15 -10  
 ttg tat gct ttg gcc aac atc tcc cca atc ccc cag acg g 269  
 Leu Tyr Ala Leu Ala Asn Ile Ser Pro Ile Pro Gln Thr  
 -5 1 5

<210> 604  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 297..350

<221> sig\_peptide  
 <222> 297..344  
 <223> Von Heijne matrix

score 4  
seq VIFYFVLFLGIMT/QR

<400> 604  
aagaacatta tatttttcaaa tggaataata ataccatcag tgaaataaat gttaaaattt 60  
ttagggcaga gattaatgcc caccagaaag gtaactttga tgagggtagc aagcatgctt 120  
tcactgaaaa gtattttttt ttcctctttt caagattctc ataattataa cccataaaac 180  
taagttagac ttgtttctta tgtgcattta tgatttaatt aacgagagta cactttgtat 240  
gacaaaatgc aattttaagg taaacactat ggagaataat ttcttttcct agtgaa atg 299  
Met  
gtg cac gtt ata ttt tat ttt gtt tta ttt cta ggg ata atg aca cag 347  
Val His Val Ile Phe Tyr Phe Val Leu Phe Leu Gly Ile Met Thr Gln  
-15 -10 -5 1  
cgg g 351  
Arg

<210> 605  
<211> 195  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 37..195  
  
<221> sig\_peptide  
<222> 37..111  
<223> Von Heijne matrix  
score 4  
seq LIYFFQLHSCCHD/KV

<400> 605  
agtgaagaat ctaagkccag agaggtggta gttaac atg cac aaa ttc ttt aga 54  
Met His Lys Phe Phe Arg  
-25 -20  
cat ttc tat tca gat ttt ctg att tat ttc ttt cag ctc cat tca tgt 102  
His Phe Tyr Ser Asp Phe Leu Ile Tyr Phe Phe Gln Leu His Ser Cys  
-15 -10 -5  
tgt cac gat aaa gtr act gcm cra agg gcc tat rtt cac tac agc agc 150  
Cys His Asp Lys Val Thr Ala Xaa Arg Ala Tyr Xaa His Tyr Ser Ser  
1 5 10  
ctc tta act cct tac ctc tct cag cac ccc tgc ccc cat ccc ggg 195  
Leu Leu Thr Pro Tyr Leu Ser Gln His Pro Cys Pro His Pro Gly  
15 20 25

<210> 606  
<211> 426  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 63..425  
  
<221> sig\_peptide  
<222> 63..140  
<223> Von Heijne matrix  
score 4  
seq LLRELRYLSAATG/HP

<221> misc\_feature  
<222> 174  
<223> n=a, g, c or t

<400> 606  
ggaggagggg ttttcagggt cgtaggacgc cggtgggcac cacgctcgga gaagacagga 60  
ca atg gcg gcc tta ggg tcc ccg tcg cac act ttt cga gga ctt ctg 107  
Met Ala Ala Leu Gly Ser Pro Ser His Thr Phe Arg Gly Leu Leu  
-25 -20 -15  
cgg gag ttg cgc tac ctg agc gcg gcc acc ggc cac cct atc gcg aca 155  
Arg Glu Leu Arg Tyr Leu Ser Ala Ala Thr Gly His Pro Ile Ala Thr  
-10 -5 1 5  
ccg cgg cct atc ggt acc ntt gtg aag gct ttc cgt gca cat cgg gtc 203  
Pro Arg Pro Ile Gly Thr Xaa Val Lys Ala Phe Arg Ala His Arg Val  
10 15 20  
acc agt gaa aag ttg tgc aga gcc caa cat gag ctt cat ttc caa gct 251  
Thr Ser Glu Lys Leu Cys Arg Ala Gln His Glu Leu His Phe Gln Ala  
25 30 35  
gcc acc tat ctc tgc ctc ctg cgt asa tcc gga aac atg tgg ccc tac 299  
Ala Thr Tyr Leu Cys Leu Leu Arg Xaa Ser Gly Asn Met Trp Pro Tyr  
40 45 50  
atc agg aat ttc atg gca agg gtg agc gct cgg tgg agg agt ctg ctg 347  
Ile Arg Asn Phe Met Ala Arg Val Ser Ala Arg Trp Arg Ser Leu Leu  
55 60 65  
gct tgg tgg gtc tca agt tgc ccc atc agc ctg gag gga agg gct ggg 395  
Ala Trp Trp Val Ser Ser Cys Pro Ile Ser Leu Glu Gly Arg Ala Gly  
70 75 80 85  
agc cat gaa cat gga gaa tat cct tgg atg c 426  
Ser His Glu His Gly Glu Tyr Pro Trp Met  
90 95

<210> 607  
<211> 161  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 71..160  
<221> sig\_peptide  
<222> 71..154  
<223> Von Heijne matrix  
score 4  
seq VSLFLLVVLHYHA/AV

<400> 607  
agttccggtc caggtctctg acttcgggct tggtcgctgg tggcgctcgga gccgagccgg 60  
actggtcagg atg atc acg gac gtg cag ctc gcc atc ttc gcc aac atg 109  
Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met  
-25 -20  
ctg ggc gtg tcg ctc ttc ttg ctt gtc gtt ctc tat cac tac gcg gcc 157  
Leu Gly Val Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Ala Ala  
-15 -10 -5 1  
gtg g 161  
Val

<210> 608  
<211> 357  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 283..357

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<221> sig_peptide
<222> 283..336
<223> Von Heijne matrix
      score 4
      seq LSFLCSLSQNALN/IS

<400> 608
tgaaccttgc tttatatacaa atcacttttt tggtatttga ggaacaagat aacattttct      60
tggcaggatt actatagtcc cccaacaag ctctaccama gaagataata gaacttattg      120
agcttaaata aattatagga magttcctga aaagtccaar gtaaatgtga agagaacccg      180
attctcttaa cctcacccaa cccagcactt gattctccct tgtttcctgg ttttcataca      240
cacactggga aaggamaagg aagaagaaac aaggatgtcg tt atg gct gaa gga      294
                                   Met Ala Glu Gly
                                   -15
gct ttg agc ttc ctt tgc tct tta tcg caa aat gca ttg aat att tcc      342
Ala Leu Ser Phe Leu Cys Ser Leu Ser Gln Asn Ala Leu Asn Ile Ser
               -10               -5               1
ctc att tct cgt aag      357
Leu Ile Ser Arg Lys
      5

<210> 609
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..201

<221> sig_peptide
<222> 133..180
<223> Von Heijne matrix
      score 4
      seq SFLLCFTLVGTQL/RN

<400> 609
ttatatgttc tgcttatggg actttgcatg ttctacaaac tacaagtatc tttttctact      60
ctgaattgaa tttagctctg tttacggttt tcttttctgt gagcagaagt tcttaatgat      120
tactgtagtc aa atg tat cca tct ttt ctt tta tgc ttc aca ctc gta ggg      171
               Met Tyr Pro Ser Phe Leu Leu Cys Phe Thr Leu Val Gly
               -15               -10               -5
act cag tta aga aat tct tcc tta gcc atg      201
Thr Gln Leu Arg Asn Ser Ser Leu Ala Met
      1               5

<210> 610
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..279

<221> sig_peptide
<222> 223..267
<223> Von Heijne matrix
      score 4
      seq SCTVGCATASSWG/CT

<400> 610

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327

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accgccttcc cacatcggat cgcagggctc ccaaaatggc gagtgagact gcgggggactc   60
gctgagcagc ggagggggag cgtgcagarm mgctgcggcc ctcacagtcc ggagcccggc   120
cgtgccgtgc cgtaggggaa atgcactttt ccattcccga aaccgagtcc cgcagcgggg   180
acagcggcgg ctccgcctac gtggcctata acattcacgt ga atg gag tcc tgc   234
                                     Met Glu Ser Cys
                                     -15

```

```

act gtc ggg tgc gct aca gcc agc tcc tgg ggc tgy acg agc agg gg   281
Thr Val Gly Cys Ala Thr Ala Ser Ser Trp Gly Cys Thr Ser Arg
   -10                -5                1

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<210> 611  
 <211> 241  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 28..240

<221> sig\_peptide  
 <222> 28..156  
 <223> Von Heijne matrix  
       score 4  
       seq AAWCSLVLSFCRL/HK

```

<400> 611
agcttccggg tttcctgggc tactacg atg gcg atg agt ttc gag tgg ccg tgg   54
                                     Met Ala Met Ser Phe Glu Trp Pro Trp
                                     -40                -35
cag tat cgc ttc cca ccc ttc ttt acg tta caa ccg aat gtg gac act   102
Gln Tyr Arg Phe Pro Pro Phe Phe Thr Leu Gln Pro Asn Val Asp Thr
               -30                -25                -20
cgg cag aag cag ctg gcc gcc tgg tgc tgc ctg gtc ctg tcc ttc tgc   150
Arg Gln Lys Gln Leu Ala Ala Trp Cys Ser Leu Val Leu Ser Phe Cys
               -15                -10                -5
cgc ctg cac aaa cag tcc agc atg acg gtg atg gaa gct cag gag agc   198
Arg Leu His Lys Gln Ser Ser Met Thr Val Met Glu Ala Gln Glu Ser
      1                5                10
ccg ctc ttc aac aac gtc aag cta cag cga aag ctt cct gtg g       241
Pro Leu Phe Asn Asn Val Lys Leu Gln Arg Lys Leu Pro Val
   15                20                25

```

<210> 612  
 <211> 176  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 106..174

<221> sig\_peptide  
 <222> 106..147  
 <223> Von Heijne matrix  
       score 3.90000009536743  
       seq RLHVHSLSPFSFA/CL

```

<400> 612
aagagccttg gaacatctct ctgaagaata aaacaaatct tttctgcatg tataatcgat   60
ataaatttga ttatattgta ctttttattt cgtgtgtgtg tgtac atg aga tta cat   117
                                     Met Arg Leu His
gta cat tcc ctt tct ccc ttt tcc ttt gct tgt ctc cct ttt ctg tcc   165
Val His Ser Leu Ser Pro Phe Ser Phe Ala Cys Leu Pro Phe Leu Ser

```

-10	-5	1	5	
ccc ccg ctg gg				176
Pro Pro Leu				
<210> 613				
<211> 342				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> 258..341				
<221> sig_peptide				
<222> 258..335				
<223> Von Heijne matrix				
score 3.90000009536743				
seq RMCILQLLSAVLY/RF				
<400> 613				
catttctatk aaaatacaaaa tttaaggctg tagatttaat atgtagtatg ttcattrrgt				60
tccaaataca ttctaatttc cactgtgatt tctwctttga ctcmtgaawt atttagvagg				120
tgwttttgwh ttabdwattt ctgactgtat ggggattttc tagttagttt wctactctta				180
atttgtcttc agagamaata ctccacaaga ttccagtctt tcaattttgt tgcaacttgc				240
tacaaacttg gcctaac atg ttg cat ttt wta tat atg atc caw gtg tgc				290
Met Leu His Phe Xaa Tyr Met Ile Xaa Val Cys				
-25 -20				
ttg gaa aga atg tgc att ctg caa ttg ttg agt gct gtg ttg tat aga				338
Leu Glu Arg Met Cys Ile Leu Gln Leu Leu Ser Ala Val Leu Tyr Arg				
-15 -10 -5 1				
ttt g				342
Phe				
<210> 614				
<211> 154				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> 48..152				
<221> sig_peptide				
<222> 48..137				
<223> Von Heijne matrix				
score 3.90000009536743				
seq VGLLDTPLGAVSA/HH				
<221> misc_feature				
<222> 17				
<223> n=a, g, c or t				
<400> 614				
agtcggagcg aaggvcntgg cggasagaac ggattgcagg gtcagcc atg tca tct				56
			Met Ser Ser	
			-30	
gag cct ccc cca cca cca cag ccc ccc acc cat caa gct tca gtc ggg				104
Glu Pro Pro Pro Pro Pro Gln Pro Pro Thr His Gln Ala Ser Val Gly				
-25 -20 -15				
ctg ctg gac acc ccc ctc gga gcc gtg agc gct cac cat ccc ctc tgc				152
Leu Leu Asp Thr Pro Leu Gly Ala Val Ser Ala His His Pro Leu Cys				
-10 -5 1 5				

cc

154

<210> 615  
 <211> 272  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 185..271

<221> sig\_peptide  
 <222> 185..244  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq FLTSISFLALVLW/NV

<400> 615  
 caactataat agctttttaaa cttgtttctc ttctcttttc cttcatttca gtccatctta 60  
 ttatctttga caaaataatt tctctgatgc ctgactgcct gcccccaac aacaaagctt 120  
 ttattatact tcttaactaa tcaactatwm cyttacccat ctagccaaag tagactaccc 180  
 atat atg ttt ctt gac cat gtc agg ttt tta acc tcc ata tct ttt ctt 229  
 Met Phe Leu Asp His Val Arg Phe Leu Thr Ser Ile Ser Phe Leu  
 -20 -15 -10  
 gct ctg gtc ctg tgg aat gtc ttt ctc aac tct acc cgt ctg g 272  
 Ala Leu Val Leu Trp Asn Val Phe Leu Asn Ser Thr Arg Leu  
 -5 1 5

<210> 616  
 <211> 114  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 36..113

<221> sig\_peptide  
 <222> 36..92  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq PALTSSELPALA/SQ

<400> 616  
 aggttttttag tcttgacctc ttgacctgct tatag atg aga gaa aag cca caa 53  
 Met Arg Glu Lys Pro Gln  
 -15  
 cca gcg ctc ctg act tca agt gar ctg cct gcc ttg gcc tct caa ata 101  
 Pro Ala Leu Leu Thr Ser Ser Glu Leu Pro Ala Leu Ala Ser Gln Ile  
 -10 -5 1  
 cat tgc cgc gtc c 114  
 His Cys Arg Val  
 5

<210> 617  
 <211> 171  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 56..169

<221> sig\_peptide  
 <222> 56..133  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq VPVLCIWRAWLRA/EV

<400> 617  
 aaaatgacga tttctcagga aatcatttcg actcctcttt ccctgcccaa ggagg atg 58  
 Met  
 ccc cac aac cac ttg gag gga gat gct ttg ctg aga gtc cct gtc ctc 106  
 Pro His Asn His Leu Glu Gly Asp Ala Leu Leu Arg Val Pro Val Leu  
 -25 -20 -15 -10  
 tgc atc tgg aga gct tgg ctc aga gct gag gtg gga ggg agg gct cct 154  
 Cys Ile Trp Arg Ala Trp Leu Arg Ala Glu Val Gly Gly Arg Ala Pro  
 -5 1 5  
 ctt cca ggt cgc atg gg 171  
 Leu Pro Gly Arg Met  
 10

<210> 618  
 <211> 240  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 160..240

<221> sig\_peptide  
 <222> 160..225  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq CLFWIXLPPHTCT/HT

<400> 618  
 caaaaaggaa aactgataat atcttaaaaa taatatTTaa ctgagtgtg gagaaagggg 60  
 attgaaatgt gagctccttt atatttttagc tttgccacgt cattgttttt ccctcagaaa 120  
 ctgtgaaata ctttaaatat gagttgttgg gaaagttaa atg aaa aat act ctt 174  
 Met Lys Asn Thr Leu  
 -20  
 tat tat aat ttt tgt tta ttt tgg att ytc cta cct ccc cac aca tgc 222  
 Tyr Tyr Asn Phe Cys Leu Phe Trp Ile Xaa Leu Pro Pro His Thr Cys  
 -15 -10 -5  
 aca cac aca gac aca cat 240  
 Thr His Thr Asp Thr His  
 1 5

<210> 619  
 <211> 257  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 97..255

<221> sig\_peptide  
 <222> 97..201  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq CTFLSLSLHPWGG/FF

<400> 619

331

```

acttcagaac tgggggagag ggagaggact ggagggcggga ggggtggccgc tggccagtgc      60
gcactctttc ctctgcatcc ccttcctgc ggcccc atg tgc ctg aac ccc gcc      114
                               Met Cys Leu Asn Pro Ala
                               -35                               -30
tgc tcg gga ccg ctt tcc ctc cgt tcc cct cgg ctt ccc cct ctc ttt      162
Cys Ser Gly Pro Leu Ser Leu Arg Ser Pro Arg Leu Pro Pro Leu Phe
                               -25                               -20                               -15
tgc act ttt ctt tcc ctt tct ttg cat ccc tgg ggg ggt ttc ttt ttg      210
Cys Thr Phe Leu Ser Leu Ser Leu His Pro Trp Gly Gly Phe Phe Leu
                               -10                               -5                               1
tgt gcc tgg att tct bkt ttc ctc ccg tgg gtg tgt gtg tgk gcg gg      257
Cys Ala Trp Ile Ser Xaa Phe Leu Pro Trp Val Cys Val Xaa Ala
      5                               10                               15

```

&lt;210&gt; 620

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 47..349

&lt;221&gt; sig\_peptide

&lt;222&gt; 47..313

&lt;223&gt; Von Heijne matrix

score 3.90000009536743

seq RLLVACCLADIFR/IY

&lt;400&gt; 620

```

agcggagtak ygagtcggca acccggaggg tagaaatatt tctgtc atg gct cat      55
                               Met Ala His
tca aag act agg acc aat gat gga aaa att aca tat ccg cct ggg gtc      103
Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr Pro Pro Gly Val
      -85                               -80                               -75
aag gaa ata tca gat aaa ata tct aaa gag gag atg gtg aga cga tta      151
Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val Arg Arg Leu
      -70                               -65                               -60                               -55
aag atg gtt gtg aaa act ttt atg gat atg gac cag gac tct gaa gaa      199
Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp Ser Glu Glu
                               -50                               -45                               -40
gaa aag gag ctt tat tta aac cta gct tta cat ctt gct tca gat ttt      247
Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu Ala Ser Asp Phe
      -35                               -30                               -25
ttt ctc aag cat cct gat aaa gat gtt cgc tta ctg gta gcc tgc tgc      295
Phe Leu Lys His Pro Asp Lys Asp Val Arg Leu Leu Val Ala Cys Cys
      -20                               -15                               -10
ctt gct gat att ttc agg att tat gct cct gaa gct cct tac aca tcc      343
Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro Tyr Thr Ser
      -5                               1                               5                               10
cct aag gg      351
Pro Lys

```

&lt;210&gt; 621

&lt;211&gt; 118

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 40..117

&lt;221&gt; sig\_peptide

<222> 40..93  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq IAWTATPSSAAFA/QA

<400> 621  
 atatcctgcc tgmgcctggg mcgggtggag gtgtcctgc atg gmg tct tgt gaa 54  
 Met Xaa Ser Cys Glu  
 -15  
 atc gcg tgg act gca aca ccc agc agc gcg gcc ttt gca caa gct ttt 102  
 Ile Ala Trp Thr Ala Thr Pro Ser Ser Ala Ala Phe Ala Gln Ala Phe  
 -10 -5 1  
 ccc aca gcc tgc aac a 118  
 Pro Thr Ala Cys Asn  
 5

<210> 622  
 <211> 221  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 83..220

<221> sig\_peptide  
 <222> 83..157  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq LLYILSRSSGRRG/KN

<400> 622  
 aaagatttga aggaagatgt aagctttacc aaaattaaaa agtaaagggg gtaagtgggg 60  
 ggaaaagggtg cagaacagtg ta atg tgt cac tac ttg tgg aaa aaa tta tac 112  
 Met Cys His Tyr Leu Trp Lys Lys Leu Tyr  
 -25 -20  
 tca aca ctt ttg tat ata ctc agc aga tct tct gga aga aga ggt aag 160  
 Ser Thr Leu Leu Tyr Ile Leu Ser Arg Ser Ser Gly Arg Arg Gly Lys  
 -15 -10 -5 1  
 aat ctg ata act gca gtt gcc tcc agg gca ggg aat tta ggt gtc tgg 208  
 Asn Leu Ile Thr Ala Val Ala Ser Arg Ala Gly Asn Leu Gly Val Trp  
 5 10 15  
 aca gaa aag ggg g 221  
 Thr Glu Lys Gly  
 20

<210> 623  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 344..430

<221> sig\_peptide  
 <222> 344..424  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq SRMVLLSSALLST/EN

<221> misc\_feature  
 <222> 348..349

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 623

```

gtttattgca ttttbcacaa ctcattaaat ttaggcttat aagtagctgt atcctggttt    60
ggtttcactt gttttaatta ttttttgatg atttaagaca ctagccatat ggattcaagt    120
tttttagttt ttattttcct acaccatacc atagtagaac tattactgtt gttatttata    180
ttttttaaaa aattcacttg tttttctcga gaatttgtga ctgattttta tggtatactg    240
cataattcag taatttcaca cattaacaac atccagggtc atgtgaggat gagttttcta    300
gcttctgaaa tgttctgagg atgtaatttt ttaataagag gaa atg tnn tct cac    355

```

Met Xaa Ser His

-25

```

aga cta ttt ggg tgt ttt cca agt gac ttg tca cga atg gtt ttg ctc    403
Arg Leu Phe Gly Cys Phe Pro Ser Asp Leu Ser Arg Met Val Leu Leu

```

-20

-15

-10

```

tct agt gca ctt ctg agt aca gaa aac ca    432
Ser Ser Ala Leu Leu Ser Thr Glu Asn

```

-5

1

&lt;210&gt; 624

&lt;211&gt; 233

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 91..231

&lt;221&gt; sig\_peptide

&lt;222&gt; 91..153

&lt;223&gt; Von Heijne matrix

score 3.90000009536743

seq YLCLHLCAFSTEG/WM

&lt;400&gt; 624

```

agaggaaaga gaaaaacatg taacatgtaa caaattgttt tcctaaatga caactcagaa    60
caatagaagg cattagaaga gaccttccat atg cgc cca tca cat tct tca gcc    114

```

Met Arg Pro Ser His Ser Ser Ala

-20

-15

```

tac cta tgt ctg cac ctt tgt gct ttc agt act gaa ggt tgg atg aac    162
Tyr Leu Cys Leu His Leu Cys Ala Phe Ser Thr Glu Gly Trp Met Asn

```

-10

-5

1

```

cgt ctg tcc tct tct cta agg ctg gct cct cta cct ttg tac cct ttt    210
Arg Leu Ser Ser Ser Leu Arg Leu Ala Pro Leu Pro Leu Tyr Pro Phe

```

5

10

15

```

tgc cta ccc agc aat tca ccc ca    233
Cys Leu Pro Ser Asn Ser Pro

```

20

25

&lt;210&gt; 625

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 10..378

&lt;221&gt; sig\_peptide

&lt;222&gt; 10..57

&lt;223&gt; Von Heijne matrix

score 3.90000009536743

seq RLVWLGLRAPLGG/RQ

<400> 625  
aaggaagaa atg tgg tcg cgg ttg gtg tgg ctg ggm ctt cgg gcc cct ctg 51  
Met Trp Ser Arg Leu Val Trp Leu Gly Leu Arg Ala Pro Leu  
-15 -10 -5  
ggt ggg cgc cag ggc ttc acc tcc aag gcg gat cct cag ggc agt ggc 99  
Gly Gly Arg Gln Gly Phe Thr Ser Lys Ala Asp Pro Gln Gly Ser Gly  
1 5 10  
cgg atc acg gct gcg gtg atc gag cac ctg gag cgt cta gcg ctt gtg 147  
Arg Ile Thr Ala Ala Val Ile Glu His Leu Glu Arg Leu Ala Leu Val  
15 20 25 30  
gac ttc ggc agc cgc gag gca gtg gcg cga ctg gag aaa gct atc gcc 195  
Asp Phe Gly Ser Arg Glu Ala Val Ala Arg Leu Glu Lys Ala Ile Ala  
35 40 45  
ttc gcc gac cgg cta cgc gcc gtg gac aca gac ggg gtg gag ccc atg 243  
Phe Ala Asp Arg Leu Arg Ala Val Asp Thr Asp Gly Val Glu Pro Met  
50 55 60  
gaa tcg gtc ctg gag gac aga tgt cta tac ctg aga tcc gac aat gtg 291  
Glu Ser Val Leu Glu Asp Arg Cys Leu Tyr Leu Arg Ser Asp Asn Val  
65 70 75  
gta gaa ggc aac tgt gct gat gaa tta cta caa aac tcc cat cgc gtc 339  
Val Glu Gly Asn Cys Ala Asp Glu Leu Leu Gln Asn Ser His Arg Val  
80 85 90  
gtg gag gag tac ttt gtg gcc ccc cca ggt aat atc tct tt 380  
Val Glu Glu Tyr Phe Val Ala Pro Pro Gly Asn Ile Ser  
95 100 105

<210> 626

<211> 276

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 27..275

<221> sig\_peptide

<222> 27..269

<223> Von Heijne matrix

score 3.90000009536743

seq AIVTCKSLASIHA/LP

<400> 626  
atcctgtgttt tgggacagcg gcaatc atg gcg cca cct gtg aga tac tgc atc 53  
Met Ala Pro Pro Val Arg Tyr Cys Ile  
-80 -75  
ccc ggc gaa cgt ctg tgt aac ttg gag gag ggc agc ccg ggc agc ggc 101  
Pro Gly Glu Arg Leu Cys Asn Leu Glu Glu Gly Ser Pro Gly Ser Gly  
-70 -65 -60  
acc tac acc cgc cac ggc tac atc ttt tcg tcg ctw rcc ggc tgt ctg 149  
Thr Tyr Thr Arg His Gly Tyr Ile Phe Ser Ser Leu Xaa Gly Cys Leu  
-55 -50 -45  
atg aag agc agc gag aat ggc gcg ctt cca gtg gtg tct gta gtg aga 197  
Met Lys Ser Ser Glu Asn Gly Ala Leu Pro Val Val Ser Val Val Arg  
-40 -35 -30 -25  
gaa aca gag tcc cag tta ctg cca gat gtg gga gct att gta acc tgt 245  
Glu Thr Glu Ser Gln Leu Leu Pro Asp Val Gly Ala Ile Val Thr Cys  
-20 -15 -10  
aag tct cta gca tca att cac gct ttg cca a 276  
Lys Ser Leu Ala Ser Ile His Ala Leu Pro  
-5 1

<210> 627

<211> 415  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 174..413

<221> sig\_peptide  
 <222> 174..353  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq RLLVARLHMASLA/RR

<221> misc\_feature  
 <222> 7  
 <223> n=a, g, c or t

<400> 627  
 accggangtg gagcctggga gccttgacgt taggaacgaa gtctaacctg gatctggagc 60  
 cgggtgagat caaattggga atgctttcat aatgaacgtc aaccagtcag ttccacctgt 120  
 gccaccattt gggcagcccc agcccatcta cccagggtat catcagtcga gct atg 176  
 Met  
 -60  
 gtg ggc aat cag ggt cca cag ccc ccg cca ttc cct atg gag cct aca 224  
 Val Gly Asn Gln Gly Pro Gln Pro Pro Phe Pro Met Glu Pro Thr  
 -55 -50 -45  
 atg gcc cag tac cag gct atc agc aaa cac ctc ccc aag gta tgt caa 272  
 Met Ala Gln Tyr Gln Ala Ile Ser Lys His Leu Pro Lys Val Cys Gln  
 -40 -35 -30  
 gag ccc cac ctt cct cgg ggg cac ctc cag cct caa cag cac agg ctc 320  
 Glu Pro His Leu Pro Arg Gly His Leu Gln Pro Gln Gln His Arg Leu  
 -25 -20 -15  
 ctt gtg gcc agg ctg cat atg gcc agt ttg gca agg aga tgt aca gaa 368  
 Leu Val Ala Arg Leu His Met Ala Ser Leu Ala Arg Arg Cys Thr Glu  
 -10 -5 1 5  
 tgg gcc aag ctc cac tgt tca gat gca agg ctg ccc tgg gtc tca gc 415  
 Trp Ala Lys Leu His Cys Ser Asp Ala Arg Leu Pro Trp Val Ser  
 10 15 20

<210> 628  
 <211> 318  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 214..318

<221> sig\_peptide  
 <222> 214..297  
 <223> Von Heijne matrix  
 score 3.90000009536743  
 seq GVAGVCFRRSDA/SE

<221> misc\_feature  
 <222> 8  
 <223> n=a, g, c or t

<400> 628  
 amattgmkh hataractct taccatcatt ttaactggat aaaaagtga gtgtctaaag 60

336

atgtatatat ttsgcacggt tgarttcaca agaggaagaa caawtttcta gccasgawac 120  
 catgahagga ttccaaacag agattaaact tgtcctttga ggataggtaa tgagtccaga 180  
 attggtgggt tcttggtttt gctgacttca aga atg aag cca cag acc ctc gca 234  
 Met Lys Pro Gln Thr Leu Ala

-25

gtg agt gtt aca gtt ctt aaa gat ggt gtg gct gga gtt tgt ttc ttc 282  
 Val Ser Val Thr Val Leu Lys Asp Gly Val Ala Gly Val Cys Phe Phe  
 -20 -15 -10  
 aga cgt tca gat gcg tct gaa gtt tct tcc ttc tgg 318  
 Arg Arg Ser Asp Ala Ser Glu Val Ser Ser Phe Trp  
 -5 1 5

&lt;210&gt; 629

&lt;211&gt; 170

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 29..169

&lt;221&gt; sig\_peptide

&lt;222&gt; 29..157

&lt;223&gt; Von Heijne matrix

score 3.90000009536743

seq KCLFLSFAHFLMG/RT

&lt;400&gt; 629

cattttgact ggtgtaagat gatattctc atg gtg gtt ttg att tgc ctt tct 52  
 Met Val Val Leu Ile Cys Leu Ser  
 -40

ctc atg atc agt aat act gag ctt ttt ttc ata cgc ttc ttg act gca 100  
 Leu Met Ile Ser Asn Thr Glu Leu Phe Phe Ile Arg Phe Leu Thr Ala  
 -35 -30 -25 -20

tgt atg cct tct ttt gaa aag tgt ctg ttc tta tct ttt gcc cac ttc 148  
 Cys Met Pro Ser Phe Glu Lys Cys Leu Phe Leu Ser Phe Ala His Phe  
 -15 -10 -5

ttg atg gga aga acc cac cgt g 170  
 Leu Met Gly Arg Thr His Arg  
 1

&lt;210&gt; 630

&lt;211&gt; 196

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 87..194

&lt;221&gt; sig\_peptide

&lt;222&gt; 87..152

&lt;223&gt; Von Heijne matrix

score 3.90000009536743

seq SLLSDILFANIFS/HS

&lt;400&gt; 630

gccatttgta tatatttgav aaatatctat tcaaatacat tgcctgcttt aaaatactgt 60  
 tattggtctt tttatcattg gattgt atg agt tct tta tat att ttg gat att 113  
 Met Ser Ser Leu Tyr Ile Leu Asp Ile  
 -20 -15

agt ctc tta tca gat ata tta ttt gca aat att ttc tcc cat tct tgg 161  
 Ser Leu Leu Ser Asp Ile Leu Phe Ala Asn Ile Phe Ser His Ser Trp

1

196

<220>  
<221> CDS  
<222> 53..337

[illegible]

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<220>  
<221> CDS  
<222> 171..431
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```
<221> misc_feature
<222> 376..377
<223> n=a, g, c or t
```

<400> 632

338

```

actctgaaag cagtcttcac agaaactttt cacagaagtc aaatagttaa agcaaattct 60
agatacatgg tagagaccag gagaaaatat gaataacttt cttctaaaca aggagctcag 120
tggtataaacc atacctctag attccttgct tccattttcc cagaaacaag atg agg 176
                                     Met Arg
aag aga aag atc agt gtg tgt caa caa act tgg gcc tta tta tgc aag 224
Lys Arg Lys Ile Ser Val Cys Gln Gln Thr Trp Ala Leu Leu Cys Lys
-45 -40 -35
aac ttt ctt aaa aaa tgg aga atg aaa aga gag tcc tta atg gaa tgg 272
Asn Phe Leu Lys Lys Trp Arg Met Lys Arg Glu Ser Leu Met Glu Trp
-30 -25 -20 -15
ctg aat tca ttg ctc cta cta ctt tgt ttg tat ata tat cct cat agt 320
Leu Asn Ser Leu Leu Leu Leu Cys Leu Tyr Ile Tyr Pro His Ser
-10 -5 1
cat caa gta aat gaw tdd tct tca ctg ctt acc atg gac ctg gga cgg 368
His Gln Val Asn Xaa Xaa Ser Ser Leu Leu Thr Met Asp Leu Gly Arg
5 10 15
gta gat rnn tkt aat gaa tcc aga ttt tct gtt gta tac aca cct gtc 416
Val Asp Xaa Xaa Asn Glu Ser Arg Phe Ser Val Val Tyr Thr Pro Val
20 25 30
acc aac acg acc cct gg 433
Thr Asn Thr Thr Pro
35

```

<210> 633  
 <211> 154  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 54..152

<221> sig\_peptide  
 <222> 54..143  
 <223> Von Heijne matrix  
 score 3.79999995231628  
 seq XFVFVCXLLKCMS/VP

```

<400> 633
cagttaagtg tatctgtgtg tgagcaagtt tatatgtgta cacatgtttg ccc atg 56
                                     Met
                                     -30
tgt act tgt ctt tgt gtg tgt ctg tat atg tay aat atg caa ttt tta 104
Cys Thr Cys Leu Cys Val Cys Leu Tyr Met Tyr Asn Met Gln Phe Leu
-25 -20 -15
kyt ttt gtg ttt gtk tgc gww ttg cta aag tgt atg agt gtg cct ttg 152
Xaa Phe Val Phe Val Cys Xaa Leu Leu Lys Cys Met Ser Val Pro Leu
-10 -5 1
tg 154

```

<210> 634  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 34..390

<221> sig\_peptide  
 <222> 34..126  
 <223> Von Heijne matrix  
 score 3.79999995231628

seq PVCLLLVLGMAGSG/KT

&lt;221&gt; misc\_feature

&lt;222&gt; 224

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 634

```

ctctatggctc ggggtgggtgg ggccaggagg aag atg gcg gcg tcc gca gct gcc      54
                               Met Ala Ala Ser Ala Ala Ala
                               -30                               -25
gct gag ctc cag gct tct ggg ggt ccg cgg cac cca gtg tgt ctg ttg      102
Ala Glu Leu Gln Ala Ser Gly Gly Pro Arg His Pro Val Cys Leu Leu
                               -20                               -10
gtg ttg gga atg gcg gga tcc ggg aaa acc act ttt gta cag agg ctc      150
Val Leu Gly Met Ala Gly Ser Gly Lys Thr Thr Phe Val Gln Arg Leu
                               -5                               1                               5
aca gga cac ctg cat gcc caa ggc act cca ccg tat gtg atc aac ctg      198
Thr Gly His Leu His Ala Gln Gly Thr Pro Pro Tyr Val Ile Asn Leu
                               10                               15                               20
gat cca gca gta cat gaa gtt ccc tnt cct gcc aat att gat att cgt      246
Asp Pro Ala Val His Glu Val Pro Xaa Pro Ala Asn Ile Asp Ile Arg
25                               30                               35                               40
gat act gta aag tat aaa gaa gta atg aaa caa tat gga ctt gga ccc      294
Asp Thr Val Lys Tyr Lys Glu Val Met Lys Gln Tyr Gly Leu Gly Pro
                               45                               50                               55
aat ggc ggc ata gtg acc tca ctc aat ctc ttt gst acc aga ttt gat      342
Asn Gly Gly Ile Val Thr Ser Leu Asn Leu Phe Xaa Thr Arg Phe Asp
                               60                               65                               70
cag gtg atg aaa tta ttg aga agg ccc aga aca tgt cca aat atg tgt      390
Gln Val Met Lys Leu Leu Arg Arg Pro Arg Thr Cys Pro Asn Met Cys
                               75                               80                               85

```

&lt;210&gt; 635

&lt;211&gt; 137

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 22..135

&lt;221&gt; sig\_peptide

&lt;222&gt; 22..81

&lt;223&gt; Von Heijne matrix

score 3.79999995231628

seq VLLTHGLIHYSFT/HH

&lt;400&gt; 635

```

caacatgcag gtttggttact t atg tat gca tgt gcc atg ttg gtg tta tta      51
                               Met Tyr Ala Cys Ala Met Leu Val Leu Leu
                               -20                               -15
act cat gga ctc atc cat tac tca ttt act cat cat tta cat tac gta      99
Thr His Gly Leu Ile His Tyr Ser Phe Thr His His Leu His Tyr Val
-10                               -5                               1                               5
ttt atc cta att ctt ccc ctc cca ccc ccg cca cag gg      137
Phe Ile Leu Ile Leu Pro Leu Pro Pro Pro Pro Gln
                               10                               15

```

&lt;210&gt; 636

&lt;211&gt; 172

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 38..172

&lt;221&gt; sig\_peptide

&lt;222&gt; 38..109

&lt;223&gt; Von Heijne matrix

score 3.79999995231628

seq SMCLLLDVSSXKS/TD

&lt;400&gt; 636

catcttgtag aaaaaagtta caaattaaca aaaaaga atg ggc ttt ctt ggc agc 55  
 Met Gly Phe Leu Gly Ser  
 -20

ccc aga cag aga aac tca atg tgt ttg ctt tta gac gtc agc tct rcc 103  
 Pro Arg Gln Arg Asn Ser Met Cys Leu Leu Leu Asp Val Ser Ser Xaa  
 -15 -10 -5

aag agc aca gat aat tth cya rtc gww wtt ttg att att tat tat ctg 151  
 Lys Ser Thr Asp Asn Xaa Xaa Xaa Xaa Xaa Leu Ile Ile Tyr Tyr Leu  
 1 5 10

att acc aga aaa ggg cca ggg 172  
 Ile Thr Arg Lys Gly Pro Gly  
 15 20

&lt;210&gt; 637

&lt;211&gt; 253

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 100..252

&lt;221&gt; sig\_peptide

&lt;222&gt; 100..228

&lt;223&gt; Von Heijne matrix

score 3.79999995231628

seq FNIFLAAPSPVWQ/PQ

&lt;400&gt; 637

acaagcactg caatgcagca accattgacc taactatgct tcctttctcca ggatcatctca 60  
 agcagacccc tcactctgaa gcccccgat ccaagcagg atg agc tgc caa mct 114  
 Met Ser Cys Gln Xaa  
 -40

mag ctt gct cdg acc ttg act tgg ctc atg atc cgt gga aga cat ccc 162  
 Xaa Leu Ala Xaa Thr Leu Thr Trp Leu Met Ile Arg Gly Arg His Pro  
 -35 -30 -25

tac ctg acc cgt cga tca gcc cga aac ttc aac atc ttt ttg gca gct 210  
 Tyr Leu Thr Arg Arg Ser Ala Arg Asn Phe Asn Ile Phe Leu Ala Ala  
 -20 -15 -10

ccg tcc cca gtt tgg cag cct cag agg acc cgc cga ccc cag k 253  
 Pro Ser Pro Val Trp Gln Pro Gln Arg Thr Arg Arg Pro Gln  
 -5 1 5

&lt;210&gt; 638

&lt;211&gt; 185

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 32..184

```

<221> sig_peptide
<222> 32..133
<223> Von Heijne matrix
      score 3.79999995231628
      seq FHQMALXPGTSRA/QA

<400> 638
acgcggcaca cagtcaccagt gctcagtcac c atg tgt cct gca tgg ctc cca      52
                                   Met Cys Pro Ala Trp Leu Pro
                                   -30
tgt tgg acg gca cag acg gaa cat ctc gat cgt tac agg aag ttc cac      100
Cys Trp Thr Ala Gln Thr Glu His Leu Asp Arg Tyr Arg Lys Phe His
      -25                -20                -15
cag atg gcg ctg tyt cca ggg aca tct agg gca cag gcc tta ctt tat      148
Gln Met Ala Leu Xaa Pro Gly Thr Ser Arg Ala Gln Ala Leu Leu Tyr
      -10                -5                1                5
aac gaa gtc cta gag aga ttt atg ttc acc cgg ctg c      185
Asn Glu Val Leu Glu Arg Phe Met Phe Thr Arg Leu
      10                15

<210> 639
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 73..204

<221> sig_peptide
<222> 73..126
<223> Von Heijne matrix
      score 3.79999995231628
      seq RICTFLLPSHSTS/GP

<400> 639
ttggatgacc ttaatgcttc aggacttagt aagaaataag cccgagtact tgtgaaatgt      60
taggctttgt tg atg aat gtc atg aag aga ata tgt acc ttt ctg ttg cct      111
      Met Asn Val Met Lys Arg Ile Cys Thr Phe Leu Leu Pro
      -15                -10
tca cac tct acc tct ggc cct ctg tgc tgt tca aat gcc cat ctt cct      159
Ser His Ser Thr Ser Gly Pro Leu Cys Cys Ser Asn Ala His Leu Pro
      -5                1                5                10
gct acc tcc tct acc ttg aaa cat tgc agg gct tgg agg gaa gcg bv      206
Ala Thr Ser Ser Thr Leu Lys His Cys Arg Ala Trp Arg Glu Ala
      15                20                25

<210> 640
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..506

<221> sig_peptide
<222> 21..383
<223> Von Heijne matrix
      score 3.79999995231628
      seq SLATLPFLSTVVT/DK

```

<221> misc\_feature  
 <222> 495  
 <223> n=a, g, c or t

<400> 640

```

aagtcacatg agccaccaaaa atg gtg gtg ttc ggg tat gag gct ggg act aag      53
                Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys
                -120                                -115

cca agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag      101
Pro Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys
-110                                -105                                -100                                -95

gtt ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta      149
Val Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu
                -90                                -85                                -80

gaa gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa      197
Glu Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys
                -75                                -70                                -65

aat ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg      245
Asn Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met
                -60                                -55                                -50

gcg aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc      293
Ala Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe
                -45                                -40                                -35

ctg ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat      341
Leu Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr
-30                                -25                                -20                                -15

gca tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag      389
Ala Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys
                -10                                -5                                1

ctt ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac      437
Leu Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn
                5                                10                                15

tgt gtt ttc aga agc tca ctg att ggc ata gtt tgt ggw gtt ttc tat      485
Cys Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr
                20                                25                                30

ccc agt tct ntg gct ttt act a      507
Pro Ser Ser Xaa Ala Phe Thr
35                                40

```

<210> 641  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 295..483

<221> sig\_peptide  
 <222> 295..408  
 <223> Von Heijne matrix  
       score 3.79999995231628  
       seq LVVCSVTVFVWS/CC

<221> misc\_feature  
 <222> 54  
 <223> n=a, g, c or t

<400> 641

```

accattcgga agaggcggag tcttcttccg aggaccattc ggaagaaggc gganctacct      60
ctcatcagga ccagtctgac tgcacctgca tccttagctc agagcatccc cggagcatct      120

```

```

taagagctga gcgcastgac aactaggggc cggaccgtcg caggaggcgt ccgctggata 180
ccttccccct tccctgacct agagctctac agctgctgcc tcggtactga ccgaggggttc 240
ccagagctgt ctyaccattg caaaaacggt atagcaacag cctctgatta cgac atg 297
                                     Met
gct gag atc acc aat atc cga cct agc ttt gat gtg tca ccg gtg gtg 345
Ala Glu Ile Thr Asn Ile Arg Pro Ser Phe Asp Val Ser Pro Val Val
      -35                -30                -25
gcc ggc ctc atc ggg gcc tct gtg ctg gtg gtg tgt gtc tcg gtg acc 393
Ala Gly Leu Ile Gly Ala Ser Val Leu Val Val Cys Val Ser Val Thr
      -20                -15                -10
gtc ttt gtc tgg tca tgc tgc crc cag cag gca gag aag aag cac aag 441
Val Phe Val Trp Ser Cys Cys Xaa Gln Gln Ala Glu Lys Lys His Lys
      -5                1                5                10
aac cca cca tac aag ttt att cac atg ctc aaa ggc wtc agc 483
Asn Pro Pro Tyr Lys Phe Ile His Met Leu Lys Gly Xaa Ser
      15                20                25

```

&lt;210&gt; 642

&lt;211&gt; 309

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 235..309

&lt;221&gt; sig\_peptide

&lt;222&gt; 235..279

&lt;223&gt; Von Heijne matrix

score 3.79999995231628

seq ILTMLILLIHEHG/IP

&lt;400&gt; 642

```

attratctat gtgtctgttg ttatacgaat atcatgctgt tttggtttct atatccttgt 60
aatatgtttt gaagtcaggt agtgtgatgc ctccagattt gttctttttg gtcaggattg 120
ctttggctgw tttgggttcw wttwtgggtc catacaaatt ttaggattat tttttctatg 180
tctgtgaaaa gtggcatggg tattacattc aatctgtaga ttgctttgga tagt atg 237
                                     Met
                                     -15
gtc att tta act atg tta att ctt tta atc cat gag cat ggt att ttc 285
Val Ile Leu Thr Met Leu Ile Leu Leu Ile His Glu His Gly Ile Phe
      -10                -5                1
ttt tca ctt gtt tgt gtc ctc ttc 309
Phe Ser Leu Val Cys Val Leu Phe
      5                10

```

&lt;210&gt; 643

&lt;211&gt; 245

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 147..245

&lt;221&gt; sig\_peptide

&lt;222&gt; 147..233

&lt;223&gt; Von Heijne matrix

score 3.79999995231628

seq LTHHTCTPPSTA/HP

&lt;221&gt; misc\_feature

&lt;222&gt; 61



<210> 646  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 258..347

<221> sig\_peptide  
 <222> 258..314  
 <223> Von Heijne matrix  
 score 3.79999995231628  
 seq LAXLPGXXHGGLS/AV

<221> misc\_feature  
 <222> 294  
 <223> n=a, g, c or t

<400> 646  
 ctttcttttc cggayycagc agtggcgccct aaagtctgcg aggaggaagt cgctctctgtg 60  
 ccccgaggtt cagaggtcta aggaagagga gataaatata tgaagggtgct gtttggcaca 120  
 gaatttaata gggaagaaaag agacagtata actcaccagt gctgggtctc atcatcctgc 180  
 aatttc dgaa caactatgaa tacaaaaaga attttaaaat cccagtcctg cctagaaagg 240  
 ggaagtcatc tctaaat atg gtg gcc ctg ggg cag ctg gcc tdc ctg cca 290  
 Met Val Ala Leu Gly Gln Leu Ala Xaa Leu Pro  
 -15 -10  
 ggc nbc tdc cat ggg ggc ctt tct gca gtg act gtg gtt ctt ccc att 338  
 Gly Xaa Xaa His Gly Gly Leu Ser Ala Val Thr Val Val Leu Pro Ile  
 -5 1 5  
 tta ctc tgt 347  
 Leu Leu Cys  
 10

<210> 647  
 <211> 143  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 78..143

<221> sig\_peptide  
 <222> 78..122  
 <223> Von Heijne matrix  
 score 3.79999995231628  
 seq VSFVCLLFRNVYS/NL

<400> 647  
 aaactggggt gagatgatat ctcaatgtag ttttcattta catctctaata gatcaataat 60  
 gttgagcaat ttttcat atg ccc gtt tca ttt gtc tgt ctt ctt ttc aga 110  
 Met Pro Val Ser Phe Val Cys Leu Leu Phe Arg  
 -15 -10 -5  
 aat gtt tat tca aat cta ttg cct tct ttt ttt 143  
 Asn Val Tyr Ser Asn Leu Leu Pro Ser Phe Phe  
 1 5

<210> 648  
 <211> 232  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 41..232

<221> sig\_peptide

<222> 41..121

<223> Von Heijne matrix

score 3.79999995231628

seq LPLLLPAHHGRHG/SG

<400> 648

```

aaaaagtgct cgggacaagg mcatagggct gagagtagcc atg ggc tct gga gga      55
                                   Met Gly Ser Gly Gly
                                   -25
gac agc ctc ctg ggg ggc agg ggt tcc ctg cct ctg ctg ctc cct gct      103
Asp Ser Leu Leu Gly Gly Arg Gly Ser Leu Pro Leu Leu Leu Pro Ala
-20                               -15          -10
cat cat ggg agg cat ggc tca gga ctc ccc gcc cca gat cct agt cca      151
His His Gly Arg His Gly Ser Gly Leu Pro Ala Pro Asp Pro Ser Pro
-5                               1              5          10
ccc cca gga cca gct gtt cca ggg ccc tgg ccc tgc cag gat gag ctg      199
Pro Pro Gly Pro Ala Val Pro Gly Pro Trp Pro Cys Gln Asp Glu Leu
15                               20              25
cca agc ctc agg cca gcc acc tcc cac cac ttt      232
Pro Ser Leu Arg Pro Ala Thr Ser His His Phe
30                               35

```

<210> 649

<211> 133

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..132

<221> sig\_peptide

<222> 4..78

<223> Von Heijne matrix

score 3.79999995231628

seq LLGRSGFSFQVSG/WG

<400> 649

```

act atg gcg gtt gga gga acg gca gtg atc aca cgt cgg ctg ctg gga      48
  Met Ala Val Gly Gly Thr Ala Val Ile Thr Arg Arg Leu Leu Gly
  -25                               -20          -15
aga tct gga ttc tcg ttt cag gtt tcg ggg tgg ggg tgg gga gaa agg      96
Arg Ser Gly Phe Ser Phe Gln Val Ser Gly Trp Gly Trp Gly Glu Arg
-10                               -5              1          5
gtc gat gat ttc ctt ttt tcg tcg ggt ata gac ggr a      133
Val Asp Asp Phe Leu Phe Ser Ser Gly Ile Asp Gly
10                               15

```

<210> 650

<211> 419

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 317..418

&lt;221&gt; sig\_peptide

&lt;222&gt; 317..379

&lt;223&gt; Von Heijne matrix

score 3.79999995231628

seq ALSSLAHHPRTSG/QK

&lt;400&gt; 650

```

ggagtggaca cggagggggcc tagaggaggg ccctagaggg gcggaggggc cgatggaaaag    60
ggaaagggtgg cctgtcctcc cctcccgaca ccaggggagg agccccagcc ccgcgacgag    120
gaggaagcggg actgragctg ctgaggcagt ttgacctggc ctggcagtac gggccctgca    180
ccgggatcac acggctgcag cgctgggtgc gggccaagca gatgggcttg gagcctcccc    240
cagagggtgtg gcagggtgct aagaccaccc ccggagaccc ccgcttcag tgcagtctct    300
ggcatctcta tcccct atg agg cac cac gta aga yct cct gcc ctt agc tct    352
                Met Arg His His Val Arg Xaa Pro Ala Leu Ser Ser
                  -20          -15          -10
ctt gct cac cac cca aga acc tca gga cag aag cga gag ccc att gct    400
Leu Ala His His Pro Arg Thr Ser Gly Gln Lys Arg Glu Pro Ile Ala
                  -5              1              5
cct gct cag ctc agc ccg g    419
Pro Ala Gln Leu Ser Pro
                10

```

&lt;210&gt; 651

&lt;211&gt; 396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 52..396

&lt;221&gt; sig\_peptide

&lt;222&gt; 52..270

&lt;223&gt; Von Heijne matrix

score 3.79999995231628

seq LAGNLALSPTGNA/KK

&lt;400&gt; 651

```

ttggaagtgg tgtggagacg gaggacagga gcagtgccca agcagcgagg g atg ctg    57
                Met Leu
atc ttg aat ggc ttc cgg ggc cat gcc aca gat tcc gtg aag aac tcc    105
Ile Leu Asn Gly Phe Arg Gly His Ala Thr Asp Ser Val Lys Asn Ser
   -70          -65          -60
atg gaa agc atg aac act gac atg gtg atc atc cca ggg ggt ctg acc    153
Met Glu Ser Met Asn Thr Asp Met Val Ile Ile Pro Gly Gly Leu Thr
   -55          -50          -45          -40
tca cag ctt cag gtg ctg gat gtc gtg gtc tac aag cca ctg aat gac    201
Ser Gln Leu Gln Val Leu Asp Val Val Val Tyr Lys Pro Leu Asn Asp
          -35          -30          -25
agt gtg cgg gcc cag tac tcc aac tgg ctt ctg gct ggg aac ctg gcg    249
Ser Val Arg Ala Gln Tyr Ser Asn Trp Leu Leu Ala Gly Asn Leu Ala
          -20          -15          -10
ctg agc cca acc ggg aat gct aag aag cca ccc ctg ggc ctc ttt ctg    297
Leu Ser Pro Thr Gly Asn Ala Lys Lys Pro Pro Leu Gly Leu Phe Leu
   -5              1              5
gag tgg gtc atg gtc gcg tgg aat agc atc tca agt gag tcc atc gtc    345
Glu Trp Val Met Val Ala Trp Asn Ser Ile Ser Ser Glu Ser Ile Val
10          15          20          25
caa ggg whc aaa gaa gtg cca tat ctc crg caa ctt gga gga gga aga    393
Gln Gly Xaa Lys Glu Val Pro Tyr Leu Xaa Gln Leu Gly Gly Gly Arg
          30          35          40
cga    396

```

Arg

<210> 652  
 <211> 170  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 67..168

<221> sig\_peptide  
 <222> 67..141  
 <223> Von Heijne matrix  
 score 3.79999995231628  
 seq YCLSNCLLXXSWG/LH

<400> 652  
 tgtatacacaa taaccagata ttctcctaag tttttcaaaa taatagaaac agatattttg 60  
 ggatcc atg atc tgt acc act gtt tat att acc atg gct cct tac tgt 108  
 Met Ile Cys Thr Thr Val Tyr Ile Thr Met Ala Pro Tyr Cys  
 -25 -20 -15  
 cta tca aac tgt tta ctt thw caw agt tgg ggc ctg cat ttg tat aga 156  
 Leu Ser Asn Cys Leu Leu Xaa Xaa Ser Trp Gly Leu His Leu Tyr Arg  
 -10 -5 1 5  
 ttt cta gcc ccc at 170  
 Phe Leu Ala Pro

<210> 653  
 <211> 178  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 131..178

<221> sig\_peptide  
 <222> 131..172  
 <223> Von Heijne matrix  
 score 3.79999995231628  
 seq VSLCVAALFPLQA/YG

<400> 653  
 agagtacctg aaaaccttag agaaccctgg ggaaatattt atagccaggc ttcttgaggaga 60  
 ctctgggaac aggaaagtca ggaaccctgc ctttcaggaa ctgctgtatc tcagtcggct 120  
 tcttcatttc atg gtt tct ctc tgt gta gct gct tta ttt cct ctt cag 169  
 Met Val Ser Leu Cys Val Ala Ala Leu Phe Pro Leu Gln  
 -10 -5  
 gct tac ggg 178  
 Ala Tyr Gly  
 1

<210> 654  
 <211> 121  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 36..119

<221> sig\_peptide

&lt;222&gt; 36..107

&lt;223&gt; Von Heijne matrix

score 3.79999995231628

seq FVYLLLRNLXSYS/LP

&lt;400&gt; 654

tgtggttttg attggcattt ccctgatcat tactg atg ttg agc att ttt tca	53
Met Leu Ser Ile Phe Ser	
-20	
ttt ttt tgt agg cca ttt gta tat ctt ctt ttg aga aat ctc krt tca	101
Phe Phe Cys Arg Pro Phe Val Tyr Leu Leu Arg Asn Leu Xaa Ser	
-15 -10 -5	
tat tct ttg ccc acc acg gg	121
Tyr Ser Leu Pro Thr Thr	
1	

&lt;210&gt; 655

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 89..370

&lt;221&gt; sig\_peptide

&lt;222&gt; 89..319

&lt;223&gt; Von Heijne matrix

score 3.79999995231628

seq LGLQCDAVNLAFG/RR

&lt;400&gt; 655

acttcgccat tttcctccgg aagtgcggat cccagcggcg gtcgtgtagc tgagcagscc	60
tggggccttg ttctatgtcc ctgtggct atg ttt cca gtg tcc tct ggg tgt	112
Met Phe Pro Val Ser Ser Gly Cys	
-75 -70	
ttc caa gag caa caa gaa acg aat aaa tct ctg ccc cgc agc gcc tcc	160
Phe Gln Glu Gln Gln Glu Thr Asn Lys Ser Leu Pro Arg Ser Ala Ser	
-65 -60 -55	
acc cca gag acc cgg acc aag ttc aca cag gac aat ctg tgc cry gcc	208
Thr Pro Glu Thr Arg Thr Lys Phe Thr Gln Asp Asn Leu Cys Xaa Ala	
-50 -45 -40	
cag cgc gag cgc ctg gac tcg gcc aac ctg tgg gtk ctk gtg gac tgc	256
Gln Arg Glu Arg Leu Asp Ser Ala Asn Leu Trp Val Leu Val Asp Cys	
-35 -30 -25	
atc ctt cgc gac acc tcc gag gac ctg gga ctc cag tgt gac gcc gtg	304
Ile Leu Arg Asp Thr Ser Glu Asp Leu Gly Leu Gln Cys Asp Ala Val	
-20 -15 -10	
aac ctg gcc ttc ggg cgc cgc tgt gag gaa ctg gag gac gcg cgg cac	352
Asn Leu Ala Phe Gly Arg Arg Cys Glu Glu Leu Glu Asp Ala Arg His	
-5 1 5 10	
aag ctg cag yac cac ctg	370
Lys Leu Gln Xaa His Leu	
15	

&lt;210&gt; 656

&lt;211&gt; 197

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 137..196

```

<221> sig_peptide
<222> 137..181
<223> Von Heijne matrix
      score 3.79999995231628
      seq LVHSFLWLSSILY/IY

<400> 656
attgtatcgt tcttatgcct ttgcatactc atagcttagc tcccacatat cagtgagaac      60
atacaatggt tgggtttcca ttcctgagtt acttcactta gaataatagt ctccaatctc      120
atccagggtca ctgcaa atg cca ttg gtt cat tcc ttc tta tgg ctg agt agt      172
                Met Pro Leu Val His Ser Phe Leu Trp Leu Ser Ser
                -15                -10                -5
atc cta tat ata tac cac ctg cgg g      197
Ile Leu Tyr Ile Tyr His Leu Arg
                1                5

<210> 657
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 79..246

<221> sig_peptide
<222> 79..150
<223> Von Heijne matrix
      score 3.79999995231628
      seq XVFXFXFLXRXLX/XX

<400> 657
tttttgacat cytattaata gccattctgg ctggtgtcag gtggtatctc attgtgggtt      60
cgattttgga tttctcta atg att agt aat ggt aag ttt ttt tgt ttt ttt      111
                Met Ile Ser Asn Gly Lys Phe Phe Cys Phe Phe
                -20                -15
ttk gtt ttt kgt ttt tkg ttt ttg ara cgg asy ttg cyc tkg ycg ccc      159
Xaa Val Phe Xaa Phe Xaa Phe Leu Xaa Arg Xaa Leu Xaa Xaa Xaa Pro
                -10                -5                1
agg ctg gag tgc aat ggm aar ayc tgc gcy cac tgm aac ctc cgc ctc      207
Arg Leu Glu Cys Asn Gly Lys Xaa Ser Ala His Xaa Asn Leu Arg Leu
                5                10                15
ctg agt yca agc aat tcy ctk gcc tca gcc ccc cga ggg      246
Leu Ser Xaa Ser Asn Ser Leu Ala Ser Ala Pro Arg Gly
20                25                30

<210> 658
<211> 335
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..333

<221> sig_peptide
<222> 31..300
<223> Von Heijne matrix
      score 3.70000004768372
      seq LRVRLTLPHSIRS/DS

<221> misc_feature

```

&lt;222&gt; 320

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 658

```

acacgcgcct cttcacgagg tggaaacaag atg gag gat tcg gcc tcg gcc tcg      54
                               Met Glu Asp Ser Ala Ser Ala Ser
                               -90                               -85
ctg tct tct gca gcc gct act gga acc tcc acc tcg act cca gcg gcc      102
Leu Ser Ser Ala Ala Ala Thr Gly Thr Ser Thr Ser Thr Pro Ala Ala
      -80                               -75                               -70
ccg aca gca cgg aag cag ctg gat aaa gaa cag gtt aga aag gca gtg      150
Pro Thr Ala Arg Lys Gln Leu Asp Lys Glu Gln Val Arg Lys Ala Val
      -65                               -60                               -55
gac gct ctc ttg acg cat tgc aag tcc agg aaa aac aat tat ggg ttg      198
Asp Ala Leu Leu Thr His Cys Lys Ser Arg Lys Asn Asn Tyr Gly Leu
      -50                               -45                               -40                               -35
ctt ttg aat gag aat gaa agt tta ttt tta atg gtg gta tta tgg aaa      246
Leu Leu Asn Glu Asn Glu Ser Leu Phe Leu Met Val Val Leu Trp Lys
      -30                               -25                               -20
att cca agt aaa gaa ctg agg gtc aga ttg acc ttg cct cat agt att      294
Ile Pro Ser Lys Glu Leu Arg Val Arg Leu Thr Leu Pro His Ser Ile
      -15                               -10                               -5
cga tca gat tca gaa gat atc tgt tna ttt acg aag gat gg      335
Arg Ser Asp Ser Glu Asp Ile Cys Xaa Phe Thr Lys Asp
      1                               5                               10

```

&lt;210&gt; 659

&lt;211&gt; 197

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 20..196

&lt;221&gt; sig\_peptide

&lt;222&gt; 20..106

&lt;223&gt; Von Heijne matrix

score 3.70000004768372

seq LIELNLXSPVALQ/WP

&lt;400&gt; 659

```

attcaacaag caatcaggt atg aat gca gaa ggg gct tcc cca gga aaa gaa      52
                               Met Asn Ala Glu Gly Ala Ser Pro Gly Lys Glu
                               -25                               -20
acg aac aca gga aca ttg ata gag cta aat ctg mcc agc cct gta gcc      100
Thr Asn Thr Gly Thr Leu Ile Glu Leu Asn Leu Xaa Ser Pro Val Ala
      -15                               -10                               -5
ctc cag tgg cca ctt tcc agc ccc tct tgc ctg agg atc ctc agc aac      148
Leu Gln Trp Pro Leu Ser Ser Pro Ser Cys Leu Arg Ile Leu Ser Asn
      1                               5                               10
aag gtg ccc agg aac ctg agg tgg cag aaa cac tac tcc acc cac cag g      197
Lys Val Pro Arg Asn Leu Arg Trp Gln Lys His Tyr Ser Thr His Gln
      15                               20                               25                               30

```

&lt;210&gt; 660

&lt;211&gt; 272

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 28..270

&lt;221&gt; sig\_peptide

&lt;222&gt; 28..216

&lt;223&gt; Von Heijne matrix

score 3.70000004768372

seq MAAAAALRAPAQSV

&lt;400&gt; 660

```

atatttgccct gtcaggtcca tccggcg atg ctg ggt ctg gac gag ctc ggg agg      54
                               Met Leu Gly Leu Asp Glu Leu Gly Arg
                               -60                               -55
agt ggt tgt ggc cat tgc aca cag gcg gat ctg agg ttc ggc gac gcc      102
Ser Gly Cys Gly His Cys Thr Gln Ala Asp Leu Arg Phe Gly Asp Ala
                               -50                               -45                               -40
gct ggy csc gaa ccc cgg gmc agg mca acg cac agg aac acc gcc gca      150
Ala Gly Xaa Glu Pro Arg Xaa Arg Xaa Thr His Arg Asn Thr Ala Ala
                               -35                               -30                               -25
gcc cgc gtt ccc ccc ccg ccc aga gtc atg gcg gca gca gcc gct ctg      198
Ala Arg Val Pro Pro Pro Pro Arg Val Met Ala Ala Ala Ala Ala Leu
                               -20                               -15                               -10
agg gcg cct gct cag agc agt gtg acc ttt gaa gat gtg gct gta aac      246
Arg Ala Pro Ala Gln Ser Ser Val Thr Phe Glu Asp Val Ala Val Asn
                               -5                               1                               5                               10
ttt tcc ctg gag gaa tgg agt ctt ct      272
Phe Ser Leu Glu Glu Trp Ser Leu
                               15

```

&lt;210&gt; 661

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 263..409

&lt;221&gt; sig\_peptide

&lt;222&gt; 263..340

&lt;223&gt; Von Heijne matrix

score 3.70000004768372

seq WGNLSFHLQEAHG/SE

&lt;400&gt; 661

```

tgaaaacaaa catctactaa tgttgtcaga tggtaggaa gcaagattct gcaactatag      60
agggtaagtg tttcttttgt tctgtgggtc ctctctaaaa ctctaagatc ttgaggggtg      120
catttcagaa agtgcagcgt gacccgcagt ttgtgggaag ccatggagct cggcactgcc      180
atcctaatac ttcctaaagc acaaaacccc agagacaatc tggggtcagg agagtggaaag      240
gggcttgtct gccacactgg tg atg agt gcc ctg aaa gac ttc aga gaa ttt      292
                               Met Ser Ala Leu Lys Asp Phe Arg Glu Phe
                               -25                               -20
ctg aac tgg tgg gga aac ctc tct ttt cat ctt cag gaa gct cat gga      340
Leu Asn Trp Trp Gly Asn Leu Ser Phe His Leu Gln Glu Ala His Gly
                               -15                               -10                               -5
agt gaa att gca gaa atg gga gct ggt att cta gag gaa aaa aat tat      388
Ser Glu Ile Ala Glu Met Gly Ala Gly Ile Leu Glu Glu Lys Asn Tyr
1                               5                               10                               15
ggv caa caa wat cac tgt aac ta      411
Gly Gln Gln Xaa His Cys Asn
                               20

```

&lt;210&gt; 662

&lt;211&gt; 146

```

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..145

<221> sig_peptide
<222> 38..127
<223> Von Heijne matrix
      score 3.70000004768372
      seq PPSLFLSLPPSL/PP

<400> 662
awbwcccgcc cacacgtggc caacctttgc gttttta atg tct ctw ccc cct ttt      55
                                   Met Ser Leu Pro Pro Phe
                                   -30                -25

ttc cac cct tct ccc gct ccc tct ctc gct ccc cct ccc tcc ctc ttt      103
Phe His Pro Ser Pro Ala Pro Ser Leu Ala Pro Pro Pro Ser Leu Phe
      -20                -15                -10

ctt tcc ctc cct ccc tct ctt tct ccc cct cta ccc gcc cgg g      146
Leu Ser Leu Pro Pro Ser Leu Ser Pro Pro Leu Pro Ala Arg
      -5                1                5

<210> 663
<211> 65
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..63

<221> sig_peptide
<222> 10..48
<223> Von Heijne matrix
      score 3.70000004768372
      seq MFFLCGFLYLCFI/SF

<400> 663
caatatgct atg ttt ttc ctt tgt ggt ttt ctg tat cta tgt ttt atc tca      51
      Met Phe Phe Leu Cys Gly Phe Leu Tyr Leu Cys Phe Ile Ser
      -10                -5                1

ttt ttt ttt ttt tt      65
Phe Phe Phe Phe
      5

<210> 664
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..182

<221> sig_peptide
<222> 30..155
<223> Von Heijne matrix
      score 3.70000004768372
      seq ALGIFLCPGETLS/AS

<400> 664

```

354

```

cgggatgccg gagccctcgg gccttgag atg aag gca ggc ccc tgc tcc tgc      53
                               Met Lys Ala Gly Pro Cys Ser Cys
                               -40                               -35
cag gag gga ggg agg cag tgg gct cat ggg tcg gtg cct ttg cag ccg      101
Gln Glu Gly Gly Arg Gln Trp Ala His Gly Ser Val Pro Leu Gln Pro
                               -30                               -25                               -20
aca gca cgc ctt gcg gcc ctg ggg atc ttt ctg tgc ccc ggc gag acc      149
Thr Ala Arg Leu Ala Ala Leu Gly Ile Phe Leu Cys Pro Gly Glu Thr
                               -15                               -10                               -5
ctt tcg gcc tca ctg cat tgg aac ccc att ggg                          182
Leu Ser Ala Ser Leu His Trp Asn Pro Ile Gly
      1                               5

```

<210> 665  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 160..318

<221> sig\_peptide  
 <222> 160..228  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq TNLLCLTFQRCQS/YN

```

<400> 665
tacatcagaa accagaggcg gaaaactttc cacggtgata tgcataaaca aatatttcat      60
atTTTTtaca gaaagtctgg ctattgccta tagaaagaca aaaactggta acagccttat      120
tccagctaaa tttgaatgcc aggttgacac taatcatgg atg ctt tcc cag agc      174
                               Met Leu Ser Gln Ser
                               -20
ttt cag aaa aac aaa acc aac ctg ttg tgt tta act ttc caa aga tgt      222
Phe Gln Lys Asn Lys Thr Asn Leu Leu Cys Leu Thr Phe Gln Arg Cys
                               -15                               -10                               -5
cag agt tac aat tgg ctg aat att ttt gaa gct aca tat atg acg act      270
Gln Ser Tyr Asn Trp Leu Asn Ile Phe Glu Ala Thr Tyr Met Thr Thr
      1                               5                               10
ctc ttc att tca gta att aam aca aat ttt tta aaa aga tac ctc ctg      318
Leu Phe Ile Ser Val Ile Xaa Thr Asn Phe Leu Lys Arg Tyr Leu Leu
15                               20                               25                               30
99

```

<210> 666  
 <211> 273  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 180..272

<221> sig\_peptide  
 <222> 180..254  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq QLLGCMVLYDCFS/FK

```

<400> 666
aagttgttgc atgtgtcaat ggttggttct ttttatttct gagtaatggt ccatgatatg      60
aatgtaccac agtttgttta accattcacc cactgaagga cgtttggatt gtttctaagt      120

```

```

tttgactgtg gcaagtaaag atgctatgaa cattcatgta cacatgaatt tgtaggcat      179
atg ttt tta ttt tgc tgg gag aaa agc cca aga atg cag ttg ctg ggt      227
Met Phe Leu Phe Cys Trp Glu Lys Ser Pro Arg Met Gln Leu Leu Gly
-25                      -20                      -15                      -10
tgt atg gta ttg tat gat tgt ttt tct ttt aag aaa ctg ccg ggg g      273
Cys Met Val Leu Tyr Asp Cys Phe Ser Phe Lys Lys Leu Pro Gly
                      -5                      1                      5

```

&lt;210&gt; 667

&lt;211&gt; 149

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 8..148

&lt;221&gt; sig\_peptide

&lt;222&gt; 8..97

&lt;223&gt; Von Heijne matrix

score 3.70000004768372

seq FVCFHFVFCVFC/NV

&lt;400&gt; 667

```

atttttgt atg tct ttt ata tct gtt att ttt cct tta atc ctt tta aac      49
      Met Ser Phe Ile Ser Val Ile Phe Pro Leu Ile Leu Leu Asn
      -30                      -25                      -20
cgt ttt tca ttt gtt tgt ttc ttt cat gtc ttt tac tgt gtt ttc tgc      97
Arg Phe Ser Phe Val Cys Phe Phe His Val Phe Tyr Cys Val Phe Cys
-15                      -10                      -5
aac gtc tct tct ttg ttc tcc tat cag ttt ctt ctt cat ttc tgt gat      145
Asn Val Ser Ser Leu Phe Ser Tyr Gln Phe Leu Leu His Phe Cys Asp
1                      5                      10                      15
gac t      149
Asp

```

&lt;210&gt; 668

&lt;211&gt; 122

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 16..120

&lt;221&gt; sig\_peptide

&lt;222&gt; 16..108

&lt;223&gt; Von Heijne matrix

score 3.70000004768372

seq LGMGMGFFSGVKS/WI

&lt;400&gt; 668

```

caaggaatta cagaa atg cat gaa tac tta cct aga aac ttt cat gac ttt      51
      Met His Glu Tyr Leu Pro Arg Asn Phe His Asp Phe
      -30                      -25                      -20
aat tct ccc aac tct aaa tta ggc atg gga atg ggc ttt ttc tca ggt      99
Asn Ser Pro Asn Ser Lys Leu Gly Met Gly Met Gly Phe Phe Ser Gly
-15                      -10                      -5
gtc aaa tct tgg att gga ggt ga      122
Val Lys Ser Trp Ile Gly Gly
1

```

&lt;210&gt; 669

<211> 288  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 38..286

<221> sig\_peptide  
 <222> 38..145  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq ILMRDFSPSGIFG/AF

<400> 669  
 tcgcgcgggtc ccgcacagcg gacaccagga ctccaaa atg gcg tca rtt gta cca 55  
 Met Ala Ser Xaa Val Pro  
 -35  
 gtg aag gac aag aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc 103  
 Val Lys Asp Lys Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser  
 -30 -25 -20 -15  
 tgg atc ttg atg cgg gac ttc agt cct agt ggc att ttc gga gcg ttt 151  
 Trp Ile Leu Met Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe  
 -10 -5 1  
 caa aga ggt tac tac cgg tac tac aac aag tac atc aat gtg aag aag 199  
 Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys  
 5 10 15  
 ggg agc atc tcg ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt 247  
 Gly Ser Ile Ser Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe  
 20 25 30  
 agc tac tcc ttt tcc tac aag cat ctc aag cac gag tcg gg 288  
 Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys His Glu Ser  
 35 40 45

<210> 670  
 <211> 160  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 89..160

<221> sig\_peptide  
 <222> 89..142  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq GALLWMAWDGQLS/RP

<400> 670  
 cgtcaacatt cttttcatc tgggcctgag cgcgtggatc aagccgctgc ccttgcaact 60  
 gctgagcctg aagctggact tgccggtg atg gtg ata tcg gcc ggg gca ctg 112  
 Met Val Ile Ser Ala Gly Ala Leu  
 -15  
 ctg tgg atg gcg tgg gac ggc cag ctc agc cgc ccc gaa ggc gcc cgt 160  
 Leu Trp Met Ala Trp Asp Gly Gln Leu Ser Arg Pro Glu Gly Ala Arg  
 -10 -5 1 5

<210> 671  
 <211> 137  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 44..136

<221> sig\_peptide  
 <222> 44..97  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq LELLGSSYNPISA/SP

<400> 671  
 gaattttctt cttctgctca ggctggagta caatggcaca atc atg gtt cac tgt 55  
 Met Val His Cys  
 -15  
 aat ctt gaa ctc ctg ggc tca agt tat aat ccc atc tca gcc tct cca 103  
 Asn Leu Glu Leu Leu Gly Ser Ser Tyr Asn Pro Ile Ser Ala Ser Pro  
 -10 -5 1  
 gta gct agg act ata tca tgc ccc gct att gtg g 137  
 Val Ala Arg Thr Ile Ser Cys Pro Ala Ile Val  
 5 10

<210> 672  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 111..491

<221> sig\_peptide  
 <222> 111..374  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq CDLLLARFGLIQS/MK

<400> 672  
 gccgcgctt gttgtgctga ggccgagggg gtcgccattt tggatggtga accctgaagt 60  
 cggtgtctgc tgcgttcacg gcaggattcg gttaggagga acagcacagc atg ctg 116  
 Met Leu  
 ggc tct gga ttt aaa gct gag cgc tta aga gtg aat ttg aga tta gtc 164  
 Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu Arg Leu Val  
 -85 -80 -75  
 ata aat cgc ctt aaa cta ttg gag aaa aag aaa acg gaa ctg gcc cag 212  
 Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Thr Glu Leu Ala Gln  
 -70 -65 -60 -55  
 aaa gca agg aag gag att gct gac tat ctg gct gct ggg aaa gat gaa 260  
 Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly Lys Asp Glu  
 -50 -45 -40  
 cga gct cgg atc cgt gtg gag cac att atc cgg gaa gac tac ctc gtg 308  
 Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp Tyr Leu Val  
 -35 -30 -25  
 gag gcc atg gag atc ctg gag ctg tac tgt gac ctg ctg ctg gct cgg 356  
 Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu Leu Ala Arg  
 -20 -15 -10  
 ttt ggc ctt atc cag tct atg aag gaa cta gat tct ggt ctg gct gaa 404  
 Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly Leu Ala Glu  
 -5 1 5 10  
 tct gtg tct aca ttg atc tgg gct gct cct cga ctc cag tca gaa gtg 452  
 Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln Ser Glu Val  
 15 20 25  
 gct gag ttg aaa ata gtt gct gat cag ctc tgt cca agt at 493  
 Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Pro Ser

30

35

<210> 673  
 <211> 263  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 102..263

<221> sig\_peptide  
 <222> 102..230  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq VWCLXLKLVPALC/IS

<400> 673  
 tcccagcaga aggggyagcg cctggctgtc agcagcgtgt gcctcaggag ggatctgcgg 60  
 tgacgggggtt gttacttcag taggatgagg aagagtcaca a atg cgg ggt tgg mmg 116  
 Met Arg Gly Trp Xaa  
 -40  
 gct cct gct tgg aga sgh ytg arc acy agg aga cta cca atg ggg agc 164  
 Ala Pro Ala Trp Arg Xaa Leu Xaa Thr Arg Arg Leu Pro Met Gly Ser  
 -35 -30 -25  
 agg cac ggt gcc agc ccg gcc tct gcc gtc tgg tgt ctg tmc ctc aag 212  
 Arg His Gly Ala Ser Pro Ala Ser Ala Val Trp Cys Leu Xaa Leu Lys  
 -20 -15 -10  
 tta gtc cca gct ttg tgc att agc ggg ctc acc ctc gga atc cag gga 260  
 Leu Val Pro Ala Leu Cys Ile Ser Gly Leu Thr Leu Gly Ile Gln Gly  
 -5 1 5 10  
 ttc 263  
 Phe

<210> 674  
 <211> 263  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 115..261

<221> sig\_peptide  
 <222> 115..216  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq RLILXFHDNTWG/ST

<221> misc\_feature  
 <222> 136,139..140  
 <223> n=a, g, c or t

<400> 674  
 gtcatttatg ccatattctg tccactagaa atgaattact aagtctggcc caaactcaag 60  
 tggaggcgaa ttaagctgca tctcataagg gaaagagtat cgaagaactt ctgt atg 117  
 Met  
 tat ttt aaa acc act aca nta nnb cat agt gca cat atg ctt ctg caa 165  
 Tyr Phe Lys Thr Thr Xaa Xaa His Ser Ala His Met Leu Leu Gln  
 -30 -25 -20  
 att tgc ttt ttt cgc tta aca atc tta gkt ttc cat gac aat aca tgg 213  
 Ile Cys Phe Phe Arg Leu Thr Ile Leu Xaa Phe His Asp Asn Thr Trp

```

      -15      -10      -5
ggg tca act tca ttc tct twa gtt gck gca atg cta ttc cac tac cgg      261
Gly Ser Thr Ser Phe Ser Xaa Val Ala Ala Met Leu Phe His Tyr Arg
      1              5              10              15
gg      263

<210> 675
<211> 107
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..107

<221> sig_peptide
<222> 30..101
<223> Von Heijne matrix
      score 3.70000004768372
      seq LLFLFFLFLFFFF/FF

<400> 675
tgcactggca cacactcaca gctctgacc atg tca tca aac ata cag aga ctg      53
                               Met Ser Ser Asn Ile Gln Arg Leu
                               -20
ggc ttc cct ctg ctt ttt ctt ttt ttt ctt ttt ctt ttt ttt ttt ttt      101
Gly Phe Pro Leu Leu Phe Leu Phe Phe Leu Phe Leu Phe Phe Phe Phe
      -15      -10      -5
ttt ttt      107
Phe Phe
1

<210> 676
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 70..276

<221> sig_peptide
<222> 70..270
<223> Von Heijne matrix
      score 3.70000004768372
      seq LVLPLPMLPTS NR/KR

<400> 676
gtcacagcac cctcctgaaa actgcagctt ccttctcacc ttgaagaata atcctagaaa      60
actcacaaa atg tgt gat gct ttt gta ggt acc tgg aaa ctt gtc tcc agt      111
      Met Cys Asp Ala Phe Val Gly Thr Trp Lys Leu Val Ser Ser
      -65      -60      -55
gaa aac ttt gat gat tat atg aaa gaa gta gga gtg ggc ttt gcc acc      159
Glu Asn Phe Asp Asp Tyr Met Lys Glu Val Gly Val Gly Phe Ala Thr
      -50      -45      -40
agg aaa gtg gct ggc atg gcc aaa cct aac atg atc atc agt gtg aat      207
Arg Lys Val Ala Gly Met Ala Lys Pro Asn Met Ile Ile Ser Val Asn
      -35      -30      -25
ggg gat gtg atc acc att ccc cac ctg gtc ctc ccc ctt ccc atg ctg      255
Gly Asp Val Ile Thr Ile Pro His Leu Val Leu Pro Leu Pro Met Leu
      -20      -15      -10
cca act tct aac cgc aag agg      276
Pro Thr Ser Asn Arg Lys Arg

```

-5

1

&lt;210&gt; 677

&lt;211&gt; 441

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 337..441

&lt;221&gt; sig\_peptide

&lt;222&gt; 337..399

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq GQLLSFLLGTYLG/RR

&lt;400&gt; 677

```

gggattcaag gaggcccatc atgtcagaat gctgtgggtt ggcaggaggc atcacaatga      60
aattttccat gttcccaaat ttgatattca cagtactaca tataatttct caggaagat      120
agggttggac acgatggaaa tattttgggtg aaccattcgt tcccttgggt ttcttttca      180
tttggggagt gtggtttaca atgattggag caaaagtttc ctgaatcttt ttcttgtttc      240
cattttattg catggtaaaa cacaatttat ccactttctt gtcaatgagt atctagttag      300
attcctgttt tttggctaatt tcaaataaaa ctatga atg ttt ttg tac cgg tct      354
                                     Met Phe Leu Tyr Arg Ser
                                     -20
ttt ggt ggg cag ttg ctt tcc ttt ctc ttg ggt aca tac cta gga agg      402
Phe Gly Gly Gln Leu Leu Ser Phe Leu Leu Gly Thr Tyr Leu Gly Arg
-15          -10          -5          1
agg gaa gtt gct ggg cca cag cat ggc cag ttt tct aaa      441
Arg Glu Val Ala Gly Pro Gln His Gly Gln Phe Ser Lys
          5          10

```

&lt;210&gt; 678

&lt;211&gt; 191

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 135..191

&lt;221&gt; sig\_peptide

&lt;222&gt; 135..182

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq FFCLCAFNSFLLS/PE

&lt;400&gt; 678

```

aagtgtgtgt tgctgcggca scacggaggc caaggacctc acggkwstaa aagatgacga      60
gactggcttc gggagaaaca ccatccagaa gagaccttcc aaaaaacttc tagagactcc      120
ccaagacgta tgag atg ama ggc ttc ttc tgt ctg tgt gcg ttt aac tca      170
                                     Met Xaa Gly Phe Phe Cys Leu Cys Ala Phe Asn Ser
                                     -15          -10          -5
ttt ctc ctt agc ccc gag ggg      191
Phe Leu Leu Ser Pro Glu Gly
          1

```

&lt;210&gt; 679

&lt;211&gt; 235

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 31..234

&lt;221&gt; sig\_peptide

&lt;222&gt; 31..228

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq LTSFLSIXIFVNP/TR

&lt;400&gt; 679

```

atttttcacc actgcatagt gttacattgt atg att ttc cca cat tgc atg tac      54
                                Met Ile Phe Pro His Cys Met Tyr
                                -65                    -60
tgt tta gag tgt ata act aag aat gga ttg cta ggt tta aag gtg ctt      102
Cys Leu Glu Cys Ile Thr Lys Asn Gly Leu Leu Gly Leu Lys Val Leu
                    -55                    -50                    -45
cca ctc tat ggg ata atg cta att ttt ttc cct aaa gtg gtt tat aac      150
Pro Leu Tyr Gly Ile Met Leu Ile Phe Phe Pro Lys Val Val Tyr Asn
                    -40                    -35                    -30
aat caa ccc ttg cac tac aag tca gta atg gtg ttt cag ttg act tca      198
Asn Gln Pro Leu His Tyr Lys Ser Val Met Val Phe Gln Leu Thr Ser
                    -25                    -20                    -15
ttc ttg tcg att tka att ttt gtc aac ccc act cgg g                      235
Phe Leu Ser Ile Xaa Ile Phe Val Asn Pro Thr Arg
-10                    -5                    1

```

&lt;210&gt; 680

&lt;211&gt; 410

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 173..409

&lt;221&gt; sig\_peptide

&lt;222&gt; 173..334

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq LMAXLLTVEVTHP/NS

&lt;221&gt; misc\_feature

&lt;222&gt; 305

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 680

```

taatcgaaaa gctcagtgcg cagggcgcaa gaagctggca ggggcacgag ccgggggcgg      60
gtttgaagac gcgtcggttg gttttggagg ccgtgaaaca gccgtttgag tttggctgcg      120
ggtaggagaac gtttgtcagg ggcccggcca agaaggaggc ccgcctgtta cg atg gtg      178
                                Met Val
tcc atg agt ttc aag cgg aac cgc agt gac cgg ttc tac agc acc cgg      226
Ser Met Ser Phe Lys Arg Asn Arg Ser Asp Arg Phe Tyr Ser Thr Arg
                    -50                    -45                    -40
tgc tgc ggc tgt tgc cat gtc cgc rcc ggg acg atc atc ctg ggg acc      274
Cys Cys Gly Cys Cys His Val Arg Xaa Gly Thr Ile Ile Leu Gly Thr
                    -35                    -30                    -25
tgg tac atg gta gta aac cta ttg atg gca nbt ttg ctg act gtg gaa      322
Trp Tyr Met Val Val Asn Leu Leu Met Ala Xaa Leu Leu Thr Val Glu
-20                    -15                    -10                    -5
gtg act cat cca aac tcc atg cca gct gtc aac att cag tat gaa gtc      370
Val Thr His Pro Asn Ser Met Pro Ala Val Asn Ile Gln Tyr Glu Val

```

```

          1             5             10
atc ggt aat tac tat tcg tct gag aga atg gct gat aat g      410
Ile Gly Asn Tyr Tyr Ser Ser Glu Arg Met Ala Asp Asn
          15             20             25

```

<210> 681  
 <211> 303  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 21..302

<221> sig\_peptide  
 <222> 21..113  
 <223> Von Heijne matrix  
       score 3.59999990463257  
       seq STFALTIXRXXSC/SS

<221> misc\_feature  
 <222> 102  
 <223> n=a, g, c or t

```

<400> 681
gagttkgact gtgaagaaac atg gcg gcc gcg acg ttg act tcg aaa ttg tac      53
                Met Ala Ala Ala Thr Leu Thr Ser Lys Leu Tyr
                -30                -25
tcc ctg ctg ttc cgc agg acc tcc acc ttc gcc ctc acc atc akc cgt      101
Ser Leu Leu Phe Arg Arg Thr Ser Thr Phe Ala Leu Thr Ile Xaa Arg
-20                -15                -10                -5
ngg gsg tca tgt tct tcg rgc gcg cct tcg atc aag gcg cgg acg cta      149
Xaa Xaa Ser Cys Ser Ser Xaa Ala Pro Ser Ile Lys Ala Arg Thr Leu
          1             5             10
tct acg acc aca tca acg agg gga agc tgt gga aac aca tca agc aca      197
Ser Thr Thr Thr Ser Thr Arg Gly Ser Cys Gly Asn Thr Ser Ser Thr
          15             20             25
agt atg aga aca agt agt tcc ttg gag gcc ccc atc cag gcc aga agg      245
Ser Met Arg Thr Ser Ser Ser Leu Glu Ala Pro Ile Gln Ala Arg Arg
          30             35             40
acc agg tcc acc cag cag ctg ttt gcc cag agc tgg agc ctc agc dtg      293
Thr Arg Ser Thr Gln Gln Leu Phe Ala Gln Ser Trp Ser Leu Ser Xaa
          45             50             55             60
aag atg atg c
Lys Met Met

```

<210> 682  
 <211> 328  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 79..327

<221> sig\_peptide  
 <222> 79..201  
 <223> Von Heijne matrix  
       score 3.59999990463257  
       seq LHTSVTLFLLSYC/DC

<221> misc\_feature

&lt;222&gt; 258

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 682

```

agatgattcc ctgattctcc agagagatta cacacttcgt ttgtggctaa ggttactgtg      60
acccaatgaa agaagaaa atg aaa gcc ata aag aaa agt ctt aca gaa gaa      111
                Met Lys Ala Ile Lys Lys Ser Leu Thr Glu Glu
                -40                -35
gaa tac ctg tac ctg gac ttt tct cac caa aca gaa gga tgc atc ttt      159
Glu Tyr Leu Tyr Leu Asp Phe Ser His Gln Thr Glu Gly Cys Ile Phe
-30                -25                -20                -15
cct ctt cat aca tct gta act tta ttt ctg tta tct tac tgt gac tgt      207
Pro Leu His Thr Ser Val Thr Leu Phe Leu Leu Ser Tyr Cys Asp Cys
                -10                -5                1
aaa atc ttt aaa att tgc tta gtt gtc acc aaa gag gtg agt aga gat      255
Lys Ile Phe Lys Ile Cys Leu Val Val Thr Lys Glu Val Ser Arg Asp
                5                10                15
avn tca cta cta aga gat gac ctg atc cag gat gtt gaa ata cag att      303
Xaa Ser Leu Leu Arg Asp Asp Leu Ile Gln Asp Val Glu Ile Gln Ile
                20                25                30
att tca agg cag gag ctc cca cca a      328
Ile Ser Arg Gln Glu Leu Pro Pro
35                40

```

&lt;210&gt; 683

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 386..445

&lt;221&gt; sig\_peptide

&lt;222&gt; 386..427

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq FLCVCYFIRKSTS/FF

&lt;221&gt; misc\_feature

&lt;222&gt; 307

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 683

```

ttaacatctt ccactgaaaa gaaaagataa tgatataaat aaagcaattt aaatcaagtc      60
taaggatatag gaaggatattt aagaaagaag caaacattct ctgatgttg ttatccaaaa      120
tatattctct tttgcagttt actgaaataa tttcttcagt gtgtgggaat ttcctttgca      180
tccagcttta ctatagagat gacatcacac caacagtgac acgacttggt tacaagaggg      240
tggtataaac agcaaattgtt cttccttaaa acagatttct tggtgaactt caacagaaaa      300
agaagcngta aatgtagaag gaagaacagg agatagtctt taacatgtag ggtaaaatct      360
aaggtagagg agagagcagc tgata atg ttt tta tgt gtt tgc tac ttt att      412
                Met Phe Leu Cys Val Cys Tyr Phe Ile
                -10
agg aag tct act tcc ttc ttt tcc ata tct agt ag      447
Arg Lys Ser Thr Ser Phe Phe Ser Ile Ser Ser
-5                1                5

```

&lt;210&gt; 684

&lt;211&gt; 217

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
 <221> CDS  
 <222> 5..217

<221> sig\_peptide  
 <222> 5..139  
 <223> Von Heijne matrix  
 score 3.59999990463257  
 seq AWWLLLPVWKLGG/QL

<400> 684  
 tcaa atg ggg aag ccg aga ggt ggt gag atg ctt gag gtt gta aag act 49  
 Met Gly Lys Pro Arg Gly Gly Glu Met Leu Glu Val Val Lys Thr  
 -45 -40 -35  
 gtc tcc act ttc act ttg gga ggg tgg aaa ggg act gct cct gtg tcc 97  
 Val Ser Thr Phe Thr Leu Gly Gly Trp Lys Gly Thr Ala Pro Val Ser  
 -30 -25 -20 -15  
 tgc gcc tgg tgg ctg ctt ctc cca gtt tgg aag ctg gga ggg cag ctt 145  
 Cys Ala Trp Trp Leu Leu Leu Pro Val Trp Lys Leu Gly Gly Gln Leu  
 -10 -5 1  
 gag cgc agg aag aat cca aag gaa tac tgt ctt ggc tcc tgg gtg tgg 193  
 Glu Arg Arg Lys Asn Pro Lys Glu Tyr Cys Leu Gly Ser Trp Val Trp  
 5 10 15  
 ctc agt cct cag ctg gct cca agg 217  
 Leu Ser Pro Gln Leu Ala Pro Arg  
 20 25

<210> 685  
 <211> 132  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 77..130

<221> sig\_peptide  
 <222> 77..124  
 <223> Von Heijne matrix  
 score 3.59999990463257  
 seq FTFISTLLFVFLG/VV

<400> 685  
 tgaaatccta gcttgaatat ttacattagt cttgtttctc aaacttgact ctttggtttg 60  
 atcgacattt tcccta atg ctg att ttc acc ttt att tct act ttg ctg ttt 112  
 Met Leu Ile Phe Thr Phe Ile Ser Thr Leu Leu Phe  
 -15 -10 -5  
 gta ttc ttg gga gtt gtg gg 132  
 Val Phe Leu Gly Val Val  
 1

<210> 686  
 <211> 260  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 120..260

<221> sig\_peptide  
 <222> 120..230

<223> Von Heijne matrix  
score 3.59999990463257  
seq PGSGLC SMAAVQA/GN

<400> 686  
acatctcctt ggccccgccc cactcccgcg gggctattgt ccccggtaaa ctgcagtttc 60  
tggttcgaga ctccaatcct gtttcgaatt gctgcttgct gccccttggg ctggggata 119  
atg gaa gtt ctt tcb mtt ccc aac tct ttc cag acc caa gca ctc tgg 167  
Met Glu Val Leu Ser Xaa Pro Asn Ser Phe Gln Thr Gln Ala Leu Trp  
-35 -30 -25  
gac tca ctc cat agt cca gga gtt cca ggt tcc gga tta tgt tcc atg 215  
Asp Ser Leu His Ser Pro Gly Val Pro Gly Ser Gly Leu Cys Ser Met  
-20 -15 -10  
gca gca gtc caa gca gga aac caa gcc atc tac tct gcc tgc ggg 260  
Ala Ala Val Gln Ala Gly Asn Gln Ala Ile Tyr Ser Ala Ser Gly  
-5 1 5 10

<210> 687  
<211> 473  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 332..472

<221> sig\_peptide  
<222> 332..457  
<223> Von Heijne matrix  
score 3.59999990463257  
seq LLTQAGFP RRGEA/AP

<400> 687  
tgtgtatgtg tgaaaatcag gaagagccag cggggagtgt gtgttgccat cgcgtctccg 60  
cctgcagggg cgggacccca ggaggaggga gaggacagag cactgcaga ggaccagact 120  
gggaaaacaa cgatatggca ggagccagtc ttggggcccg cttctaccgg cagatcaaaa 180  
gacatccggg gctgggacag aaagaacaac ccggagccct ggaaccgcct gagccccaat 240  
gaccaataca agttccttgc agtttcact gactataaga agctgaagaa ggaccggcca 300  
gacttctaag ccaggctggg ctgccagtgc c atg caa gcc aca gcc agc cag 352  
Met Gln Ala Thr Ala Ser Gln  
-40  
ccc atc cac ttc ttc crs tcc tcc ccg cag gcc cca agg cat cac tcc 400  
Pro Ile His Phe Phe Xaa Ser Ser Pro Gln Ala Pro Arg His His Ser  
-35 -30 -25 -20  
ggc cac cct gtc ccg cta ctg ctt aca cag gcc ggg ttc cca cgc aga 448  
Gly His Pro Val Pro Leu Leu Leu Thr Gln Ala Gly Phe Pro Arg Arg  
-15 -10 -5  
ggg gag gct gct cca ccc cta ctc c 473  
Gly Glu Ala Ala Pro Pro Leu Leu  
1 5

<210> 688  
<211> 107  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 5..106

<221> sig\_peptide  
<222> 5..94  
<223> Von Heijne matrix

score 3.59999990463257  
seq LCTFTLNLTAVRT/IX

<400> 688  
acac atg cga ggg tak aac tgh gtg ttc agg gtt ttc tct gaa agc ctg 49  
Met Arg Gly Xaa Asn Xaa Val Phe Arg Val Phe Ser Glu Ser Leu  
-30 -25 -20  
aag gga ttg tgt acw ttt aca ttg aac ttg act gca gtt aga acc att 97  
Lys Gly Leu Cys Thr Phe Thr Leu Asn Leu Thr Ala Val Arg Thr Ile  
-15 -10 -5 1  
arc cta gat g 107  
Xaa Leu Asp

<210> 689  
<211> 377  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 258..377

<221> sig\_peptide  
<222> 258..353  
<223> Von Heijne matrix  
score 3.59999990463257  
seq RLTIISTXLSTSXX/FM

<400> 689  
aaacacaaca accagattcc tcctctaaag aagcccctgg gagcacagct catcaccatg 60  
gactggacct ggaggttcct ctttttggtg acagcagcta cagatgtcca gtcccaggtc 120  
cagctggtgc aagtctgggt actgaggtga agaggcctgg gtccctcggg aaggtctcct 180  
gtaagacttc tggaggcacc ttcagtagta atgccatcac gtgggtgcga caggcccctg 240  
gacaagggct tgagtgg atg ggr agg atc atc ccc atg gtt gaa aaa gcg 290  
Met Gly Arg Ile Ile Pro Met Val Glu Lys Ala  
-30 -25  
gac acc gca cag aag ttc cag ggc aga ctc act att agt aca dkv cta 338  
Asp Thr Ala Gln Lys Phe Gln Gly Arg Leu Thr Ile Ser Thr Xaa Leu  
-20 -15 -10  
tcg acg agc asa gsc ttc atg gaa ctg agc agt ctg aga 377  
Ser Thr Ser Xaa Xaa Phe Met Glu Leu Ser Ser Leu Arg  
-5 1 5

<210> 690  
<211> 388  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 53..388

<221> sig\_peptide  
<222> 53..253  
<223> Von Heijne matrix  
score 3.59999990463257  
seq IIMVFVFICFCYL/HY

<400> 690  
ataaattcag tagttacctt agtagacaaa tcatttgaac caagttgcgg ac atg aat 58  
Met Asn  
ctt gtt att tgt gtc cta ctt ttg tcc att tgg aaa aat aat tgc atg 106  
Leu Val Ile Cys Val Leu Leu Leu Ser Ile Trp Lys Asn Asn Cys Met

367

-65		-60		-55		-50	
act aca aac caa acc aat gga tct tct act aca gga gat aaa cct gtt							154
Thr Thr Asn Gln Thr Asn Gly Ser Ser Thr Thr Gly Asp Lys Pro Val							
	-45		-40		-35		
gaa tca atg cag aca aaa ttg aac tac ctt aga aga aat cta ctc att							202
Glu Ser Met Gln Thr Lys Leu Asn Tyr Leu Arg Arg Asn Leu Leu Ile							
	-30		-25		-20		
tta gtt ggt att atc atc atg gtt ttt gtc ttt atc tgt ttt tgt tat							250
Leu Val Gly Ile Ile Ile Met Val Phe Val Phe Ile Cys Phe Cys Tyr							
	-15		-10		-5		
ctc cat tat aat tgt ctg agc gat gat gcg tcc aaa gca gga atg gtc							298
Leu His Tyr Asn Cys Leu Ser Asp Asp Ala Ser Lys Ala Gly Met Val							
	1		5		10		15
aag aaa aaa ggc ata gca gcc aag tca tct aaa aca tca ttc agt gaa							346
Lys Lys Lys Gly Ile Ala Ala Lys Ser Ser Lys Thr Ser Phe Ser Glu							
	20		25		30		
gcc aag aca gcc tct caa tgc agt tca gaa aca caa acc ggg							388
Ala Lys Thr Ala Ser Gln Cys Ser Ser Glu Thr Gln Thr Gly							
	-35		-40		-45		

&lt;210&gt; 691

&lt;211&gt; 408

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 304..408

&lt;221&gt; sig\_peptide

&lt;222&gt; 304..387

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq IFFSLTLTGCKFS/KL

&lt;400&gt; 691

cttgacttct gtgcactcac aggcttgatc aacaccacaa ggaagctgcc aaggccatcc	60
tctgaaacca cagcccgagc tctatgttgg ccccttttag ccatggctgg aatggctgag	120
acacaggaca ccaagtcctt aggctgtaca cagcactggg accctgggcc ctgcccattg	180
aacaattttt tcttcctaaa tcttcaggcc tgtgatggga ggggctaccg caaaggtctc	240
tgacatgccc cagatacatt ttcctattg tcttggggat taacatttgg ctctctgcta	300
ctt atg caa att tct gca gcc agc ttg aat ttc tcc tca aaa aat gga	348
Met Gln Ile Ser Ala Ala Ser Leu Asn Phe Ser Ser Lys Asn Gly	
	-25
att ttc ttt tct tta aca ttg tca ggc tgc aaa ttt tcc aaa ctt tta	396
Ile Phe Phe Ser Leu Thr Leu Ser Gly Cys Lys Phe Ser Lys Leu Leu	
	-10
tgc cct ttt ggg	408
Cys Pro Phe Gly	
	5

&lt;210&gt; 692

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 106..321

&lt;221&gt; sig\_peptide

&lt;222&gt; 106..261

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq LVWDCLLPPPSFF/LL

&lt;221&gt; misc\_feature

&lt;222&gt; 284..285

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 692

tgttacctgt	gtgcatatat	tatatctact	taagttttat	tctaaataag	gagcttgtga	60
tarttgtttc	cgttttgtaa	ttagaaggta	ttatatgttc	ctatc atg att ttt gag		117

Met Ile Phe Glu

-50

cct gtg gtt	ctg aaa cca	gtg ttt cta	aat att ttt	ttc ttt tca	cat	165
Pro Val Val	Leu Lys Pro	Val Phe Leu	Asn Ile Phe	Phe Phe Phe	Ser His	

-45

-40

-35

cat gta ttt	aca gtg ttt	ttc agt ggt	agt cat gtt	gac atc ctg	agt	213
His Val Phe	Thr Val Phe	Phe Ser Gly	Ser His Val	Asp Ile Leu	Ser	

-30

-25

-20

cgc aca gtt	ctt gtt tgg	gac tgt ctt	ctt cct cct	cct tcc ttc	ttc	261
Arg Thr Val	Leu Val Trp	Asp Cys Leu	Leu Pro Pro	Pro Ser Phe	Phe	

-15

-10

-5

ctc ctt ctt	ctt tct tct	tcc tnn tcc	ttv ctc ctc	ctt vct dct	tct	309
Leu Leu Leu	Leu Ser Ser	Ser Xaa Ser	Xaa Leu Leu	Leu Xaa Xaa	Ser	

1

5

10

15

tcc tcc tcc	cgg g					322
Ser Ser Ser	Arg					

20

&lt;210&gt; 693

&lt;211&gt; 153

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 93..152

&lt;221&gt; sig\_peptide

&lt;222&gt; 93..134

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq LVPLLSHLLFKFT/WP

&lt;400&gt; 693

cttttttagt	aggggagctt	gataatggaa	aacagtatga	ggaattgtca	cactgtatga	60
gatttttaaac	taaggcataa	gaatgaaacc	gg atg tta	gtt cct ctt	tta tca	113

Met Leu Val Pro Leu Leu Ser

-10

cac ttg ctc	ttc aag ttt	acc tgg cca	aaa tkg tcc	cag g		153
His Leu Leu	Phe Lys Phe	Thr Trp Pro	Lys Xaa Ser	Gln		

-5

1

5

&lt;210&gt; 694

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 23..232

&lt;221&gt; sig\_peptide

&lt;222&gt; 23..169

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq FGVLSGLXQXVSP/GK

&lt;400&gt; 694

```

aagcgcggga cgcwrcaaag tc atg gac cgc aac ccc tcg ccg ccg ccg      52
                               Met Asp Arg Asn Pro Ser Pro Pro Pro
                               -45                               -40
ggt cgc gac aag gag gag gag gag gag gtg gcc ggt gga gac tgc ata    100
Gly Arg Asp Lys Glu Glu Glu Glu Val Ala Gly Gly Asp Cys Ile
                               -35                               -30                               -25
ggg agc acg gtc tac agc aaa cac tgg ctc ttc ggc gtc ctc agc gga    148
Gly Ser Thr Val Tyr Ser Lys His Trp Leu Phe Gly Val Leu Ser Gly
                               -20                               -15                               -10
ctc akc cag rtt gtt agc cct gga aaa cac caa aat cta ggc tca grt    196
Leu Xaa Gln Xaa Val Ser Pro Gly Lys His Gln Asn Leu Gly Ser Xaa
                               -5                               1                               5
gmt gag gag cag ctg acg gag ctt gat gaa cga aat gg                234
Xaa Glu Glu Gln Leu Thr Glu Leu Asp Glu Arg Asn
10                               15                               20

```

&lt;210&gt; 695

&lt;211&gt; 455

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 344..454

&lt;221&gt; sig\_peptide

&lt;222&gt; 344..412

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq LGCHFFSLALLNT/GP

&lt;221&gt; misc\_feature

&lt;222&gt; 285,342..343

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 695

```

tgttatatgg gtctcttgaa gacaatatac agttgggtct ttcttcttta ttcaacttac    60
cactctgtgc cttttaagtg gggcatttag ctaakwtaca ttcaagggtta atattgatat    120
gtgcatattt gatcctgtca tsatgttamc tggtcgttat tcagactaga ttgtgtagtt    180
tttttatagt gtgtcagtag ttacgttttg tgggtggtcag tgacagtgat ttttttcccc    240
atgttttagca tccctttaag gacctattgt aaagcaggtc tagtngtaac aaatttcctt    300
ggcatttact tatcaggaaa ggatcttttt ttctcctttg cnn atg aag ctt agt      355
                               Met Lys Leu Ser
                               -20
ttg gct gga tat gaa att ctt ggt tgt cat ttc ttt tct tta gca ctg      403
Leu Ala Gly Tyr Glu Ile Leu Gly Cys His Phe Phe Ser Leu Ala Leu
                               -15                               -10                               -5
cta aat aca ggc ccc caa tat ctt ttg gct tat agg gtt tct gct gaa      451
Leu Asn Thr Gly Pro Gln Tyr Leu Leu Ala Tyr Arg Val Ser Ala Glu
                               1                               5                               10
agg t                                                                455
Arg

```

&lt;210&gt; 696

&lt;211&gt; 153

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 8..151

&lt;221&gt; sig\_peptide

&lt;222&gt; 8..127

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq ITALSQSLQPLRK/LP

&lt;400&gt; 696

agacaag atg gcg acg tcc gtg ggg cac cga tgt ctg gga tta ctg cac	49
Met Ala Thr Ser Val Gly His Arg Cys Leu Gly Leu Leu His	
-40 -35 -30	
ggg gtc gcg ccg tgg cgg agc agc ctc cat ccc tgt gag atc act gcc	97
Gly Val Ala Pro Trp Arg Ser Ser Leu His Pro Cys Glu Ile Thr Ala	
-25 -20 -15	
ctg agc caa tcc cta cag ccc tta cgg aag ctg cct ttt aga gcc tct	145
Leu Ser Gln Ser Leu Gln Pro Leu Arg Lys Leu Pro Phe Arg Ala Ser	
-10 -5 1 5	
ygc acg gg	153
Xaa Thr	

&lt;210&gt; 697

&lt;211&gt; 493

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 116..493

&lt;221&gt; sig\_peptide

&lt;222&gt; 116..262

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq YCLVTLVFFYSSA/SF

&lt;400&gt; 697

aaaagctgac gacttcggtc tgcgccggaa gtgcatgagc tgccgatgtg gtgcttagtg	60
attgcgggttt cggtcgctct cccgtgtttc ccgggctggg tatttgctc gcacc atg	118
Met	
gcg ccc aag ggc aaa gtg ggc acg aga ggg aag aag cag ata ttt gaa	166
Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe Glu	
-45 -40 -35	
gag aac aga gag act ctg aag ttc tac ctg cgg atc ata ctg ggg gcc	214
Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly Ala	
-30 -25 -20	
aat gcc att tac tgc ctt gtg acg ttg gtc ttc ttt tac tca tct gcc	262
Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser Ala	
-15 -10 -5	
tca ttt tgg gcc tgg ttg gcc ctg ggc ttt agt ctg gca gtg tat ggg	310
Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr Gly	
1 5 10 15	
gcc agc tac cac tct atg agc tcg atg gca cga gca gcg ttc tct gag	358
Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser Glu	
20 25 30	
gat ggg gcc ctg atg gat ggt ggc atg gac ctc aac atg gag cag ggc	406
Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln Gly	
35 40 45	
atg gca gag cac ctt aag gat gtk atc cta ctg aca gcc atc gtg cag	454

Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val Gln  
 50 55 60  
 gtg ctc agc tgc ttc tct ctc tat gtc tgg tcc ttc tgg 493  
 Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp  
 65 70 75

<210> 698  
 <211> 174  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 8..172

<221> sig\_peptide  
 <222> 8..94  
 <223> Von Heijne matrix  
 score 3.59999990463257  
 seq AFNKAVWFPCSC/QE

<400> 698  
 aacaaag atg gcg gcg gtg act gtg acg gtg acg aag acg gcg gcg gcg 49  
 Met Ala Ala Val Thr Val Thr Val Thr Lys Thr Ala Ala Ala  
 -25 -20  
 gcg acg gca ttt aac aag gcg gtg tgg ttt act cca tgc agt tgt cag 97  
 Ala Thr Ala Phe Asn Lys Ala Val Trp Phe Thr Pro Cys Ser Cys Gln  
 -15 -10 -5 1  
 gag gta agt agc agg ctg ccg gct cgg acg gcg gcg acg cgg cag gac 145  
 Glu Val Ser Ser Arg Leu Pro Ala Arg Thr Ala Ala Thr Arg Gln Asp  
 5 10 15  
 agg gcg gat aag aag gag cgg ccc tgt gg 174  
 Arg Ala Asp Lys Lys Glu Arg Pro Cys  
 20 25

<210> 699  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 199..300

<221> sig\_peptide  
 <222> 199..255  
 <223> Von Heijne matrix  
 score 3.59999990463257  
 seq PGSAICLWHSTLG/GX

<221> misc\_feature  
 <222> 261  
 <223> n=a, g, c or t

<400> 699  
 atttgtctc ggcagcgggtg gccgwagctc catcgcattht tatgtttctg gcgagaaggg 60  
 aacggagttt tcatcaggta gattggtttt trtgcggccg tcctccaccg tttctccag 120  
 gacagcacct agtcgtggcc ggaggagtct catagctgtc agaaagaata agactgattt 180  
 tatgggaaaa ttaagcag atg ctc cag ttt gag aaa cct gga tct gcg atc 231  
 Met Leu Gln Phe Glu Lys Pro Gly Ser Ala Ile  
 -15 -10  
 tgt ttg tgg cac agc act ttg gga ggy ymn ggc ggg cgt gag att gds 279

372

Cys Leu Trp His Ser Thr Leu Gly Gly Xaa Gly Gly Arg Glu Ile Xaa  
 -5 1 5  
 agt ttg aga cca gcc tgc ggg 300  
 Ser Leu Arg Pro Ala Cys Gly  
 10 15

<210> 700  
 <211> 159  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 86..157

<221> sig\_peptide  
 <222> 86..139  
 <223> Von Heijne matrix  
 score 3.59999990463257  
 seq LAILLKWVSNSKS/FL

<400> 700  
 ttttatagct atcacaaatg agattgcttt ctttaattttt tttcagatta atcatagtta 60  
 acaaatagaa actattgatt ttygt atg ttg att tcg tat ctt gca att tta 112  
 Met Leu Ile Ser Tyr Leu Ala Ile Leu  
 -15 -10  
 cta aaa tgg gtt agc aat tct aag agt ttt ttg gtg aag gca tcg gg 159  
 Leu Lys Trp Val Ser Asn Ser Lys Ser Phe Leu Val Lys Ala Ser  
 -5 1 5

<210> 701  
 <211> 274  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 46..273

<221> sig\_peptide  
 <222> 46..90  
 <223> Von Heijne matrix  
 score 3.59999990463257  
 seq LQTLAFWSAYVPC/QT

<400> 701  
 agtgtgtccg gaattgggtgg gttcttggtc tcaactgagtt ctaga atg aag ctg cag 57  
 Met Lys Leu Gln  
 -15  
 acc ctc gca ttc tgg tca gcc tat gtg cca tgc cag acc cag gac cgg 105  
 Thr Leu Ala Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg  
 -10 -5 1 5  
 gat gcc ccg cgc ctc acc ctg gag cag att gac ctc ata cgc cgc atg 153  
 Asp Ala Pro Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg Met  
 10 15 20  
 tgt gcc tcc tat tct gag ctg gag ctt gtg acc tcg gct aaa gct ctg 201  
 Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys Ala Leu  
 25 30 35  
 aac gac act cag aaa ttg gcc tgc ctc atc ggt gta gag ggt ggc cac 249  
 Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu Gly Gly His  
 40 45 50  
 tcg ctg gac aat agc ctc tcc agg g 274  
 Ser Leu Asp Asn Ser Leu Ser Arg

55

60

<210> 702  
 <211> 175  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 107..175

<221> sig\_peptide  
 <222> 107..148  
 <223> Von Heijne matrix  
 score 3.5  
 seq PACLSSFVIPSSL/SP

<400> 702  
 ttgctttcta agacacttac tttcatcggc actttcagat ttttgaatta tacttttctca 60  
 atttgatttt tcaagtgagt tattaggata taggtgggag tggaga atg cct gcc 115  
 Met Pro Ala  
 tgc ctt tct tcc ttt gtc att ccc tct ctg ctt tct ccc tcc tcc cct 163  
 Cys Leu Ser Ser Phe Val Ile Pro Ser Leu Leu Ser Pro Ser Ser Pro  
 -10 -5 1 5  
 ccc tcc ata ggg 175  
 Pro Ser Ile Gly

<210> 703  
 <211> 298  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 197..298

<221> sig\_peptide  
 <222> 197..244  
 <223> Von Heijne matrix  
 score 3.5  
 seq SFAGSCTILGASS/HS

<400> 703  
 ttttcatgtg tctgttggt gcataaatgt cttcttctga gaagtgtctg ttcatactct 60  
 tgcgccactt gttgatgagg ttgttttttt cttgttaaatt tgtttgtgtt cattgtaagt 120  
 tctggatatt agccctttgt cagatgagta gattgtaaaa attttctccc attctacagg 180  
 ttgcctgttc actctg atg gta gtt tct ttt gct ggt tct tgc aca att cta 232  
 Met Val Val Ser Phe Ala Gly Ser Cys Thr Ile Leu  
 -15 -10 -5  
 ggc gcc agt agc cat tca ttc ccc att gaa gtc agc ctg ttc cca gtg 280  
 Gly Ala Ser Ser His Ser Phe Pro Ile Glu Val Ser Leu Phe Pro Val  
 1 5 10  
 gac tgt ggc ttc ctg ttg 298  
 Asp Cys Gly Phe Leu Leu  
 15

<210> 704  
 <211> 136  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 41..136

<221> sig\_peptide

<222> 41..100

<223> Von Heijne matrix

score 3.5

seq AVSQSWLAAPSTS/WV

<400> 704

```

ttcttatttaa agatttattt ttgtagagac agatgtctca atg tgt tgc cca ggc      55
                                         Met Cys Cys Pro Gly
                                         -20
tgg aac gca gtg tgc caa tct tgg ctc gct gca cct tcc acc tcc tgg      103
Trp Asn Ala Val Ser Gln Ser Trp Leu Ala Ala Pro Ser Thr Ser Trp
-15                               -10                               -5                               1
gtt caa gag att ctc gta ctt cag cct cca ggg      136
Val Gln Glu Ile Leu Val Leu Gln Pro Pro Gly
                    5                               10

```

<210> 705

<211> 433

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 225..431

<221> sig\_peptide

<222> 225..386

<223> Von Heijne matrix

score 3.5

seq IRCPLIFLXXVSG/TX

<400> 705

```

agaggactay gcgagagcgt ctacggttgt gccaaaggaa aaaaaatggt cctaagaaaa      60
gagtatacaa agttgtgttc atcaaagtct ggaacccaaa ggtgtccctc caaagctgta      120
cacgacagag aaaacgcgaa ctgaaagaag aagcaggtcc caaggggcca ggcgcctcct      180
ccacctctc ctctcctag gattaacctc catttcagct aatc atg gga gag att      236
                                         Met Gly Glu Ile
aaa gtc tct cct gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa      284
Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys
-50                               -45                               -40                               -35
aab dtw atk gtg gat gat gat gac agt aag ata tgg tgc chc tat gac      332
Xaa Xaa Xaa Val Asp Asp Asp Ser Lys Ile Trp Ser Xaa Tyr Asp
                    -30                               -25                               -20
gcg ggc ccc cga agt atc agg tgt cct ctc ata ttc ctg cyc yct gtc      380
Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe Leu Xaa Xaa Val
                    -15                               -10                               -5
agt gga act gha gat gtc ttt ttc cgg cag att ttg gct ctg act gga      428
Ser Gly Thr Xaa Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly
                    1                               5                               10
tgg gg      433
Trp
15

```

<210> 706

<211> 419

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

&lt;222&gt; 284..418

&lt;221&gt; sig\_peptide

&lt;222&gt; 284..331

&lt;223&gt; Von Heijne matrix

score 3.5

seq SHSHLSLVGHSRA/CG

&lt;400&gt; 706

```

attgaaaatc attaaaaatc ttagcaattg ttttaaatta tctaattttt ttctccaaat      60
aatatctatt ttagcagcca aatcaccaca aatcattggg ttttatcttt agttgtgggt      120
gcacagcggg tgcgtgtatt ttggggcatg tgagggtgtc tgatgcgttc atgcagtgtg      180
taacagtcac atcagggtaa atgggacatc tttcacctca agcatttatt ctctcgtgta      240
tggacaccct cagctggaaa ggggggctgc gtcgtgagta tga atg gat gca agt      295
                                     Met Asp Ala Ser
                                     -15
cat agc cac ctg agc ctg gtg ggg cac agc agg gcc tgt gga gtc aca      343
His Ser His Leu Ser Leu Val Gly His Ser Arg Ala Cys Gly Val Thr
      -10      -5      1
tcc cgg cct cat gct cgg cat agg gga cgc tgc tta ggt cca tgc agt      391
Ser Arg Pro His Ala Arg His Arg Gly Arg Cys Leu Gly Pro Cys Ser
      5      10      15      20
cgc tca ggg ccc agg ctg tgc agc gcc a      419
Arg Ser Gly Pro Arg Leu Cys Ser Ala
      25

```

&lt;210&gt; 707

&lt;211&gt; 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 200..382

&lt;221&gt; sig\_peptide

&lt;222&gt; 200..301

&lt;223&gt; Von Heijne matrix

score 3.5

seq LISHDPWPRGAFA/LS

&lt;221&gt; misc\_feature

&lt;222&gt; 365

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 707

```

gttacttatg gttgagagag aatatttttc agatttttatt ggacattgat atttgtaaat      60
tgttcattcc ttttgcccag ttttctattg agtggttcat agtttctcat gggatccaa      120
gagttctgga tatgtagagg tggagggtca atctcatcay ttccttgttt taaaaatctt      180
ccatggtttt gtcactact atg ggc tca aac gcc gtg gtg tgg cat aca aag      232
                                     Met Gly Ser Asn Ala Val Val Trp His Thr Lys
                                     -30      -25
ccc tca ctt ctg aac cac cct gct tcc agc ctc atc tcc cat gat ccc      280
Pro Ser Leu Leu Asn His Pro Ala Ser Ser Leu Ile Ser His Asp Pro
      -20      -15      -10
tgg cca cgc ggt gcg ttt gcg ctt tca tgt cca agt gct tcc ttc atg      328
Trp Pro Arg Gly Ala Phe Ala Leu Ser Cys Pro Ser Ala Ser Phe Met
      -5      1      5
ttg ttt tct tcc tta caa tgc cct ttc cct tat tgd naa aca gag tgc      376
Leu Phe Ser Ser Leu Gln Cys Pro Phe Pro Tyr Xaa Xaa Thr Glu Cys
      10      15      20      25
aac gwg      382

```

```
<210> 708
<211> 384
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 215..382
```

```
<221> sig_peptide
<222> 215..268
<223> Von Heijne matrix
      score 3.5
      seq ACLFRAVADQVYG/DQ
```

<400> 708																
aagt	gac	gct	acagggg	cca	gctat	gctcc	cgggag	agtgtt	gatgttttcc	agtcatttccg		60				
gctg	acagcg	ttcaag	ttgg	aatcct	ggag	gggaggt	gtttt	cctgtcg	tacgtgggac		120					
aggcc	acgct	gtccg	tccgc	agtacc	gacg	cctgcag	cag	gagcatt	tggt	ttgaaaaggc		180				
cctac	gagac	aagaagg	gct	tc	atcat	caa	gcag	atg	aag	gag	gat	ggc	gcc	tgt	235	
Met Lys Glu Asp Gly Ala Cys																
-15																
ctc	ttc	cg	g	g	g	g	g	g	g	g	g	g	g	g	283	
Leu	Phe	Arg	Ala	Val	Ala	Asp	Gln	Val	Tyr	Gly	Asp	Gln	Asp	Met	His	
		-10				-5				1				5		
gag	gtt	gtg	cga	aag	cat	trc	atg	gac	tat	ctg	atg	aag	aat	gcc	gac	331
Glu	Val	Val	Arg	Lys	His	Xaa	Met	Asp	Tyr	Leu	Met	Lys	Asn	Ala	Asp	
				10						15		20				
tay	ttc	tcc	arc	tat	gtc	aca	gag	gac	ttt	acc	acc	tac	att	akc	agg	379
Tyr	Phe	Ser	Xaa	Tyr	Val	Thr	Glu	Asp	Phe	Thr	Thr	Tyr	Ile	Xaa	Arg	
				25						30		35				
aag cg																
Lys																
384																

```
<210> 709
<211> 149
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 76..147
```

```
<221> sig_peptide
<222> 76..138
<223> Von Heijne matrix
      score 3.5
      seq VLIMIXEAXNVWC/GD
```

```
<221> misc_feature
<222> 123..124
<223> n=a, g, c or t
```

```

<400> 709
acctaataatt aaaaatcttc ttctctaaaa gtggcatata accctgatca agaggtcatg      60
ggctcagttt gatat atg gtt cac ctc att ctt act gaa gtc ctc att atg      111
          Met Val His Leu Ile Leu Thr Glu Val Leu Ile Met
                    -20                    -15                    -10
atc akc gag gcn nsg aat gtg tgg tgt ggg gat tgc gg      149
Ile Xaa Glu Ala Xaa Asn Val Trp Cys Gly Asp Ser

```

377

-5

1

<210> 710  
 <211> 167  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 15..167

<221> sig\_peptide  
 <222> 15..155  
 <223> Von Heijne matrix  
 score 3.5  
 seq CLXFGILASEVYS/WN

<400> 710  
 atatttcatg gcga atg tac cac aat tta ttt gct ctg ttg ttg ata gac 50  
 Met Tyr His Asn Leu Phe Ala Leu Leu Leu Ile Asp  
 -45 -40  
 att cat gtt gtt cta gtt ttt tac tgc ctg gat ctc tta atg att cat 98  
 Ile His Val Val Leu Val Phe Tyr Cys Leu Asp Leu Leu Met Ile His  
 -35 -30 -25 -20  
 att ttc tat tgt aaa tac tgc ctt gka ttt ggk att tta gca agt gaa 146  
 Ile Phe Tyr Cys Lys Tyr Cys Leu Xaa Phe Gly Ile Leu Ala Ser Glu  
 -15 -10 -5  
 gtc tat tct tgg aac att tac 167  
 Val Tyr Ser Trp Asn Ile Tyr  
 1

<210> 711  
 <211> 215  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 84..215

<221> sig\_peptide  
 <222> 84..170  
 <223> Von Heijne matrix  
 score 3.5  
 seq SPLCSXSSGYCXA/FP

<400> 711  
 ccgcttttgg ctgcatcagc cggggattgc cggcgccagg tgctgggggc gactcggaca 60  
 gcgggagcgt ggggtggagt agg atg gag tct ccc tcc cga gct ggg ggt gtr 113  
 Met Glu Ser Pro Ser Arg Ala Gly Gly Val  
 -25 -20  
 grc ctm vga aag gct gct tcg ccg ctg tgt tcg gmv agc tct gga tac 161  
 Xaa Leu Xaa Lys Ala Ala Ser Pro Leu Cys Ser Xaa Ser Ser Gly Tyr  
 -15 -10 -5  
 tgc rgg gct ttt ccg cgg agg agc gcc cgc cgg cat ctg cat ccg gga 209  
 Cys Xaa Ala Phe Pro Arg Arg Ser Ala Arg Arg His Leu His Pro Gly  
 1 5 10  
 cac ggg 215  
 His Gly  
 15

<210> 712  
 <211> 241

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 59..241

<221> sig\_peptide  
<222> 59..133  
<223> Von Heijne matrix  
score 3.5  
seq LISLSVLMPVQHS/PD

```

<400> 712
actatccttt cctcattgaa ttgctgtgat acctttgttg caaatcagct gtctgcag      58
atg tgg agg tat gtt tct aga ctt tct tct gtt cca ttg atc agc ttg      106
Met Trp Arg Tyr Val Ser Arg Leu Ser Ser Val Pro Leu Ile Ser Leu
-25                -20                -15                -10
tct gtc ttg atg cca gta cag cac tcc cct gat ttt tgt agc ttt att      154
Ser Val Leu Met Pro Val Gln His Ser Pro Asp Phe Cys Ser Phe Ile
-5                1                5
gta agt aca gtt atc cct tgg ttt cct tgg gga att ggt tcc agg acc      202
Val Ser Thr Val Ile Pro Trp Phe Pro Trp Gly Ile Gly Ser Arg Thr
10                15                20
ctc atg gat ata aaa atc ctg gga tgc tcg agt cca ggg      241
Leu Met Asp Ile Lys Ile Leu Gly Cys Ser Ser Pro Gly
25                30                35

```

<210> 713  
<211> 376  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 276..374

<221> sig\_peptide  
<222> 276..365  
<223> Von Heijne matrix  
score 3.5  
seq NLLKLSSHPTCA/CK

<221> misc\_feature  
<222> 154,217  
<223> n=a, g, c or t

```

<400> 713
tatgtacatt tgtcaaaact cagaaaatgt atatataata tgtgtgcata tgattttaag      60
tagttttaca taaaaagata agcaaatttt ggatgctggg taactactaag catgctgaaa      120
tatttagagg gaagagtatt attgtctaca atyngcttta aagacaccaa aaataagggtg      180
grttaattwa wkggsywwgg grmdwtggat aaatggnkag awatgtgata aagcaagtct      240
aatagaatttt tgtggcagaa tctaattggcg gctat atg gat gtt agc tgt aaa      293
                                Met Asp Val Ser Cys Lys
                                -30                -25
att ctt tac aat gtg att gaa aaa ttt tgc aat aat ctg ttg aag ctt      341
Ile Leu Tyr Asn Val Ile Glu Lys Phe Cys Asn Asn Leu Leu Lys Leu
-20                -15                -10
tct tcc cat tcc cct act tgt gct tgc aaa cta aa      376
Ser Ser His Ser Pro Thr Cys Ala Cys Lys Leu
-5                1

```

<210> 714  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 216..302

<221> sig\_peptide  
 <222> 216..275  
 <223> Von Heijne matrix  
 score 3.5  
 seq SHLSGSSSLQLCVA/QF

<400> 714  
 gtatgtgtga tttgatttta tttgcccttt gaactatgac ccaatactcc ccaaacctgt 60  
 tattcagttt ttgccagag ttattatata tggggaataa acagaggaca cacacccaga 120  
 ggctgccagt agcaaaaatc actgtaattc aaaaagcatg acactacggg agtgaaatta 180  
 tcacactttt ctttgcatag agcagttttac ttgtg atg att ttc aaa gat gtg 233  
 Met Ile Phe Lys Asp Val  
 -20 -15  
 ttc tcc cac ttg tca ggt tca tct ctt caa ctg tgt gtc gca caa ttt 281  
 Phe Ser His Leu Ser Gly Ser Ser Leu Gln Leu Cys Val Ala Gln Phe  
 -10 -5 1  
 ctc gaw ctc agt gct gtt gac at 304  
 Leu Xaa Leu Ser Ala Val Asp  
 5

<210> 715  
 <211> 242  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 91..240

<221> sig\_peptide  
 <222> 91..222  
 <223> Von Heijne matrix  
 score 3.5  
 seq SFSFLFFFLSFF/FF

<400> 715  
 gtttgtgatt aagtgatttc ctctagtggg atgctttgac tcctctttag cttttgtgta 60  
 aatactatag gtttttgctt tgtgggtaac atg aag ctt aca aaa aat atc tta 114  
 Met Lys Leu Thr Lys Asn Ile Leu  
 -40  
 twa gta ata ata ggc tgt ttt aag ctg ata gcc tac aaa aac tct gta 162  
 Xaa Val Ile Ile Gly Cys Phe Lys Leu Ile Ala Tyr Lys Asn Ser Val  
 -35 -30 -25  
 ctg tac ttt tac tct aac ttc tca ttt tct ttt ctt ttc ttt ttt ttc 210  
 Leu Tyr Phe Tyr Ser Asn Phe Ser Phe Ser Phe Leu Phe Phe Phe Phe  
 -20 -15 -10 -5  
 ctt tct ttc ttt ttt ttc ttt ttt ttt tt 242  
 Leu Ser Phe Phe Phe Phe Phe Phe Phe Phe  
 1 5

<210> 716  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 100..375

&lt;221&gt; sig\_peptide

&lt;222&gt; 100..360

&lt;223&gt; Von Heijne matrix

score 3.5

seq VAGXMLAPGGTLA/DD

&lt;400&gt; 716

```

ctggcgtyag ttccggtcgc agaggagaca ccgcccagcagc tgccgggtaca tcggggattt      60
ctggctcttt cctcttcgcc tttaaattcgg gtgtctttt atg aat aat caa aag      114
                                     Met Asn Asn Gln Lys
                                     -85
cag caw rag cca acg cta tca ggc cag cgt ttt aaa act aga aaa aga      162
Gln Xaa Xaa Pro Thr Leu Ser Gly Gln Arg Phe Lys Thr Arg Lys Arg
      -80                               -75                               -70
gat gaa aaa gag agg ttt gac cct act cag ttt caa gac tgt att att      210
Asp Glu Lys Glu Arg Phe Asp Pro Thr Gln Phe Gln Asp Cys Ile Ile
      -65                               -60                               -55
caa ggc tta act gaa acc ggt act gat ttg gaa gca gta gct aag ttt      258
Gln Gly Leu Thr Glu Thr Gly Thr Asp Leu Glu Ala Val Ala Lys Phe
      -50                               -45                               -40                               -35
ctt gat gct tct gga gca aaa ctt gat tac cgt cga tat gca gaa aca      306
Leu Asp Ala Ser Gly Ala Lys Leu Asp Tyr Arg Arg Tyr Ala Glu Thr
      -30                               -25                               -20
ctc ttt gac att ctg gtg gct ggt kga atg ctg gcc cca ggt ggt aca      354
Leu Phe Asp Ile Leu Val Ala Gly Xaa Met Leu Ala Pro Gly Gly Thr
      -15                               -10                               -5
ctg gca gat gac atg atg cvg      375
Leu Ala Asp Asp Met Met Xaa
      1                               5

```

&lt;210&gt; 717

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 324..428

&lt;221&gt; sig\_peptide

&lt;222&gt; 324..374

&lt;223&gt; Von Heijne matrix

score 3.5

seq LEIKLPFLPFAQQ/ID

&lt;400&gt; 717

```

aacagtctat ttctgtttgt aaatattagt atttctgtgg attctgtact tgttccttgt      60
tatcctttca ttctcttagg ttcatttggt ctgatggatt caggtaccat tgaaattctg      120
atagtttcaa aatcttttat ctccagggtt gatctctctt gtgaactctg gaactgtatt      180
cccaattgtc aattggacat ccctacgtat gggacctcag atatttcaaa catgatgtgt      240
ccaagtctgt atcacttctg gccatcatat tgttctttta tttttccaaa tttcacatca      300
ccagtaacaa actagctgtg atc atg gca gat agc ctg gaa ata aaa ctc ccc      353
                                     Met Ala Asp Ser Leu Glu Ile Lys Leu Pro
                                     -15                               -10
ttt tta ccc ttt gca cag caa att gac atc aaa tcc tgt ttc tac ttt      401
Phe Leu Pro Phe Ala Gln Gln Ile Asp Ile Lys Ser Cys Phe Tyr Phe
      -5                               1                               5
ttt ttt ttw aac wat kgc ttc cct agg g      429

```

381

Phe Phe Xaa Asn Xaa Xaa Phe Pro Arg  
10 15

<210> 718  
<211> 350  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 4..348

<221> sig\_peptide  
<222> 4..108  
<223> Von Heijne matrix  
score 3.5  
seq ATAAATAASATTG/AS

<221> misc\_feature  
<222> 155  
<223> n=a, g, c or t

<400> 718  
tga atg gac aga aaa tgg acc tgg aag aga ggg caa agg tca cat ctg 48  
Met Asp Arg Lys Trp Thr Trp Lys Arg Gly Gln Arg Ser His Leu  
-35 -30 -25  
gag tca ggc cag gct gcc ccg gcc act gca gca gct acg gca gca tct 96  
Glu Ser Gly Gln Ala Ala Pro Ala Thr Ala Ala Thr Ala Ala Ser  
-20 -15 -10 -5  
gcc aca acg ggg gca agt gtg tgg aga agc aca atg ggc wac ctg tgt 144  
Ala Thr Thr Gly Ala Ser Val Trp Arg Ser Thr Met Gly Xaa Leu Cys  
1 5 10  
gat tgc acc anb dca cct tat gaa ggg ccc ttt tgc aaa aaa gag gtt 192  
Asp Cys Thr Xaa Xaa Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val  
15 20 25  
tct gct gtt ttt gag gct ggc acg tcg gtt act tac atg ttt caa gaa 240  
Ser Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu  
30 35 40  
ccc tat cct gtg acc aag aat ata agc ctc tca tcc tca gct att tac 288  
Pro Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr  
45 50 55 60  
aca gat tca gct cca tcc aag gaa aac att gca ctt agc ttt gtg aca 336  
Thr Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr  
65 70 75  
acc caa gca ccg gg 350  
Thr Gln Ala Pro  
80

<210> 719  
<211> 305  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 84..305

<221> sig\_peptide  
<222> 84..212  
<223> Von Heijne matrix  
score 3.5  
seq VLSIKHLPPQLRA/FQ

&lt;400&gt; 719

```

gttttttccct tttcatttca gcctgactgc cggaatcaga gccgcgggtg agatccccag      60
ccctgtgagc ctgtaggagt aga atg gct ccc caa atg tat gag ttc cat ctg      113
                               Met Ala Pro Gln Met Tyr Glu Phe His Leu
                               -40                               -35
cca tta tcc cca gag gag ttg ttg aaa agt gga ggg gtg aat cag tat      161
Pro Leu Ser Pro Glu Glu Leu Leu Lys Ser Gly Gly Val Asn Gln Tyr
                               -30                               -25                               -20
gtt gtg caa gag gta ctg tcc atc aaa cat ctt cca cca cag ctt aga      209
Val Val Gln Glu Val Leu Ser Ile Lys His Leu Pro Pro Gln Leu Arg
                               -15                               -10                               -5
gct ttt cag gct gcc ttt cga gct cag ggg ccc ctg gct atg ctg cag      257
Ala Phe Gln Ala Ala Phe Arg Ala Gln Gly Pro Leu Ala Met Leu Gln
    1                               5                               10                               15
cac ttt gat act atc tac agc att ttg cat cac ttt cga agt ata gat      305
His Phe Asp Thr Ile Tyr Ser Ile Leu His His Phe Arg Ser Ile Asp
                               20                               25                               30

```

&lt;210&gt; 720

&lt;211&gt; 257

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 6..257

&lt;221&gt; sig\_peptide

&lt;222&gt; 6..50

&lt;223&gt; Von Heijne matrix

score 3.5

seq AVQVVGSWPSVQP/RE

&lt;400&gt; 720

```

aaaag atg gct gct gtg caa gtt gtc ggt tgc tgg cct tcc gtg cag ccg      50
Met Ala Ala Val Gln Val Val Gly Ser Trp Pro Ser Val Gln Pro
    -15                               -10                               -5
cgg gag gca ccg cgg gaa gca atc cct gag cga ggc aat ggg ttt cgc      98
Arg Glu Ala Pro Arg Glu Ala Ile Pro Glu Arg Gly Asn Gly Phe Arg
    1                               5                               10                               15
ctc ttg tct gcc agg ctc tgc gcc ctg cgc ccg gat gac agc agc tcc      146
Leu Leu Ser Ala Arg Leu Cys Ala Leu Arg Pro Asp Asp Ser Ser Ser
    20                               25                               30
gcc cgm acc gag atc cac ctg mtc ttc gat cag ctc atc tcc gag aac      194
Ala Arg Thr Glu Ile His Leu Xaa Phe Asp Gln Leu Ile Ser Glu Asn
    35                               40                               45
tac agc gag ggc agt ggc gtg gcc ccg gag gac gtw agt gct ctt ctt      242
Tyr Ser Glu Gly Ser Gly Val Ala Pro Glu Asp Val Ser Ala Leu Leu
    50                               55                               60
gtc cag gct tgc ggg      257
Val Gln Ala Cys Gly
65

```

&lt;210&gt; 721

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 217..360

```
<221> sig_peptide
<222> 217..306
<223> Von Heijne matrix
      score 3.5
      seq FLFFLQFSFPLY/LF
```

```
<221> misc_feature
<222> 316,319
<223> n=a, g, c or t
```

[illegible]

```
<210> 722
<211> 191
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 64..189
```

```
<221> sig_peptide
<222> 64..141
<223> Von Heijne matrix
      score 3.5
      seq LVLYPWPVPLLL/AF
```

```

<400> 722
ttctctcttt gtgaaggcag ctctcagat ccagggagta tctgcacgga cctcatttat      60
ggt atg tat aga cat tcc aaa cag cgt aat aat gtc cca tgc ctt gta      108
    Met Tyr Arg His Ser Lys Gln Arg Asn Asn Val Pro Cys Leu Val
        -25                -20                -15

ctc tac gcc cct tgg gtc cct ccc ctc ctc cta gct ttc tgg ggc tgg      156
Leu Tyr Ala Pro Trp Val Pro Pro Leu Leu Leu Ala Phe Trp Gly Trp
    -10                -5                1                5

tgg ctc ctg gag cag ggt ctt ttt ttt ttt tt      191
Trp Leu Leu Glu Gln Gly Leu Phe Phe Phe
        10                15

```

```
<210> 723
<211> 473
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 63..473
```

&lt;221&gt; sig\_peptide

&lt;222&gt; 63..212

&lt;223&gt; Von Heijne matrix

score 3.5

seq ITYGVFLCIDCSG/SH

&lt;400&gt; 723

```

tttttttttc gtcgactctt accggttggc tgggccagct gcgccgcggc tcacagctga      60
cg atg ggg gac ccc agc aag cag gac atc ttg acc atc ttc aag cgc      107
  Met Gly Asp Pro Ser Lys Gln Asp Ile Leu Thr Ile Phe Lys Arg
    -50          -45          -40
ctc cgc tcg gtg ccc act aac aag gtg tgt ttt gat tgt ggt gcc aaa      155
Leu Arg Ser Val Pro Thr Asn Lys Val Cys Phe Asp Cys Gly Ala Lys
  -35          -30          -25          -20
aat ccc agc tgg gca agc ata acc tat gga gtg ttc ctt tgc att gat      203
Asn Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val Phe Leu Cys Ile Asp
          -15          -10          -5
tgc tca ggg tcc cac cgg tca ctt ggt gtt cac ttg agt ttt att cga      251
Cys Ser Gly Ser His Arg Ser Leu Gly Val His Leu Ser Phe Ile Arg
          1          5          10
tct aca gag ttg gat tcc aac tgg tca tgg ttt cag ttg cga tgc atg      299
Ser Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe Gln Leu Arg Cys Met
          15          20          25
caa gtc gga gga aac gct agt gca tct tcc ttt ttt cat caa cat ggg      347
Gln Val Gly Gly Asn Ala Ser Ala Ser Ser Phe Phe His Gln His Gly
          30          35          40          45
tgt tcc acc aat gac acc aat gcc aag tac aac agt cgt gct gct cag      395
Cys Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn Ser Arg Ala Ala Gln
          50          55          60
ctc tat agg gag aaa atc aaa tcg ctc gcc tct caa gca aca cgg aag      443
Leu Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser Gln Ala Thr Arg Lys
          65          70          75
cat ggc act gat ctg tgg ctt gat agt tgt      473
His Gly Thr Asp Leu Trp Leu Asp Ser Cys
          80          85

```

&lt;210&gt; 724

&lt;211&gt; 139

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 60..137

&lt;221&gt; sig\_peptide

&lt;222&gt; 60..125

&lt;223&gt; Von Heijne matrix

score 3.5

seq LLLHLVHFQRTLI/SL

&lt;400&gt; 724

```

tttagcattc aagccgtgat tagtgctttc ttttctcccc agcctgcctt tcagaacag      59
atg cct ctc cct ccc aat cag tcc cct cta ctg ctg cac ctg gtg ttt      107
Met Pro Leu Pro Pro Asn Gln Ser Pro Leu Leu Leu His Leu Val Phe
  -20          -15          -10
cat caa agg acc ctg att tcc ctc ccg ccg cc      139
His Gln Arg Thr Leu Ile Ser Leu Pro Pro
  -5          1

```

&lt;210&gt; 725

&lt;211&gt; 187

385

<212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 125..187

<221> sig\_peptide  
 <222> 125..163  
 <223> Von Heijne matrix  
 score 3.5  
 seq MFLTFFFCTQVHG/PS

<400> 725  
 tcttcgggaa ctctcactct ctcataaact actttattac catcccacca tatcctgtcc 60  
 tctttttttg gcctacttag atctgttttc ctttcttgcc ttaaattggga attgctagag 120  
 gmat atg ttt cta act ttt ttt ttc tgc aca caa gtt cat ggt cct tct 169  
 Met Phe Leu Thr Phe Phe Phe Cys Thr Gln Val His Gly Pro Ser  
 -10 -5 1  
 ata ctt gat agc cca gct 187  
 Ile Leu Asp Ser Pro Ala  
 5

<210> 726  
 <211> 207  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 39..206  
 <221> sig\_peptide  
 <222> 39..80  
 <223> Von Heijne matrix  
 score 3.5  
 seq VTLWIFQFFLCLT/CK

<221> misc\_feature  
 <222> 154  
 <223> n=a, g, c or t

<400> 726  
 aatataaata ccaaatacat aaatagtttt ggtgttag atg gtc act tta tgg att 56  
 Met Val Thr Leu Trp Ile  
 -10  
 ttt caa ttt ttc ttg tgt ttg act tgt aaa gct tat aat tta aga aac 104  
 Phe Gln Phe Phe Leu Cys Leu Thr Cys Lys Ala Tyr Asn Leu Arg Asn  
 -5 1 5  
 tgt aat gat ggg aag ggh wga gsm tca gwg gtg ctt gga ttg gaa caa 152  
 Cys Asn Asp Gly Lys Gly Xaa Ser Xaa Val Leu Gly Leu Glu Gln  
 10 15 20  
 mnr cta cct gaa tct gct ggt atg gta caw ttt tta ggt ttg aaa cac 200  
 Xaa Leu Pro Glu Ser Ala Gly Met Val Xaa Phe Leu Gly Leu Lys His  
 25 30 35 40  
 agg tgg g 207  
 Arg Trp

<210> 727  
 <211> 164  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 54..164

<221> sig\_peptide  
 <222> 54..95  
 <223> Von Heijne matrix  
 score 3.5  
 seq VLWAGPXVPLLCA/AX

<400> 727  
 agacaatggg gmmaatgtca cacatcacag accaagaggc ctaggaggav aag atg 56  
 Met  
 gtt ttg tgg gct ggg ccc akg gtc ccc ctg ctg tgt gca gcc tas gga 104  
 Val Leu Trp Ala Gly Pro Xaa Val Pro Leu Leu Cys Ala Ala Xaa Gly  
 -10 -5 1  
 ctt ggt gcc ctg cat ccc aga tgc tct agt caa ggc ttg agg ctt gcr 152  
 Leu Gly Ala Leu His Pro Arg Cys Ser Ser Gln Gly Leu Arg Leu Ala  
 5 10 15  
 sct tct gaa gcc 164  
 Xaa Ser Glu Ala  
 20

<210> 728  
 <211> 321  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 139..321

<221> sig\_peptide  
 <222> 139..261  
 <223> Von Heijne matrix  
 score 3.5  
 seq FNIQLLWVPXXXG/AV

<400> 728  
 catggaaatc actccaatca gaccggcccg aggatacgt ttcttgtgat ccgcagcagc 60  
 gccattagca tcataaacca ggtgattggc tggatctact ttgtggcctg gtccatctcc 120  
 ttctaccctc aggtgmtc atg aat tgg agg cgg aaa agt gtc att ggt ctg 171  
 Met Asn Trp Arg Arg Lys Ser Val Ile Gly Leu  
 -40 -35  
 agc ttc gac ttc gtg gct ctg aac ctg acg ggc ttc gtg gcc tac agt 219  
 Ser Phe Asp Phe Val Ala Leu Asn Leu Thr Gly Phe Val Ala Tyr Ser  
 -30 -25 -20 -15  
 gta ttc aac atc ggc ctc ctc tgg gtg ccc twc wtc daa gga gca gtt 267  
 Val Phe Asn Ile Gly Leu Leu Trp Val Pro Xaa Xaa Xaa Gly Ala Val  
 -10 -5 1  
 tct cct caa ata ccc caa cgg agt gaa ccc cgt gaa cag caa cga cgt 315  
 Ser Pro Gln Ile Pro Gln Arg Ser Glu Pro Arg Glu Gln Gln Arg Arg  
 5 10 15  
 ctt ctt 321  
 Leu Leu  
 20

<210> 729  
 <211> 472  
 <212> DNA  
 <213> Homo sapiens

387

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 25..471

&lt;400&gt; 729

```

gacttccttc tagaatcctc caac atg gag cct ctt gca gct tac ccg cta      51
          Met Glu Pro Leu Ala Ala Tyr Pro Leu
          1              5
aaa tgt tcc ggg ccc aga gca aag gta ttt gca gtt ttg ctg tct ata      99
Lys Cys Ser Gly Pro Arg Ala Lys Val Phe Ala Val Leu Leu Ser Ile
10              15              20              25
ggt cta tgc aca gta acg cta ttt ctt cta caa cta aaa wtc ctc aaa      147
Val Leu Cys Thr Val Thr Leu Phe Leu Leu Gln Leu Lys Xaa Leu Lys
          30              35              40
cct aaa atc aac agc ttt tat gcc ttt gaa gtg aag gat gca aaa gga      195
Pro Lys Ile Asn Ser Phe Tyr Ala Phe Glu Val Lys Asp Ala Lys Gly
          45              50              55
aga act gtt tct ctg gaa aag tat aaa ggc aaa gtt tca cta gtt gta      243
Arg Thr Val Ser Leu Glu Lys Tyr Lys Gly Lys Val Ser Leu Val Val
          60              65              70
aac gtg gcc agt gac tgc caa ctc aca gac aga aat tac tta ggg ctg      291
Asn Val Ala Ser Asp Cys Gln Leu Thr Asp Arg Asn Tyr Leu Gly Leu
          75              80              85
aag gaa ctg cac aaa gag ttt gga cca tcc cac ttc agc gtg ttg gct      339
Lys Glu Leu His Lys Glu Phe Gly Pro Ser His Phe Ser Val Leu Ala
          90              95              100              105
ttt ccc tgc aat cag ttt gga gaa tgc gag ccc cgc cca agc aag gaa      387
Phe Pro Cys Asn Gln Phe Gly Glu Ser Glu Pro Arg Pro Ser Lys Glu
          110              115              120
gta gaa tct ttt gca aga aaa aac tac gga gta act ttc ccc atc ttc      435
Val Glu Ser Phe Ala Arg Lys Asn Tyr Gly Val Thr Phe Pro Ile Phe
          125              130              135
cac aag att aag att cta gga tct gaa gga gaa ctg c      472
His Lys Ile Lys Ile Leu Gly Ser Glu Gly Glu Leu
          140              145

```

&lt;210&gt; 730

&lt;211&gt; 465

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 70..465

&lt;400&gt; 730

```

actcgaggag actccaaaca gtgagcctag agctggagac tagcggttaac cggcggggcg      60
gccggtttt atg aat gaa gct atg gct aca gat tcc cca aga aga ccc agt      111
          Met Asn Glu Ala Met Ala Thr Asp Ser Pro Arg Arg Pro Ser
          1              5              10
cgt tgt act ggt gga gtt gtg gtt cgc ccc cag gct gtc aca gag cag      159
Arg Cys Thr Gly Gly Val Val Val Arg Pro Gln Ala Val Thr Glu Gln
          15              20              25              30
tcc tac atg gaa agt gtt gtg act ttt ctg cag gat gtt gtg cca cag      207
Ser Tyr Met Glu Ser Val Val Thr Phe Leu Gln Asp Val Val Pro Gln
          35              40              45
gct tac agt gga aca cct cta aca gaa gaa aag gag aaa ata gtc tgg      255
Ala Tyr Ser Gly Thr Pro Leu Thr Glu Glu Lys Glu Lys Ile Val Trp
          50              55              60
gtc aga ttt gaa aat gca gat tta aat gat aca tca aga aat ctg gaa      303
Val Arg Phe Glu Asn Ala Asp Leu Asn Asp Thr Ser Arg Asn Leu Glu
          65              70              75
ttt cat gaa ata cat agt act ggg agt gaa ccg cct ttg att atg      351

```

388

Phe	His	Glu	Ile	His	Ser	Thr	Gly	Ser	Glu	Pro	Pro	Leu	Leu	Ile	Met	
80						85				90						
att	ggc	tac	agt	gat	gga	atg	cag	gtc	tgg	agc	atc	cct	atc	akt	ggc	399
Ile	Gly	Tyr	Ser	Asp	Gly	Met	Gln	Val	Trp	Ser	Ile	Pro	Ile	Xaa	Gly	
95					100					105					110	
gaa	sac	aag	agc	tct	tct	ctg	ttc	gac	atg	gcc	caa	ttc	gag	cgg	cta	447
Glu	Xaa	Lys	Ser	Ser	Ser	Leu	Phe	Asp	Met	Ala	Gln	Phe	Glu	Arg	Leu	
				115					120					125		
gaa	tct	tgc	ctg	ctc	cac											465
Glu	Ser	Cys	Leu	Leu	His											
				130												

&lt;210&gt; 731

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 207..344

&lt;400&gt; 731

agacgcgacg	gtgctgggat	cccgaggagg	akcggaacgg	acctgggctt	ggtcgcctcc	60
aagccggcgg	gaccgagtgc	tttaggccgc	tygaaagaaa	gttgctcoga	cccggaaaaa	120
ggagaagatg	aaggaagcca	aggatgcccg	ctataccaat	gggcacctct	tcaccacat	180
ttcagtttca	ggcatgacca	tgtgct atg	cct gta aca	aga gca tca	cag cca	233
		Met Pro Val Thr	Arg Ala Ser	Gln Pro		
		1		5		
agg aag ccc	tca tct gcc	caa caa cag	aaa gcg gcc	ctg ctg aak	aac	281
Arg Lys Pro	Ser Ser Ala	Gln Gln Gln	Lys Ala Ala	Leu Leu Xaa	Asn	
10		15		20	25	
aac acc gcc	ttg cag tcc	gtt tct ctt	cga agt aag	aca acc atc	cgg	329
Asn Thr Ala	Leu Gln Ser	Val Ser Leu	Arg Ser Lys	Thr Thr Ile	Arg	
	30		35		40	
gag cgg cca	agc tcg g					345
Glu Arg Pro	Ser Ser					
	45					

&lt;210&gt; 732

&lt;211&gt; 398

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 274..396

&lt;400&gt; 732

agcaaccaag	tcgcacctgg	agctgtccta	gcgcctagtt	ctctcccggc	cgagagctg	60
gccgcccagg	gggagtcgca	gagtttgaa	gatctctcta	acacctctcg	gccaacttca	120
gaagtgtata	agatcagctt	tatctttcca	aatggagaca	agtatgatgg	tgactgtaca	180
agaacatctt	ctggaatcta	cgagagaaat	ggaataggta	ttcataccac	tcctaattggg	240
attgtctaca	caggaagctg	gaaagatgac	aag atg aat	ggt ttt gga	aga ctt	294
		Met Asn Gly	Phe Gly Arg	Leu		
		1		5		
gag cat ttt	tca gga gca	gta tat gaa	gga caa ttt	aag gat aat	atg	342
Glu His Phe	Ser Gly Ala	Val Tyr Glu	Gly Gln Phe	Lys Asp Asn	Met	
	10		15		20	
ttt cat gga	ctg ggg act	tac aca ttc	cca aat ggg	gca aag tat	act	390
Phe His Gly	Leu Gly Thr	Tyr Thr Phe	Pro Asn Gly	Ala Lys Tyr	Thr	
	25		30		35	
gga att tc						398
Gly Ile						

40

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<210> 733
<211> 443
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 49..441
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<400> 733																	
ggaagttctt gggagcgcca gttccgtctg tgtgttcgag tggacaaa atg gcg aag																	57
Met Ala Lys																	
1																	
atc gcc aag act cac gaa gat att gaa gca cag att cga gaa att caa																	105
Ile Ala Lys Thr His Glu Asp Ile Glu Ala Gln Ile Arg Glu Ile Gln																	
5 10 15																	
ggc aag aag gca gct ctt gat gaa gct caa gga gtg ggc ctc gat tct																	153
Gly Lys Lys Ala Ala Leu Asp Glu Ala Gln Gly Val Gly Leu Asp Ser																	
20 25 30 35																	
aca ggt tat tat gac cag gaa att tat ggt gga agt gac agc aga ttt																	201
Thr Gly Tyr Tyr Asp Gln Glu Ile Tyr Gly Gly Ser Asp Ser Arg Phe																	
40 45 50																	
gct gga tac gtg aca tca att gct gca act gaa ctt gaa gat gat gac																	249
Ala Gly Tyr Val Thr Ser Ile Ala Ala Thr Glu Leu Glu Asp Asp Asp																	
55 60 65																	
gat gac tat tca tca tct acg agt ttg ctt ggt cag aag aag cca gga																	297
Asp Asp Tyr Ser Ser Ser Thr Ser Leu Leu Gly Gln Lys Lys Pro Gly																	
70 75 80																	
tat cat gcc cct gtg gca ttg ctt aat gat ata cca cag tca aca gaa																	345
Tyr His Ala Pro Val Ala Leu Leu Asn Asp Ile Pro Gln Ser Thr Glu																	
85 90 95																	
cag tat gat cca ttt gct gag cac aga cct cca aag att gca gac cgg																	393
Gln Tyr Asp Pro Phe Ala Glu His Arg Pro Pro Lys Ile Ala Asp Arg																	
100 105 110 115																	
gaa gat gaa tac aaa aag cat agg cgg acc atg ata att tcc cag agc																	441
Glu Asp Glu Tyr Lys Lys His Arg Arg Thr Met Ile Ile Ser Gln Ser																	
120 125 130																	
gt																	443

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<210> 734
<211> 373
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 128..373
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<400> 734
gagaagccgc agtctcgaga gcgtcaacga ggtgttttcgg tagtctctgg ccatacctttc      60
tgcgcaccgc gtgtcgctgg gctgcacccc gggcggggac gtccgcgggg caggggaggg      120
ggccaag atg ccg atc aat aaa tca gag aag cca gaa agc tgc gat aat      169
      Met Pro Ile Asn Lys Ser Glu Lys Pro Glu Ser Cys Asp Asn
      1              5              10
gtg aag gtt gtt gtt agg tgc cgg ccc ctc aat gag aga gag aaa tca      217
Val Lys Val Val Val Arg Cys Arg Pro Leu Asn Glu Arg Glu Lys Ser
15              20              25              30
atg tgc tac aaa cag gct gtc agt gtg gat gag atg agg gga act atc      265
Met Cys Tyr Lys Gln Ala Val Ser Val Asp Glu Met Arg Gly Thr Ile
      35              40              45
act gta cat aag act gat tct tcc aat gaa cct cca aag aca ttt act      313

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390

Thr	Val	His	Lys	Thr	Asp	Ser	Ser	Asn	Glu	Pro	Pro	Lys	Thr	Phe	Thr		
			50					55					60				
ttt	gat	act	ggt	ttt	gga	cca	gag	agt	aaa	caa	ctt	gat	ggt	tat	aac		361
Phe	Asp	Thr	Val	Phe	Gly	Pro	Glu	Ser	Lys	Gln	Leu	Asp	Val	Tyr	Asn		
			65				70					75					
tta	act	gca	aga														373
Leu	Thr	Ala	Arg														
			80														

<210> 735  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 202..321

<400> 735																	
agagcgggtg	cgccggctgc	gcsggctgtg	agtctctcgc	cgccggagga	agatgaggt												60
gaagattgga	ttcatcttac	gcagtttctg	ggtggtggga	agcttctctg	ggctagtgg												120
cctctgtct	tcctgaccc	cgccggccga	cgaccaagc	ccgctgagca	ggatgagga												180
agacagagat	gtcatgacc	c atg	ccc aac	cga ggc	ggc aat	gga cta	gct										231
			Met	Pro	Asn	Arg	Gly	Gly	Asn	Gly	Leu	Ala					
			1				5					10					
cct	ggg	gag	gac	aga	ttc	aaa	cct	gtg	gta	cca	tgg	cct	cat	ggt	gaa		279
Pro	Gly	Glu	Asp	Arg	Phe	Lys	Pro	Val	Val	Pro	Trp	Pro	His	Val	Glu		
						15			20					25			
gga	gta	gaa	gtg	gac	tta	gag	tct	att	aga	aga	ata	aac	aag	g			322
Gly	Val	Glu	Val	Asp	Leu	Glu	Ser	Ile	Arg	Arg	Ile	Asn	Lys				
			30				35					40					

<210> 736  
 <211> 181  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 75..179

<400> 736																	
acttcgcat	tttctccgg	aagtgcggat	cccagcgcg	gtcgtgtagc	tgagcagacc												60
tggggcttgg	ttct atg	tcc ctg	tgg cta	tgt ttc	cag tgt	cct ctg	ggt										110
		Met	Ser	Leu	Trp	Leu	Cys	Phe	Gln	Cys	Pro	Leu	Gly				
		1				5					10						
ggt	tcc	aag	agc	aac	aag	aaa	cga	ata	aat	ctc	tgt	aat	ggt	ttc	tgg		158
Val	Ser	Lys	Ser	Asn	Lys	Lys	Arg	Ile	Asn	Leu	Cys	Asn	Gly	Phe	Trp		
		15				20					25						
aat	gaa	aaa	ata	aaa	aac	agg	ag										181
Asn	Glu	Lys	Ile	Lys	Asn	Arg											
		30				35											

<210> 737  
 <211> 160  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 18..158

<400> 737

391

tgaatgactg gctatatt atg ggc acc cat gtt ttt gct ata aat aaa cgt 50  
 Met Gly Thr His Val Phe Ala Ile Asn Lys Arg  
 1 5 10  
 aca tat gta att tca aga gac cga gaa tta tca act gca aag ccc awr 98  
 Thr Tyr Val Ile Ser Arg Asp Arg Glu Leu Ser Thr Ala Lys Pro Xaa  
 15 20 25  
 tgt agc agt cta ctc acg gcc cct gta ctt tgc tac tgg agg gcc tgt 146  
 Cys Ser Ser Leu Leu Thr Ala Pro Val Leu Cys Tyr Trp Arg Ala Cys  
 30 35 40  
 cct ctg caa acc ca 160  
 Pro Leu Gln Thr  
 45

<210> 738  
 <211> 234  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 66..233

<400> 738  
 gttgttagtt ttcttttttag ctgaattacc cactcacatc cttattatatt tatgccactg 60  
 atttc atg ttt tgt ttt cta ttt tca tgg tgg ctt aga gga ggt ctt cat 110  
 Met Phe Cys Phe Leu Phe Ser Trp Trp Leu Arg Gly Gly Leu His  
 1 5 10 15  
 gta tta tta aac aca tgc tta tat gta cct tat ggg tat ttg tca ctt 158  
 Val Leu Leu Asn Thr Cys Leu Tyr Val Pro Tyr Gly Tyr Leu Ser Leu  
 20 25 30  
 att tgt tta ctt tgt tta tgg tat ctt aat cta tac aaa ttc tca att 206  
 Ile Cys Leu Leu Cys Leu Trp Tyr Leu Asn Leu Tyr Lys Phe Ser Ile  
 35 40 45  
 ttc ttt tct ttt ctt tct ttt ttt ttt t 234  
 Phe Phe Ser Phe Leu Ser Phe Phe Phe  
 50 55

<210> 739  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 424..588

<400> 739  
 atcaaaagaa ctcttatata caggagccca ggcaccatac tgtctttttcg aggtaggagt 60  
 cgactcctgt gaggtatggt gctgggtgca gatgcagtgt ggctctggat agcaccttat 120  
 ggacagttgt gtccccaagg aaggatgaga atagctactg aagtcctaaa gagcaagcct 180  
 aactcaagcc attggcacac aggcattaga cagaaagctg gaagttgaaa tgggtggagtc 240  
 caacttgccct ggaccagctt aatgggtctg ctcttggttaa cgttttttatc catggatgac 300  
 ttgcttggtt atggagagtc ggcttgacta cactgtgtgg agcaagtttt aaagaagcaa 360  
 aggactcaga attcatgatt gaagaaatgc aggcagacct gttatcctaa actagggttt 420  
 tta atg acc aca aca agc aag cat gca gct tac tgc ttg aaa ggg tct 468  
 Met Thr Thr Thr Ser Lys His Ala Ala Tyr Cys Leu Lys Gly Ser  
 1 5 10 15  
 tgc ctc amc caa gct aga gtg cag tgg cct ttg aag cwt act aca gcc 516  
 Cys Leu Xaa Gln Ala Arg Val Gln Trp Pro Leu Lys Xaa Thr Thr Ala  
 20 25 30  
 tca aac ttc tgg gct caa gtg atc ctc agc ctc cca gtg gtc ttt gta 564  
 Ser Asn Phe Trp Ala Gln Val Ile Leu Ser Leu Pro Val Val Phe Val  
 35 40 45

392

gac tgc ctg atg gag tmt cat ggc a  
 Asp Cys Leu Met Glu Xaa His Gly  
 50 55

589

<210> 740  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 26..388

<400> 740  
 aaaaaacgct gttggaaatc tcgctg atg gag gga gga gga ggt ata ccc cta 52  
 Met Glu Gly Gly Gly Gly Ile Pro Leu  
 1 5  
 gaa aca ctt aaa gaa gaa agt cag tca aga cat gtt cta cct gca agt 100  
 Glu Thr Leu Lys Glu Glu Ser Gln Ser Arg His Val Leu Pro Ala Ser  
 10 15 20 25  
 ttt gaa gtc aac agt ttg cag aaa agc aac tgg ggg ttc tta ctt act 148  
 Phe Glu Val Asn Ser Leu Gln Lys Ser Asn Trp Gly Phe Leu Leu Thr  
 30 35 40  
 ggg ctt gtg ggt ggc acc ctg gtg gct gtg tac gct gta gcc acg ccg 196  
 Gly Leu Val Gly Gly Thr Leu Val Ala Val Tyr Ala Val Ala Thr Pro  
 45 50 55  
 ttt gta acg cca gcc ctt cga aaa gtc tgt ttg cca ttt gta cct gca 244  
 Phe Val Thr Pro Ala Leu Arg Lys Val Cys Leu Pro Phe Val Pro Ala  
 60 65 70  
 act atg aag cag att gaa aat gtt gtg aaa atg ttg cga tgc cga aga 292  
 Thr Met Lys Gln Ile Glu Asn Val Val Lys Met Leu Arg Cys Arg Arg  
 75 80 85  
 gga tcc ctt gtg gac atc ggt agt ggg gac gga cgc att gtc ata gcg 340  
 Gly Ser Leu Val Asp Ile Gly Ser Gly Asp Gly Arg Ile Val Ile Ala  
 90 95 100 105  
 gct gcg aag aaa ggg ttc ama gca gtt ggt tat gaa tta aac cca tgg 388  
 Ala Ala Lys Lys Gly Phe Xaa Ala Val Gly Tyr Glu Leu Asn Pro Trp  
 110 115 120

<210> 741  
 <211> 478  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 15..476

<400> 741  
 agtgcgcctc taag atg gcg acg cct ttg gcg gta aat tcg gct gct agt 50  
 Met Ala Thr Pro Leu Ala Val Asn Ser Ala Ala Ser  
 1 5 10  
 cta tgg ggt cct tac aaa gac att tgg cat aaa gtg gga aat gct ctt 98  
 Leu Trp Gly Pro Tyr Lys Asp Ile Trp His Lys Val Gly Asn Ala Leu  
 15 20 25  
 tgg aga aga caa cct gaa gct gtt cam ctt ctt gat aag att ttg aag 146  
 Trp Arg Arg Gln Pro Glu Ala Val Xaa Leu Leu Asp Lys Ile Leu Lys  
 30 35 40  
 aaa cac aaa cct gac ttc atc tca ttg ttc aaa aat ccg cca aaa aat 194  
 Lys His Lys Pro Asp Phe Ile Ser Leu Phe Lys Asn Pro Pro Lys Asn  
 45 50 55 60  
 gtt caa cag cat gag aag gtt cag aaa gcc agt aca gag gga gtc gcc 242  
 Val Gln Gln His Glu Lys Val Gln Lys Ala Ser Thr Glu Gly Val Ala

393

65	70	75	
att cag ggt caa cag gga act cga ctt ctt cct gaa cag ctc att aaa			290
Ile Gln Gly Gln Gln Gly Thr Arg Leu Leu Pro Glu Gln Leu Ile Lys			
80	85	90	
gaa gcc ttt att ctc agt gac ctt ttt gat att gga gaa ttg gca gct			338
Glu Ala Phe Ile Leu Ser Asp Leu Phe Asp Ile Gly Glu Leu Ala Ala			
95	100	105	
ggt gag ctt ctt ctt gct gga gag cat caa cag cca cat ttt cct ggc			386
Val Glu Leu Leu Leu Ala Gly Glu His Gln Gln Pro His Phe Pro Gly			
110	115	120	
ctt acc aga gga tta gta gct gtt ctt ctg tac tgg gat gga aag cga			434
Leu Thr Arg Gly Leu Val Ala Val Leu Leu Tyr Trp Asp Gly Lys Arg			
125	130	135	140
tgc att gcg aat tcc ttg aaa gcc ttg ata cag tct aga cgg gg			478
Cys Ile Ala Asn Ser Leu Lys Ala Leu Ile Gln Ser Arg Arg			
145	150		

&lt;210&gt; 742

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 377..751

&lt;400&gt; 742

atttcctgcc gtaagtatac agtgccctccg ggtcgcggtc attttgagcc cctgtctgga	60
tgacttcttg cggtgttct accctcccc ctcccgcgt cggcctgmct gctgtcgtcg	120
ggaggtgggt gaggtgacgc aaacagcccc gttgttgccc tccgcgtatc ccctcaccac	180
ctttgcggcc atccacgact ttgcacctt ccgccatttt cctgcctgtg aggggtggaca	240
gatcgcgtc ggggtctcggc ctctgagtg ccggtgactg cgggaggcga cggagtgtt	300
ctgggggtgt gagctgggga agttcgtggt cacggatgcg tgtgggggtg ctgctcagtc	360
tgtaacggca ggaaag atg aat ggg agg gct gat ttt cga gag ccg aat gca	412
Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala	
1 5 10	
gag gtt cca aga cca att ccc cac ata ggg cct gat tac att cca aca	460
Glu Val Pro Arg Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr	
15 20 25	
gag gaa gaa agg aga gtc ttc gca gaa tgc aat gat gaa agc ttc tgg	508
Glu Glu Glu Arg Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp	
30 35 40	
ttc aga tct gtg cct ttg gct gca aca agt atg ttg att act caa gga	556
Phe Arg Ser Val Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly	
45 50 55 60	
tta att agt aaa gga ata ctt tca agt cat ccc aaa tat ggt tcc atc	604
Leu Ile Ser Lys Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile	
65 70 75	
cct aaa ctt ata ctt gct tgt atc atg gga tac ttt gct gga aaa ctt	652
Pro Lys Leu Ile Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu	
80 85 90	
tct tat gtg aaa act tgc caa gag aaa ttc aag aaa ctt gaa aat tcc	700
Ser Tyr Val Lys Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser	
95 100 105	
ccc ctt gga gaa gct tta cga tca gga caa gca cga cga tct tca cca	748
Pro Leu Gly Glu Ala Leu Arg Ser Gly Gln Ala Arg Arg Ser Ser Pro	
110 115 120	
cct g	752
Pro	
125	

&lt;210&gt; 743

&lt;211&gt; 459

<212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 353..457

<221> misc\_feature  
 <222> 438  
 <223> n=a, g, c or t

<400> 743  
 cctatcactg gagaatgggt ttggtgcttt gagctgtggt tctacataaa aaagaaggaa 60  
 tcaaagtgat gctggtgtga caatataaca tttgaagctg ctccaaacaa ctttgactgt 120  
 aagaaaatgg ccaagagaat acaagaggct ctaaccaagg actctgactt cactaagcca 180  
 ctgaaacatt cctggcacta cctacctcct gccttttcgt tatgggagga aaccctattg 240  
 gttaggtcac tgggttataaa cacgtccttt aaattgcaga ggaagaaaag gcttggaggt 300  
 gataaaggaa tayagttcat tcccttsmtt atggtgatgg tttcataggc at atg cat 358  
 Met His  
 1  
 atg tcc aaa ctc atc aac ttg tat aca tca rat atg tgc aat tta ctg 406  
 Met Ser Lys Leu Ile Asn Leu Tyr Thr Ser Xaa Met Cys Asn Leu Leu  
 5 10 15  
 tmt atc cac cty mtc tym ata agc tgt tta ant aat aat aar rta aca 454  
 Xaa Ile His Leu Xaa Xaa Ile Ser Cys Leu Xaa Asn Asn Lys Xaa Thr  
 20 25 30  
 tta cg 459  
 Leu  
 35

<210> 744  
 <211> 411  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 79..411

<400> 744  
 atggggacgg ggctgttccc ggggaggetg tgatggggtg acaggtgcgt gacagtggga 60  
 gctgctctcg gcacaagc atg tac ggc aaa ggc aag agt aac agc agc gcc 111  
 Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala  
 1 5 10  
 gtc ccg tcc gac agc cag gcc cgg gag aag tta gca ctc tac gta tat 159  
 Val Pro Ser Asp Ser Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr  
 15 20 25  
 gaa tat ctg ctc cat gta gga gct cag aaa tca gct caa aca ttt tta 207  
 Glu Tyr Leu Leu His Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu  
 30 35 40  
 tca gag ata aga tgg gaa aaa aac atc aca ttg ggg gaa cca cca gga 255  
 Ser Glu Ile Arg Trp Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly  
 45 50 55  
 ttc tta cat tct tgg tgg tgt gta ttt tgg gat ctc tac tgt gca gct 303  
 Phe Leu His Ser Trp Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala  
 60 65 70 75  
 cca gag aga cgt gaa aca tgt gaa cac tca agt gaa gca aaa gcc ttc 351  
 Pro Glu Arg Arg Glu Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe  
 80 85 90  
 cat gat tac agt gct gca gca gct ccc agt cca gtg cta gga aac att 399  
 His Asp Tyr Ser Ala Ala Ala Ala Pro Ser Pro Val Leu Gly Asn Ile  
 95 100 105

395

ccc cca gga gat 411  
 Pro Pro Gly Asp  
 110

<210> 745  
 <211> 404  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 83..403

<400> 745  
 ctctggggcg gasggccacc atcttggaac gggaggcgga sagagtcgac tgggagcgac 60  
 cgagcggggcc gccgccgccg cc atg aac ccc gaa tat gac tac ctg ttt aag 112  
 Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys  
 1 5 10  
 ctg ctt ttg att ggc gac tca ggc gtg ggc aag tca tgc ctg ctc ctg 160  
 Leu Leu Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Cys Leu Leu Leu  
 15 20 25  
 cgg ttt gct gat gac acg tac aca gag agc tac atc agc acc atc ggg 208  
 Arg Phe Ala Asp Thr Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly  
 30 35 40  
 gtg gac ttc aag atc cga acc atc gag ctg gat ggc aaa act atc aaa 256  
 Val Asp Phe Lys Ile Arg Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys  
 45 50 55  
 ctt cag atc tgg gac aca gcg ggc cag gaa cgg ttc cgg acc atc act 304  
 Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr  
 60 65 70  
 tcc agc tac tac cgg ggg gct cat ggc atc atc gtg gtg tat gac gtc 352  
 Ser Ser Tyr Tyr Arg Gly Ala His Gly Ile Ile Val Val Tyr Asp Val  
 75 80 85 90  
 act gac cag gaa tcc tac gcc ary gtg aag cag tgg ctg cag gag att 400  
 Thr Asp Gln Glu Ser Tyr Ala Xaa Val Lys Gln Trp Leu Gln Glu Ile  
 95 100 105  
 gac c 404  
 Asp

<210> 746  
 <211> 429  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 336..428

<221> misc\_feature  
 <222> 393  
 <223> n=a, g, c or t

<400> 746  
 ggctttcttc agtcacctcg gcccgatcg ggaagtgtca agcgggcgct ccccatctc 60  
 cgccgctatt accactgaac cgggacccc taccagggtc cagggccagc cgccatgacg 120  
 aacgtgtact ccttgatgg gattctggtg tttggtttg tctttgtttg cactgtgcc 180  
 tacttcaaga aagtacctcg tctcaaaacc tggctgctat cagagaagaa ggggtgtttg 240  
 ggtgtgtttt acaaagccgs tgtgattgga accaggctgc atgctgctgt ggcaattgct 300  
 tgtgttgtaa tgggctttta cgctctgttt ataaa atg aat tcc aaa gca scc 353  
 Met Asn Ser Lys Ala Xaa  
 1 5  
 aag tca tca act gcc aac caa ggg gac ggg gat gaa gaa nct gtt ggg 401

396

Lys Ser Ser Thr Ala Asn Gln Gly Asp Gly Asp Glu Glu Xaa Val Gly  
 10 15 20  
 mga mct gaa scc agt gta gga gag ttc a 429  
 Arg Xaa Glu Xaa Ser Val Gly Glu Phe  
 25 30

<210> 747  
 <211> 179  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 35..178

<221> misc\_feature  
 <222> 140  
 <223> n=a, g, c or t

<400> 747  
 gaaatataca atacccttatg ttgtatatatta catt atg ttg tat agt acg ttg aaa 55  
 Met Leu Tyr Ser Thr Leu Lys  
 1 5  
 cat aca cta caa tac gtt atc att aat tgt ggt cac cat gct gtg caa 103  
 His Thr Leu Gln Tyr Val Ile Ile Asn Cys Gly His His Ala Val Gln  
 10 15 20  
 aag atc tct aaa acg tat tcc tcc tgt ctg act gaa nyt ttg tat cct 151  
 Lys Ile Ser Lys Thr Tyr Ser Ser Cys Leu Thr Glu Xaa Leu Tyr Pro  
 25 30 35  
 ttg cct aat atc tcc cca atc cct cca c 179  
 Leu Pro Asn Ile Ser Pro Ile Pro Pro  
 40 45

<210> 748  
 <211> 383  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 101..382

<400> 748  
 ctatattagt tgtggagaag aacacacagc agttctcaca aagagwggag gtgtgtttac 60  
 ctttggcgct gggtcctgtg ggcaacttgg acacgactcc atg aat gat gag gtt 115  
 Met Asn Asp Glu Val  
 1 5  
 aac cct aga aga gtt cta gag ctg atg ggt agt gaa gta act caa att 163  
 Asn Pro Arg Arg Val Leu Glu Leu Met Gly Ser Glu Val Thr Gln Ile  
 10 15 20  
 gct tgt ggc aga caa cat acc cta gsm ttc gtg cct tct tct gga ctc 211  
 Ala Cys Gly Arg Gln His Thr Leu Xaa Phe Val Pro Ser Ser Gly Leu  
 25 30 35  
 atc tat gca ttt ggt tgt gga gca aga ggt caa tta gga act ggg cac 259  
 Ile Tyr Ala Phe Gly Cys Gly Ala Arg Gly Gln Leu Gly Thr Gly His  
 40 45 50  
 act tgt aat gtt aag tgc cca tct cct gtc aag ggt tac tgg gct gcc 307  
 Thr Cys Asn Val Lys Cys Pro Ser Pro Val Lys Gly Tyr Trp Ala Ala  
 55 60 65  
 cac agt ggc cag ctt tca gcc cga gct gat cgc ttt aaa tat cat atc 355  
 His Ser Gly Gln Leu Ser Ala Arg Ala Asp Arg Phe Lys Tyr His Ile  
 70 75 80 85

gtt aag cag atc ttc tct gga gga gac c 383  
 Val Lys Gln Ile Phe Ser Gly Gly Asp  
 90

<210> 749  
 <211> 446  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 381..446

<400> 749  
 aacaatcaca gctccgggca ttgggggaac cssagccggc tgcgccgggg gaatccgtgc 60  
 gggcgccctc cgtcccggtc ccatcctcgc cgcgctccag cacctctgaa gttttgcagc 120  
 gccagaaaag gaggcgagga aggcagggag tgtgtgagag gagggagcaa aaagctcacc 180  
 ctaaaacatt tatttcaagg agaaaagaaa aagggggggc gcaaaaatgg ctggggcaat 240  
 tatagaaaac atgagcacca agaagctgtg cattgttggg gggattctgc tcgtgttcca 300  
 aatcatcgcc tttctggtgg gaggttgat tgctccaggg sccacaacgg cagtgtccta 360  
 catgtcggtg aaatgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 413  
 Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly  
 1 5 10  
 tcg gtg cct tgg gga ccc aat cat tgt gac aag 446  
 Ser Val Pro Trp Gly Pro Asn His Cys Asp Lys  
 15 20

<210> 750  
 <211> 410  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 129..410

<400> 750  
 ttttctctc ctcctcaggg ctccagtcag gccgatccgc tccgctcacg gaaggaaaac 60  
 agaaataact tgctggcttg tctggagtca catggtgaca atttacagaa agtcatctct 120  
 gcagcttg atg ggc gac aac cct ttt caa cca aaa agt aat tca aaa atg 170  
 Met Gly Asp Asn Pro Phe Gln Pro Lys Ser Asn Ser Lys Met  
 1 5 10  
 gca gaa ctg ttt atg gaa tgt gaa gaa gag gag ctg gaa cca tgg cag 218  
 Ala Glu Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu Pro Trp Gln  
 15 20 25 30  
 aag aaa gta aaa gaa gtt gag gat gac gat gat gat gag cca atc ttt 266  
 Lys Lys Val Lys Glu Val Glu Asp Asp Asp Asp Asp Glu Pro Ile Phe  
 35 40 45  
 gtt ggc gag ata tca agt tca aaa cca gca att tca aat att ttg aac 314  
 Val Gly Glu Ile Ser Ser Ser Lys Pro Ala Ile Ser Asn Ile Leu Asn  
 50 55 60  
 aga gtt aac ccc agc tca tat tca agg gga cta aag aat ggt gca ctc 362  
 Arg Val Asn Pro Ser Ser Tyr Ser Arg Gly Leu Lys Asn Gly Ala Leu  
 65 70 75  
 agt cga ggt att act gct gca ttc aag cct aca agt caa cac tac acg 410  
 Ser Arg Gly Ile Thr Ala Ala Phe Lys Pro Thr Ser Gln His Tyr Thr  
 80 85 90

<210> 751  
 <211> 536  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 334..534

&lt;221&gt; misc\_feature

&lt;222&gt; 148

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 751

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cctccctccc accggaaaac tctgaggaca tgaatagtcg ccaggcttgg cggtctttgc      60
tctcccaagg cagaggagat cgttgggttt caaggccccc cgggcatttc tcgccggccc      120
tgcgagagaga gttcttcact accacaancm arggagggat atgataggcg gccagtggat      180
ataactcctt tagaaciaaag gaaattaact tttgataccc atgcattggg tcaggacttg      240
gaaactcatg gatttgacaa aacacaagca gaaacaattg tatcagcggt aactgcttta      300
tcaaattgtca gcctggatac tatctataaa gag atg gtc act caa gct caa cag      354
                               Met Val Thr Gln Ala Gln Gln
                               1           5
gaa ata aca gta caa cag cta atg gct cat ttg gat gct atc agg aaa      402
Glu Ile Thr Val Gln Gln Leu Met Ala His Leu Asp Ala Ile Arg Lys
      10           15           20
gac atg gtc atc cta gag aaa agt gaa ttt gca aat ctg aga gca gag      450
Asp Met Val Ile Leu Glu Lys Ser Glu Phe Ala Asn Leu Arg Ala Glu
      25           30           35
aat gag aaa atg aaa att gaa tta gac caa gtt aag caa caa cta atg      498
Asn Glu Lys Met Lys Ile Glu Leu Asp Gln Val Lys Gln Gln Leu Met
      40           45           50           55
cat gaa acc agt yga atc aga gca gat aat aaa ctg ga      536
His Glu Thr Ser Xaa Ile Arg Ala Asp Asn Lys Leu
      60           65

```

&lt;210&gt; 752

&lt;211&gt; 139

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 25..138

&lt;400&gt; 752

```

cttggaatctt tgggtgttacc ttaa atg aaa ttt gga aat gtt agg atg tya      51
                               Met Lys Phe Gly Asn Val Arg Met Xaa
                               1           5
tct att caa ata ttt att gtg tcc atc tgg agc ttc ttc ctt ttc tat      99
Ser Ile Gln Ile Phe Ile Val Ser Ile Trp Ser Phe Phe Leu Phe Tyr
      10           15           20           25
ggc aag tat aca tat att aga ctg atc ttg tcc caa ggc c      139
Gly Lys Tyr Thr Tyr Ile Arg Leu Ile Leu Ser Gln Gly
      30           35

```

&lt;210&gt; 753

&lt;211&gt; 193

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 87..191

&lt;400&gt; 753

```

tattacagag tttgcagact gaaagagagt ctagctaagg cttgctcctc ataccagga      60
tttgatctaa tccaacaagc ctttgt atg acc ttt gac ctc agt gtg ttc agt      113

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399

Met Thr Phe Asp Leu Ser Val Phe Ser  
 1 5  
 act ttg tca gat cac ttt tac tca tca tca ttg tcc aat act gca agg 161  
 Thr Leu Ser Asp His Phe Tyr Ser Ser Ser Leu Ser Asn Thr Ala Arg  
 10 15 20 25  
 aat ctg tat att tgt tta ttt cat atc aca ca 193  
 Asn Leu Tyr Ile Cys Leu Phe His Ile Thr  
 30 35

&lt;210&gt; 754

&lt;211&gt; 395

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 310..393

&lt;400&gt; 754

cggcctcgca cttccggtgg ggagattccg gcctggagct cccagggccg agcagacctt 60  
 gggacctgtg agcgtgcat ccaattaacc atgggaaggg tcagcaccag ccaccagccc 120  
 cttaggtgag gactctgcct ggggctctgc tgatggttcc gaatcatgga gctgcagaga 180  
 gctcctccag cctggagacg ttcttggtga aagctgtggt ctaactccac cggtcttcc 240  
 tgacatttgt attcaagagg ggtgcctgcc cccgctgact caggagctcc ggtgctgcag 300  
 ccgccacga atg ggg agg tgg gcc ctc gat gtg gcc ttt ttg tgg aag gcg 351  
 Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala  
 1 5 10  
 gtg ttg acc ctg ggg ctg gtg ctt ctc tac tac tgc ttc tcc at 395  
 Val Leu Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser  
 15 20 25

&lt;210&gt; 755

&lt;211&gt; 460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 76..459

&lt;400&gt; 755

agaaggctgt gcgtgctcct cgctttctcc gcggtcttcc gagcggctgc gtgaactgct 60  
 tcctgcaggc tggcc atg gcg ctt cac gtt ccc aag gct ccg ggc ttt gcc 111  
 Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala  
 1 5 10  
 cag atg ctc aag gag gga gcg aaa cac ttt tca gga tta gaa gag gct 159  
 Gln Met Leu Lys Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala  
 15 20 25  
 gtg tat aga aac ata caa gct tgc aag gag ctt gcc caa acc act cgt 207  
 Val Tyr Arg Asn Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg  
 30 35 40  
 aca gca tat gga cca aat gga atg aac aaa atg gtt atc aac cac ttg 255  
 Thr Ala Tyr Gly Pro Asn Gly Met Asn Lys Met Val Ile Asn His Leu  
 45 50 55 60  
 gag aag ttg ttt gtg aca aac gat gca gca act att tta aga gaa cta 303  
 Glu Lys Leu Phe Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu  
 65 70 75  
 gaa gta cag cat cct gct gca aaa atg att gta atg gct tct cat atg 351  
 Glu Val Gln His Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met  
 80 85 90  
 caa gag caa gaa gtt gga gat ggc aca aac ttt gtt ctg gta ttt gct 399  
 Gln Glu Gln Glu Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala  
 95 100 105

400

gga gct ctc ctg gaa tta gct gaa gaa ctt ctg agg att ggc ctg tca 447  
 Gly Ala Leu Leu Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser  
 110 115 120

gtt tca gag gtc a 460  
 Val Ser Glu Val  
 125

&lt;210&gt; 756

&lt;211&gt; 142

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 42..140

&lt;400&gt; 756

aagcctgact tcagegctcc cactctcggc cgacaccct c atg gcc aac cgt tac 56  
 Met Ala Asn Arg Tyr  
 1 5

acc atg gat ctg act gcc atc tac gag agc ctc ctg tcg ctg agc cct 104  
 Thr Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu Leu Ser Leu Ser Pro  
 10 15 20

gac gts acc ctc acc cac ttc gcc cac tgc aac ctc ca 142  
 Asp Val Thr Leu Thr His Phe Ala His Cys Asn Leu  
 25 30

&lt;210&gt; 757

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 158..361

&lt;400&gt; 757

atcttgtagg cggggacacg ccgaggtaac ttccagggtg cgccttcggt gtctttctcca 60  
 agctgtagtt ctacgtcccg acctccctat cataccacac tcttcagcga ccacgcaggc 120  
 actttcccg tccccagtat accataattg aagaaaa atg atg gaa gag agt gga 175  
 Met Met Glu Glu Ser Gly  
 1 5

ata gag aca aca cca cct ggg act cct cca cca aat cct gca ggg ctg 223  
 Ile Glu Thr Thr Pro Pro Gly Thr Pro Pro Pro Asn Pro Ala Gly Leu  
 10 15 20

gct gct act gct atg tct tct acc cct gtt cca tta gcg gca acc agt 271  
 Ala Ala Thr Ala Met Ser Ser Thr Pro Val Pro Leu Ala Ala Thr Ser  
 25 30 35

tct ttt tct tct cca aat gta tcc tcc atg gag tcc ttc cca cca ctc 319  
 Ser Phe Ser Ser Pro Asn Val Ser Ser Met Glu Ser Phe Pro Pro Leu  
 40 45 50

gca tac tct act cct cag ccg ccc ctt cct cct gtg agg cct t 362  
 Ala Tyr Ser Thr Pro Gln Pro Pro Leu Pro Pro Val Arg Pro  
 55 60 65

&lt;210&gt; 758

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 219..368

&lt;221&gt; misc\_feature

&lt;222&gt; 317

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 758

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gaagaaggct cttacagcat ggccgccggt actgcagctg ccttagcggt tttgagtcag      60
gagagccgaa cgccgggccgg ggggtgtcggg ggcctacggg tcccggcccc ggctactatg    120
gacagttttt tcttcggctg tgagctctcc ggccacaccc gtccttcac ctttaaggta      180
gaggaagagg atgatgcgga sacgtgctgg cactaacc atg ctc tgc ctc acc gag      236
                               Met Leu Cys Leu Thr Glu
                               1           5
gga gcc aaa gac gag tgt aat gtg gta gaa gtt gtg gcc cgg aac cat      284
Gly Ala Lys Asp Glu Cys Asn Val Val Glu Val Val Ala Arg Asn His
                               10          15          20
gac cat cag gag atc gca gtc cct gtg gcc aan ctc aag ctg tcc tgc      332
Asp His Gln Glu Ile Ala Val Pro Val Ala Xaa Leu Lys Leu Ser Cys
                               25          30          35
caa ccc atg ctc agt ctg gat gac ttc cag ctc caa      368
Gln Pro Met Leu Ser Leu Asp Asp Phe Gln Leu Gln
                               40          45          50

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&lt;210&gt; 759

&lt;211&gt; 452

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 36..452

&lt;400&gt; 759

```

agctcgctgc gcaggcgcag tgagttcgac acacc atg ccg act gtc agc gtg      53
                               Met Pro Thr Val Ser Val
                               1           5
aag cgt gat ctg ctc ttc caa gcc ctg ggc cgc acc tac act gac gaa      101
Lys Arg Asp Leu Leu Phe Gln Ala Leu Gly Arg Thr Tyr Thr Asp Glu
                               10          15          20
gaa ttt gat gaa cta tgt ttt gaa ttt ggt ctg gag ctt gat gaa att      149
Glu Phe Asp Glu Leu Cys Phe Glu Phe Gly Leu Glu Leu Asp Glu Ile
                               25          30          35
aca tct gag aag gaa ata ata agt aaa gaa caa ggt aat gta aag gca      197
Thr Ser Glu Lys Glu Ile Ile Ser Lys Glu Gln Gly Asn Val Lys Ala
                               40          45          50
gca gga gcc tct gat gtt gtt ctt tac aaa att gac gtc cct gcc aat      245
Ala Gly Ala Ser Asp Val Val Leu Tyr Lys Ile Asp Val Pro Ala Asn
55                               60          65          70
aga tat gat ctc ctg tgt ctg gaa gga ttg gtt cga gga ctt cag gtc      293
Arg Tyr Asp Leu Leu Cys Leu Glu Gly Leu Val Arg Gly Leu Gln Val
                               75          80          85
ttc aaa gaa agg ata aag gct cca gtg tat aaa cgg gta atg cct gat      341
Phe Lys Glu Arg Ile Lys Ala Pro Val Tyr Lys Arg Val Met Pro Asp
90                               95          100
gga aaa atc cag aaa ttg att atc aca gaa gag aca gct aag ata cgt      389
Gly Lys Ile Gln Lys Leu Ile Ile Thr Glu Glu Thr Ala Lys Ile Arg
105                               110          115
cct ttt gcg gta gca gca gtt ctc cgt aat ata aag ttt act aaa gat      437
Pro Phe Ala Val Ala Ala Val Leu Arg Asn Ile Lys Phe Thr Lys Asp
120                               125          130
cga tat gac agc ttc      452
Arg Tyr Asp Ser Phe
135

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<210> 760  
 <211> 295  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 83..295

<400> 760  
 aagctgctgg tcgaaaatss tgacagcaca gggcttcttg ggctctgcag agcaaaactgg 60  
 aaagagctgg gatccaggca ct atg ttc tct gaa gaa ctg tgg ctg gaa aat 112  
 Met Phe Ser Glu Glu Leu Trp Leu Glu Asn  
 1 5 10  
 gag aaa aag tgt gct gtg gtt cgg aag tct aag cag ggc agg aaa cgc 160  
 Glu Lys Lys Cys Ala Val Val Arg Lys Ser Lys Gln Gly Arg Lys Arg  
 15 20 25  
 caa gaa ctg ctg gcc gta gcc ttc ggg gtg aag gtc cac acg ttc cga 208  
 Gln Glu Leu Leu Ala Val Ala Phe Gly Val Lys Val His Thr Phe Arg  
 30 35 40  
 ggc cca cac tgg tgt gaa tat tgt gcc aat ttc atg tgg ggg ctc atc 256  
 Gly Pro His Trp Cys Glu Tyr Cys Ala Asn Phe Met Trp Gly Leu Ile  
 45 50 55  
 gcc caa ggg gtc cgg tgc tca gac tgt gga ttg aac gta 295  
 Ala Gln Gly Val Arg Cys Ser Asp Cys Gly Leu Asn Val  
 60 65 70

<210> 761  
 <211> 212  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 124..210

<400> 761  
 ttggccattt ttttcttttg gctttgattt gtgaactata tccaagactc attggagtaa 60  
 tagttaactg attgcagtgg atttcgaggt gtggcaacta gtggcaatgc tcatgcgaca 120  
 gtg atg gtg gtt ttc atg aca tat gta act tta ccc ttt ttt ttt tct 168  
 Met Val Val Phe Met Thr Tyr Val Thr Leu Pro Phe Phe Phe Ser  
 1 5 10 15  
 ttc atc tct tcc ctt ctt tca ttt ttt ttt ctt ttt cta ctc tc 212  
 Phe Ile Ser Ser Leu Leu Ser Phe Phe Phe Leu Phe Leu Leu  
 20 25

<210> 762  
 <211> 623  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 474..623

<400> 762  
 agtggggagt ttaggcaagt gcctgatttg ggtaatcgaa agcaccagct gattgtattt 60  
 gatgactttt aagctttcat atgccgttat ttaatacctg tcacttccaa atgagagatg 120  
 taagggcaac ggccgttagc gttctgwttt ggatcaggct ctggagtggc cgcccctagc 180  
 ttagggttcc ttctaggcag ccagaaaact gcggaaaatg gtagcgatgg cggctggggc 240  
 gagtgggtgt ctggtgccgg cgtttgggct acggttggtg ttggcgactg tgcttcaagc 300  
 ggtgtctgct tttggggcag agttttcatc ggaggcatgc agagagttrg gcttttctag 360

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caacttgctt tgcagctctt gtgatcttct cggacagttc aacctgcttc agctggatcc 420
tgattgcaga ggatgstgtc aggaggaagc acaatttgaa accaaaaagc tgt atg 476
                                     Met
                                     1
cag gag cta ttc ttg aag ttt gtg gat gaa aat tgg gaa ggt tcc ctc 524
Gln Glu Leu Phe Leu Lys Phe Val Asp Glu Asn Trp Glu Gly Ser Leu
      5              10              15
aag tcc aag tat gtc cgt ggt tca gac cct gta tta aag ctt ttg gac 572
Lys Ser Lys Tyr Val Arg Gly Ser Asp Pro Val Leu Lys Leu Leu Asp
      20              25              30
gac aat ggg aac att gct gaa gaa ctg agc att ctc aaa tgg aca cag 620
Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu Lys Trp Thr Gln
      35              40              45
aca 623
Thr
50

```

&lt;210&gt; 763

&lt;211&gt; 261

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 58..261

&lt;400&gt; 763

```

gacatccacg gggcgcgagt gacacgcggg agggagagca gtgttctgct ggagccg 57
atg cca aaa acc atg cat ttc tta ttc aga ttc att gtt ttc ttt tat 105
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr
1      5              10              15
ctg tgg ggc ctt ttt act gct cag aga caa aag aaa gag gag agc acc 153
Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr
      20              25              30
gaa gaa gtg aaa ata gaa gtt ttg cat cgt cca gaa aac tgc tct aag 201
Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys
      35              40              45
aca agc aag aag gga gac cta cta aat gcc cat tat gac ggc tac ctg 249
Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu
      50              55              60
gct aaa gac ggc 261
Ala Lys Asp Gly
65

```

&lt;210&gt; 764

&lt;211&gt; 160

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 4..159

&lt;400&gt; 764

```

agt atg ctt gag gaa ttg aaa gct ggc cag gag ttg gag gaa cag acc 48
Met Leu Glu Glu Leu Lys Ala Gly Gln Glu Leu Glu Glu Gln Thr
1      5              10              15
att agc cac ggc ttt gca cgt ggt gtg agg agg ggt gtg gct att gtg 96
Ile Ser His Gly Phe Ala Arg Gly Val Arg Arg Gly Val Ala Ile Val
      20              25              30
ggc aag ggt ctg gaa tgg cat ggg tgt tgg tgg atg tgc cac gga tac 144
Gly Lys Gly Leu Glu Trp His Gly Cys Trp Trp Met Cys His Gly Tyr
      35              40              45

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agg att cta gcc ggg a  
Arg Ile Leu Ala Gly  
50

160

<210> 765  
<211> 516  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 404..514

<400> 765  
aagaaagaga gaggcaagcg aaattcctga atggatagac agatgctacg tcatcggagc 60  
tgcatacctcc actccacaag aggctaggag ctgggggggag agaggcagtc cagccgcagg 120  
gccacccgaa cagtctctcc tcctcacaga agcctggagc tgggcatcca agaagaagca 180  
gcctcatttg ttttctggtg tcatcgtagg tggccaccta tggcttttgg gcttctcacc 240  
tggggcgggg gggttctgca ccaccctccc accctccttc ctccgtgtgg acgatagagc 300  
cacatccagc accacggaca gctcccgggc gacaaaaaag aagaatgtac ttcattctggt 360  
tgggctggat tccctctgat aagccttccc agttgactga aag atg agg cta ggc 415  
Met Arg Leu Gly  
1  
tct agc aag ttg aag tca aac cag ctc ctt caa gaa gct ttg agc aga 463  
Ser Ser Lys Leu Lys Ser Asn Gln Leu Leu Gln Glu Ala Leu Ser Arg  
5 10 15 20  
atg aag tgg gga gga ccc agc ttc cag ccc agg aag ccc act gta cct 511  
Met Lys Trp Gly Gly Pro Ser Phe Gln Pro Arg Lys Pro Thr Val Pro  
25 30 35  
gga gc 516  
Gly

<210> 766  
<211> 626  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 68..238

<221> sig\_peptide  
<222> 68..106  
<223> Von Heijne matrix  
score 15  
seq MLLLLLLLLPLALG/DK

<221> misc\_feature  
<222> 529  
<223> n=a, g, c or t

<400> 766  
agtttctgag agaagaaccc tgaggaacag acgttccttg gcggccctgg cgccttcaaa 60  
cccagac atg ctg ctg ctg ctg ctg ctg ccc ctt gct ctg ggg gac 109  
Met Leu Leu Leu Leu Leu Leu Leu Pro Leu Ala Leu Gly Asp  
-10 -5 1  
aaa ggg gat gga ggg aga cag aca ata tgg gga tgg tta ctt gct gca 157  
Lys Gly Asp Gly Gly Arg Gln Thr Ile Trp Gly Trp Leu Leu Ala Ala  
5 10 15  
agt gca gga gct ggt gac ggt gca gga ggg cct gtg tgt cca tgt gcc 205  
Ser Ala Gly Ala Gly Asp Gly Ala Gly Gly Pro Val Cys Pro Cys Ala  
20 25 30

ctg ctc ctt ctc cta ccc cca gga tgg ctg gac tgactctgac ccagttcatg 258  
 Leu Leu Leu Leu Leu Pro Pro Gly Trp Leu Asp

35 40  
 gctactgggt cccgggcaggg aatgatataa gctggaaggc tccagtggcc acaacaacc 318  
 cagcttgggc agtgcaggag gaaactcggg accgattcca mctycyttgg ggaccacag 378  
 accaaaaatt gcactctgag catcagagat gccagaatga gtgatgcggg gagatacttc 438  
 tttcgtatgg agaaaggaaa tataaaatgg aattataaat atgaccagct ctctgtgaac 498  
 gtgayagcct tgaccacag gcccaacats nktatccccg gtaccctgga gtctggctgc 558  
 ttccagaatc tgacctgctc tgtgccctgg gcctgtgagc aggggacgcc ccctatgatc 618  
 tcctggat 626

<210> 767

<211> 473

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 60..344

<221> sig\_peptide

<222> 60..113

<223> Von Heijne matrix

score 10.3000001907349

seq VLMLAALLLHCYA/DS

<400> 767

acagcaactt ccttgatccc tgccacgcac gactgaacac agacagcagc cgctcggc 59  
 atg aag ctg ctg atg gtc ctc atg ctg gcg gcc ctc ctc ctg cac tgc 107  
 Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys  
 -15 -10 -5  
 tat gca gat tct ggc tgc aaa ctc ctg gag gac atg gtt gaa aag acc 155  
 Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr  
 1 5 10  
 atc aat tcc gac ata tct ata cct gaa tac aaa gag ctt ctt caa gag 203  
 Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu  
 15 20 25 30  
 ttc ata gac agt gat gcc gct gca gag gct atg ggg aaa ttc aag cag 251  
 Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln  
 35 40 45  
 tgt ttc ctc aac cag tca cat aga act ctg aaa aac ttt gga ctg atg 299  
 Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met  
 50 55 60  
 atg cat aca gtg tac gac agc att tgg tgt aat atg aag agt aat 344  
 Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn  
 65 70 75  
 taactttacc caaggcggtt ggctcagagg gctacagact atggccagaa ctcatctgtt 404  
 gattgctaga aaccactttt ctttcttgtg ttgtctkttt atgwggaam tgctagacaa 464  
 ctgttgaaa 473

<210> 768

<211> 673

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 218..502

<221> sig\_peptide

<222> 218..310

<223> Von Heijne matrix

score 9.19999980926514

seq RLLLATVLQAVSA/FG

&lt;400&gt; 768

```

agtggggagt ttaggcaagt gcctgatttg ggtaatcgaa agcaccagtg gattgtattt      60
gatgactttt aagctttcat atgccgttat ttaatacctg tcacttccaa atgagagatg      120
taagggcaac ggccgtagc gttctgwttt ggatcaggct ctggagtgga cgccctagc      180
ttaggggtcc ttctaggcag ccagaaacct gcggaaa atg gta gcg atg gcg gct      235
                               Met Val Ala Met Ala Ala
                               -30
ggg ccg agt ggg tgt ctg gtg ccg gcg ttt ggg cta cgg ttg ttg ttg      283
Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu Arg Leu Leu Leu
-25          -20          -15          -10
gcg act gtg ctt caa gcg gtg tct gct ttt ggg gca gag ttt tca tcg      331
Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu Phe Ser Ser
          -5          1          5
gag gca tgc aga gag tta ggc ttt tct agc aac ttg ctt tgc agc tct      379
Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu Cys Ser Ser
          10          15          20
tgt gat ctt ctc gga cag ttc aac ctg ctt cag ctg gat cct gat tgc      427
Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp Pro Asp Cys
          25          30          35
aga gga tgc tgt cag gag gaa gca caa ttt gaa acc aaa aag ctg tat      475
Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys Lys Leu Tyr
          40          45          50          55
gca gga gct att ctt gaa gtt tgt gga tgaaaattgg gaaggttccc      522
Ala Gly Ala Ile Leu Glu Val Cys Gly
          60
tcaagtccaa gcttttggtta ggagtgataa acccaaactg ttcagaggac tgcaaataca      582
gtatgtccgt ggttcagacc ctgtattaaa gcttttggac gacaatggga acattgctga      642
agaactgagc attctcaaat ggacacagac a      673

```

&lt;210&gt; 769

&lt;211&gt; 539

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 190..492

&lt;221&gt; sig\_peptide

&lt;222&gt; 190..285

&lt;223&gt; Von Heijne matrix

score 8.80000019073486

seq VPMLLLIVGGSFG/LR

&lt;221&gt; misc\_feature

&lt;222&gt; 500..501

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 769

```

acaagtatgt tacgatggct cgattgcttt tgcctagcgg aaaccattca ctaaggaccg      60
agcaccaaata aaccaaggaa aaggaagtga gttaaggacg tactcgtctt ggtgagagcg      120
tgagctgctg agatttgga gtctgcgcta ggcccgcttg gagttctgag ccgatggaag      180
agttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac aag      231
          Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys
          -30          -25          -20
act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt tct      279
Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser
          -15          -10          -5
ttt ggt ctt cgt gag ttt tct caa atc cga tat gat gct gtg aag agt      327
Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser

```

```

      1             5             10
aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata tct      375
Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser
15             20             25             30
tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac tgg      423
Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp
35             40             45
aag aat att cga gga ccc agg cct tgg gaa gat cct gac ctc ctc caa      471
Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln
50             55             60
gga aag aaa tcc aga aag cct taagacanng acaacttgac tctgctgatt      522
Gly Lys Lys Ser Arg Lys Pro
65
cttttttccct tttttttt      539

```

&lt;210&gt; 770

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 124..468

&lt;221&gt; sig\_peptide

&lt;222&gt; 124..276

&lt;223&gt; Von Heijne matrix

score 8.10000038146973

seq VCLCGTFCFPCLG/CQ

&lt;400&gt; 770

```

aagttacctc tccccittca cgtarttttc atttgtggtg agattctctc ccaggccaca      60
agacatttcc tgctcggaac cttgtttact aatttccact gcttttaagg ccctgcaactg      120
aaa atg caa gct cag gcg ccg gtg gtc gtt gtg acc caa cct gga gtc      168
Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val
-50             -45             -40
ggt ccc ggt ccg gcc ccc cag aac tcc aac tgg cag aca ggc atg tgt      216
Gly Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys
-35             -30             -25
gac tgt ttc agc gac tgc gga gtc tgt ctc tgt ggc aca ttt tgt ttc      264
Asp Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe
-20             -15             -10             -5
ccg tgc ctt ggg tgt caa gtt gca gct gat atg aat gaa tgc tgt ctg      312
Pro Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu
1             5             10
tgt gga aca agc gtc gca atg agg act ctc tac agg acc cga tat ggc      360
Cys Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly
15             20             25
atc cct gga tct att tgt gat gac tat atg gca act ctt tgc tgt cct      408
Ile Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro
30             35             40
cat tgt act ctt tgc caa atc aag aga gat atc aac aga agg aga gcc      456
His Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala
45             50             55             60
atg cgt act ttc taaaaactga t      479
Met Arg Thr Phe

```

&lt;210&gt; 771

&lt;211&gt; 492

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> CDS  
<222> 25..402

<221> sig\_peptide  
<222> 25..96  
<223> Von Heijne matrix  
score 7  
seq LLCCFRALSGSLS/MR

<221> misc\_feature  
<222> 371  
<223> n=a, g, c or t

<400> 771  
agsetggccc tccctctttc caaa atg gac aag tcc ctc ttg ctg gaa ctc 51  
Met Asp Lys Ser Leu Leu Leu Glu Leu  
-20  
ccc atc ctg ctc tgc tgc ttt agg gca tta tct gga tca ctt tca atg 99  
Pro Ile Leu Leu Cys Cys Phe Arg Ala Leu Ser Gly Ser Leu Ser Met  
-15 -10 -5 1  
aga aat gat gca gtc aat gaa ata gtt gct gtg aaa aac aat ttt cct 147  
Arg Asn Asp Ala Val Asn Glu Ile Val Ala Val Lys Asn Asn Phe Pro  
5 10 15  
gtg ata gaa att gtt cgg tgt agg atg tgc cac ctc cag ttc cca gga 195  
Val Ile Glu Ile Val Arg Cys Arg Met Cys His Leu Gln Phe Pro Gly  
20 25 30  
gaa aag tgc tcc aga gga aga gga ata tgc aca gca aca aca gaa gag 243  
Glu Lys Cys Ser Arg Gly Arg Gly Ile Cys Thr Ala Thr Thr Glu Glu  
35 40 45  
gcc tgc atg gtt gga agg atg ttc aaa agg gat ggt aat ccc tgg tta 291  
Ala Cys Met Val Gly Arg Met Phe Lys Arg Asp Gly Asn Pro Trp Leu  
50 55 60 65  
acc ttc atg ggc tgc cta aag aac tgt gct gat gtg aaa ggc ata agg 339  
Thr Phe Met Gly Cys Leu Lys Asn Cys Ala Asp Val Lys Gly Ile Arg  
70 75 80  
tgg agt gtc tat ttg gtg aac ttc agg tgc tnm agg agc cat gac ctg 387  
Trp Ser Val Tyr Leu Val Asn Phe Arg Cys Xaa Arg Ser His Asp Leu  
85 90 95  
tgc aat gaa gac ctt tagaagttaa tggttcttct gtgactccaa tttctgggtg 442  
Cys Asn Glu Asp Leu  
100  
aggttgttgc ctcagcctct tcacaatgac tttctaaaaa aatcacacac 492

<210> 772  
<211> 396  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 7..312  
  
<221> sig\_peptide  
<222> 7..54  
<223> Von Heijne matrix  
score 6.80000019073486  
seq LWILPSLWLLLLG/GP

<400> 772  
agcaag atg gat cta ctg tgg atc ctg ccc tcc ctg tgg ctt ctc ctg 48  
Met Asp Leu Leu Trp Ile Leu Pro Ser Leu Trp Leu Leu Leu  
-15 -10 -5

```

ctt ggg ggg cct gcc tgc ctg aag acc cag gaa cac ccc agc tgc cca      96
Leu Gly Gly Pro Ala Cys Leu Lys Thr Gln Glu His Pro Ser Cys Pro
      1              5              10
gga ccc agg gaa ctg gaa gcc agc aaa gtt gtc ctc ctg ccc agt tgt      144
Gly Pro Arg Glu Leu Glu Ala Ser Lys Val Val Leu Leu Pro Ser Cys
15              20              25              30
ccc gga gct cca gga agt cct ggg gag aag gga gcc cca ggt cct caa      192
Pro Gly Ala Pro Gly Ser Pro Gly Glu Lys Gly Ala Pro Gly Pro Gln
      35              40              45
ggg cca cct gga cca cca ggc aag atg ggc ccc aag ggt gag cca gga      240
Gly Pro Pro Gly Pro Pro Gly Lys Met Gly Pro Lys Gly Glu Pro Gly
      50              55              60
gat cca gtg aac ctg ctc cgg tgc cag gaa ggc ccc aga aac tgc cgg      288
Asp Pro Val Asn Leu Leu Arg Cys Gln Glu Gly Pro Arg Asn Cys Arg
      65              70              75
gag ctg ttg agc agg gcg cca cct tgagcggctg gtamcatctg tgcctacctg      342
Glu Leu Leu Ser Arg Ala Pro Pro
      80              85
agggcagggc ctcccagtct tttgtgacat ggacaccgag gggggcggct ggct      396

```

&lt;210&gt; 773

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 50..229

&lt;221&gt; sig\_peptide

&lt;222&gt; 50..106

&lt;223&gt; Von Heijne matrix

score 6.59999990463257

seq SAVVLPSTPQASA/NP

&lt;221&gt; misc\_feature

&lt;222&gt; 206,354

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 773

```

acaggatcga tttacggycg cagagaaaaa ccaagatttc actttcaag atg gaa agt      58
                                     Met Glu Ser
ccg tca grc tca gct gtg gtt tta cct agc act cct cag gcc tct gcg      106
Pro Ser Xaa Ser Ala Val Val Leu Pro Ser Thr Pro Gln Ala Ser Ala
-15              -10              -5
aat cca tca tct ccc tat aca aat agt tcc cga aaa caa cct atg agt      154
Asn Pro Ser Ser Pro Tyr Thr Asn Ser Ser Arg Lys Gln Pro Met Ser
1              5              10              15
gca aca ctt aga gaa aga tta agg aaa aca aga ttt tca ttt aat tcc      202
Ala Thr Leu Arg Glu Arg Leu Arg Lys Thr Arg Phe Ser Phe Asn Ser
      20              25              30
tct nac aat gtg gtg aac gtc tta aag tagagagtga agaaaatgat      249
Ser Xaa Asn Val Val Asn Val Leu Lys
      35              40
cagacctttt cagagaaccc agcatcttcc acagaggraa actgtttggr attcaaagaa      309
agtttaaamc atatagrcag tgatttgaag aaaatacaaa tttgnaaaat actttgaaga      369
atctcaatgt ctgtgaatct cagtcacttg attctggatc atgcagtg      417

```

&lt;210&gt; 774

&lt;211&gt; 454

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
 <221> CDS  
 <222> 153..443

<221> sig\_peptide  
 <222> 153..200  
 <223> Von Heijne matrix  
 score 6.40000009536743  
 seq WLWPLYFLPVSGA/LR

<221> misc\_feature  
 <222> 359  
 <223> n=a, g, c or t

<400> 774  
 aggttgatcat ttcctcatcg tcaagctttg ttcctcgtgg gggctagaaa tctctttcca 60  
 gttccagatt gtgaagggtt cctgagtaag cagcgtgtct ccatccccct ctctaggggc 120  
 tcttgatggg accttgcaact ctagaaggga ca atg gac ttc tgg ctt tgg cca 173  
 Met Asp Phe Trp Leu Trp Pro  
 -15 -10  
 ctt tac ttc ctg cca gta tcr ggg gcc ctg agg atc ctc cca gaa gta 221  
 Leu Tyr Phe Leu Pro Val Ser Gly Ala Leu Arg Ile Leu Pro Glu Val  
 -5 1 5  
 aag gta gag ggg gag ctg ggc gga tca gtt acc atc aag tgc cca ctt 269  
 Lys Val Glu Gly Glu Leu Gly Gly Ser Val Thr Ile Lys Cys Pro Leu  
 10 15 20  
 cct gaa atg cat gtg agg ata tat ctg tgc cgg gag atg gct gga tct 317  
 Pro Glu Met His Val Arg Ile Tyr Leu Cys Arg Glu Met Ala Gly Ser  
 25 30 35  
 gga aca tgt ggt acc gtg gta tcc acc acc aac ttc atc aan gca gaa 365  
 Gly Thr Cys Gly Thr Val Val Ser Thr Thr Asn Phe Ile Xaa Ala Glu  
 40 45 50 55  
 tac aag ggc cga gtt act ctg aga gca ata ccc acg caa gaa tct gtt 413  
 Tyr Lys Gly Arg Val Thr Leu Arg Ala Ile Pro Thr Gln Glu Ser Val  
 60 65 70  
 cct agt gga ggt aac aca gct gac aga aag tgacagcgga g 454  
 Pro Ser Gly Gly Asn Thr Ala Asp Arg Lys  
 75 80

<210> 775  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 8..253

<221> sig\_peptide  
 <222> 8..109  
 <223> Von Heijne matrix  
 score 6.19999980926514  
 seq MAVLAPLIALVYS/XP

<400> 775  
 agtcgtt atg gtg ggg gag gcg ggg cga gac cta cga cgc cgg cga gca 49  
 Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala  
 -30 -25  
 gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct 97  
 Val Ala Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala  
 -20 -15 -10 -5

```

ctc gtg tat tgc gys ccg cga ctt tca cga tgg ctc gcc caa cct tac      145
Leu Val Tyr Ser Xaa Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
              1              5              10
tac ctt ctg tgc scc ctg ctc tct gmt gcc ttc cta ctc gtg agg maa      193
Tyr Leu Leu Ser Xaa Leu Leu Ser Xaa Ala Phe Leu Leu Val Arg Xaa
              15              20              25
ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gaa smc ggt aac      241
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn
              30              35              40
ccg tcr wsa ytt tgactgggtg agcctcccgcc gtgtagtac cccgcgacsk      293
Pro Ser Xaa Xaa
45
tgactgtacc tgccttgca ggtgtatctg ggaaccctgg gggttacctc tctgaggaca      353
cctgaggttc cgagcctgta gggacttag agactattaw ktgcagggtc cgaaccatca      413
tcgagtctaa actttgtgtt taagatggga aaacggaaca tgtagtcgt agcccatgca      473
caacggccca acagcttttg actgttgagt ccaggtttct ttctgtttca ccattgag      531

```

&lt;210&gt; 776

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 220..363

&lt;221&gt; sig\_peptide

&lt;222&gt; 220..270

&lt;223&gt; Von Heijne matrix

score 6

seq WLSCFLLPALVVS/VA

&lt;221&gt; misc\_feature

&lt;222&gt; 201

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 776

```

agagggtgcc cacctgtgtg ccagcgctg tccggcgctt gcctgccgcc tccgtggcga      60
aggggacaca gaaatactca ctgagcctac actgggctca gcctgtgctt ggtcctgggg      120
tcacaaaggt gcatcagacg cagaccttgc cctcacatct cttctggcct ggtgggagag      180
gctcatctgc aaagagataa ngaggtccct gcggatgtg atg gcc cag cta tgg      234
                                   Met Ala Gln Leu Trp
                                   -15
ctg tcc tgc ttc ctc ctt cct gcc ctc gtg gtg tct gtg gca gcc aac      282
Leu Ser Cys Phe Leu Leu Pro Ala Leu Val Val Ser Val Ala Ala Asn
              -10              -5              1
gtg gcc cck wag ttc cta gcc aac atg acg tca gtg atc ctg cct gag      330
Val Ala Pro Xaa Phe Leu Ala Asn Met Thr Ser Val Ile Leu Pro Glu
              5              10              15              20
gac tgc ctg tgg gtg ccc agg cct tct ggt tgg tagcg      368
Asp Cys Leu Trp Val Pro Arg Pro Ser Gly Trp
              25              30

```

&lt;210&gt; 777

&lt;211&gt; 469

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 8..322

```
<221> sig_peptide
<222> 8..109
<223> Von Heijne matrix
      score 5.90000009536743
      seq MAVLAPLIALVYS/VP
```

```
<221> misc_feature
<222> 233,352
<223> n=a, g, c or t
```

[illegible]

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<210> 778
<211> 468
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 77..340
```

```
<221> sig_peptide
<222> 77..133
<223> Von Heijne matrix
      score 5.90000009536743
      seq AFLVCLAFSLATL/VQ
```

```

<400> 778
agctcckcct cggcctcccc ttccgggcgct ctccgcgctaa ctgtgctcct ccgggggcct      60
ccgcctgctc ccagcc atg gtg gcc tgg cgc tcg gcg ttc ctt gtc tgc ctc      112
          Met Val Ala Trp Arg Ser Ala Phe Leu Val Cys Leu
                    -15                                -10

gct ttc tcc ttg gcc acc ctg gtc cag cga gga tct ggg gac ttt gat      160
Ala Phe Ser Leu Ala Thr Leu Val Gln Arg Gly Ser Gly Asp Phe Asp
          -5                                1                                5

gat ttt aac ctg gag gat gca gtg aaa gaa act tcc tca gta aag cag      208
Asp Phe Asn Leu Glu Asp Ala Val Lys Glu Thr Ser Ser Val Lys Gln
10          15          20          25

```

```

cca tgg gac cac acc acc acc acc aca acc aat agg cca gga acc acc    256
Pro Trp Asp His Thr Thr Thr Thr Thr Thr Asn Arg Pro Gly Thr Thr
              30              35              40
aga gct ccg gca aaa cct cca ggt agt gga ttg gac ttg gct gat gct    304
Arg Ala Pro Ala Lys Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala
              45              50              55
ttg gat gat caa gat gat ggc cgc aga aac cgg gta taggaggaag    350
Leu Asp Asp Gln Asp Asp Gly Arg Arg Asn Arg Val
              60              65
agagagatgg aaccatgtaa ccaccacgac caagaggcca gtaaccacca gagctccagc    410
aaatacttta ggaaatgatt ttgacttggc tgatgcctgg atgatcgaaa tgatcgag    468

```

&lt;210&gt; 779

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 73..429

&lt;221&gt; sig\_peptide

&lt;222&gt; 73..231

&lt;223&gt; Von Heijne matrix

score 5.80000019073486

seq ILSLQVLLTTVTS/TV

&lt;400&gt; 779

```

gctctctcgc ggaastgggg aggaggcggg tgcggtagt ggaccgggac cggtaggggt    60
gctgttgcca tc atg gct gac ccc gac ccc cgg tac cct cgc tcc tcg atc    111
      Met Ala Asp Pro Asp Pro Arg Tyr Pro Arg Ser Ser Ile
              -50              -45
gag gac gac ttc aac tat ggc agc agc gtg gcc tcc gcc acc gtg cac    159
Glu Asp Asp Phe Asn Tyr Gly Ser Ser Val Ala Ser Ala Thr Val His
-40              -35              -30              -25
atc cga atg gcc ttt ctg aga aaa gtc tac agc att ctt tct ctg cag    207
Ile Arg Met Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln
              -20              -15              -10
gtt ctc tta act aca gtg act tca aca gtt ttt tta tac ttt gag tct    255
Val Leu Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser
              -5              1              5
gta cgg aca ttt gta cat gag agt cct gcc tta att ttg ctg ttt gcc    303
Val Arg Thr Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala
              10              15              20
ctc gga tct ctg ggt ttg att ttt gcg ttg ayt tta aac aga cat aag    351
Leu Gly Ser Leu Gly Leu Ile Phe Ala Leu Xaa Leu Asn Arg His Lys
25              30              35              40
tat ccc ctt aac ctg tac cta ctt ttt gga ttt acg ctg ttg gaa gct    399
Tyr Pro Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Glu Ala
              45              50              55
ctg act gtg gca gtt gtk gtt act gtt cta tgatgtatat attattctgc    449
Leu Thr Val Ala Val Val Val Thr Val Leu
              60              65
aagctttcat actgactact acagtatttt    479

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&lt;210&gt; 780

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 112..423

<221> sig\_peptide

<222> 112..276

<223> Von Heijne matrix

score 5.59999990463257

seq ELCCLFCCPPCPG/KI

<400> 780

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agtttcttcc gggtcattga cagaagcgtc aattcctggg agtagttcgt tggttttctt      60
tccctcatc cttttgcctg ctcccggcga ggggtggcct tgatttcggc g atg agc      117
                                         Met Ser
                                         -55
tcc cag aaa ggc aac gtg gct cgt tcc aga cct cag aag cac cag aat      165
Ser Gln Lys Gly Asn Val Ala Arg Ser Arg Pro Gln Lys His Gln Asn
                                         -50          -45          -40
acg ttt agc ttc aaa aat gac aag ttc gat aaa agt gtg cag acc aag      213
Thr Phe Ser Phe Lys Asn Asp Lys Phe Asp Lys Ser Val Gln Thr Lys
                                         -35          -30          -25
agc atg aat aat ctt tca ttt agt gag cta tgt tgc ctc ttc tgc tgt      261
Ser Met Asn Asn Leu Ser Phe Ser Glu Leu Cys Cys Leu Phe Cys Cys
                                         -20          -15          -10
cca cct tgt cca ggg aag att gct tca aaa tta gcg ttt ttg cca cct      309
Pro Pro Cys Pro Gly Lys Ile Ala Ser Lys Leu Ala Phe Leu Pro Pro
-5          1          5          10
gat cca act tac aca ctg atg tgt gat gaa agc gga agc gtt gga ctt      357
Asp Pro Thr Tyr Thr Leu Met Cys Asp Glu Ser Gly Ser Val Gly Leu
15          20          25
tac atc tgt ctg aac gag cag act ggc agt att ctt cta gag aaa aag      405
Tyr Ile Cys Leu Asn Glu Gln Thr Gly Ser Ile Leu Leu Glu Lys Lys
30          35          40
atg cta ttg agt gtt tca tgactagaac cagtaaaggc aacagaattg      453
Met Leu Leu Ser Val Ser
45
cttgtatgtt tgtacgttgt tcaccaatg cgaaatacac tttactcttc t      504

```

<210> 781

<211> 544

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 102..479

<221> sig\_peptide

<222> 102..287

<223> Von Heijne matrix

score 5.59999990463257

seq VIYLILLTAGAGL/LV

<221> misc\_feature

<222> 521

<223> n=a, g, c or t

<400> 781

```

agctgcagtg gttcgatggg aaggatcttt ctccaagtgg ttcctcttga ggggagcatt      60
tctgctggct ccaggacttt ggccatctat aaagcttggc a atg aga aat aag aaa      116
                                         Met Arg Asn Lys Lys
                                         -60
att ctc aag gag gac gag ctc ttg agt gag acc caa caa gct gct ttt      164
Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu Thr Gln Gln Ala Ala Phe
-55          -50          -45

```

415

```

cac caa att gca atg gag cct ttc gaa atc aat gtt cca aag ccc aag      212
His Gln Ile Ala Met Glu Pro Phe Glu Ile Asn Val Pro Lys Pro Lys
-40 -35 -30
agg aga aat ggg gtg aac ttc tcc cta gct gtg gtc atc tac ctg      260
Arg Arg Asn Gly Val Asn Phe Ser Leu Ala Val Val Val Ile Tyr Leu
-25 -20 -15 -10
atc ctg ctc acc gct ggc gct ggg ctg ctg gtg gtc caa gtt ctg aat      308
Ile Leu Leu Thr Ala Gly Ala Gly Leu Leu Val Val Gln Val Leu Asn
-5 1 5
ctg cag gcg cgg ctc cgg gtc ctg gag atg tat ttc ctc aat gac act      356
Leu Gln Ala Arg Leu Arg Val Leu Glu Met Tyr Phe Leu Asn Asp Thr
10 15 20
ctg gcg gct gag gac agc ccg tcc ttc tcc ttg ctg cag tca gca cac      404
Leu Ala Ala Glu Asp Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His
25 30 35
cct gga gaa cac ctg gct cag ggt gca tcg agg ctg cag tcc tgc agg      452
Pro Gly Glu His Leu Ala Gln Gly Ala Ser Arg Leu Gln Ser Cys Arg
40 45 50 55
ccc aac tca cct ggg tcc gcg tca sca tgagcacttg ctgcagcggg      499
Pro Asn Ser Pro Gly Ser Ala Ser Xaa
60
tagacaactt cactcagaak cnacggatgt tcagaatcaa aaggt      544

<210> 782
<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 27..428

<221> sig_peptide
<222> 27..194
<223> Von Heijne matrix
      score 5.30000019073486
      seq LAKLLPLPAITS/QL

<400> 782
aagagaggaa aaaaaatagc aggaag atg gcg ccc acc aag ccc agc ttt cag      53
Met Ala Pro Thr Lys Pro Ser Phe Gln
-55 -50
cag gat cct tcc agg cga gaa cgt tta caa gca ttg aga aag gag aaa      101
Gln Asp Pro Ser Arg Arg Glu Arg Leu Gln Ala Leu Arg Lys Glu Lys
-45 -40 -35
tcc cga gat gct gct cgc tcc cgc cgg gga aaa gaa aac ttt gag ttc      149
Ser Arg Asp Ala Ala Arg Ser Arg Arg Gly Lys Glu Asn Phe Glu Phe
-30 -25 -20
tat gaa ttg gcc aag ttg ttg cct ctt cct gca gcc att acc agc cag      197
Tyr Glu Leu Ala Lys Leu Leu Pro Leu Pro Ala Ala Ile Thr Ser Gln
-15 -10 -5 1
ctc gac aag gca tcc atc att cga ctt aca att agc tat ctg aaa atg      245
Leu Asp Lys Ala Ser Ile Ile Arg Leu Thr Ile Ser Tyr Leu Lys Met
5 10 15
agg gac ttt gct aac cag ggg gac cct ccg tgg aac ttg cga atg gaa      293
Arg Asp Phe Ala Asn Gln Gly Asp Pro Pro Trp Asn Leu Arg Met Glu
20 25 30
ggc cct cca cct aac aca tca gta aaa gtt ata ggt gca cag cga agg      341
Gly Pro Pro Pro Asn Thr Ser Val Lys Val Ile Gly Ala Gln Arg Arg
35 40 45
aga agc ccc agt gca cta gcc att gaa gta ttt gaa gca cat ttg gga      389
Arg Ser Pro Ser Ala Leu Ala Ile Glu Val Phe Glu Ala His Leu Gly
50 55 60 65

```

416

agc cac att ttg cag tcc tgg atg gct ttg tat ttg cac taaatcagga 438  
 Ser His Ile Leu Gln Ser Trp Met Ala Leu Tyr Leu His

70

75

aggaaaattt ttgtaca 455

&lt;210&gt; 783

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 85..168

&lt;221&gt; sig\_peptide

&lt;222&gt; 85..144

&lt;223&gt; Von Heijne matrix

score 5

seq ALLSVCSTDVTTA/HA

&lt;221&gt; misc\_feature

&lt;222&gt; 284

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 783

ccccctgtgg ccaagcctgg aacatcacat ctgtacgttg caatctgtgg atcagctacg 60

agactgagag aaaggaatga aagg atg gaa gaa tta caa gat cag gca ctg 111

Met Glu Glu Leu Gln Asp Gln Ala Leu

-20

-15

ctg tct gtc tgt tcc acg gat gta acc aca gca cac gcg tgg ctc acg 159

Leu Ser Val Cys Ser Thr Asp Val Thr Thr Ala His Ala Trp Leu Thr

-10

-5

1

5

gta cta gtg tgataaatgc ttgttacatg aaggcgtgaa cagggatgag 208

Val Leu Val

aagagacttc ctggagaaac aaaaggacta acaatcagga aggggaggtg atcggggcag 268

gagtaaagtg gacacntcag ctgggtcccct gggtcgtcca cccgatgtcc cccattctcc 328

ccacttggtc tccccacag gctctcggca aaggaccgtg ggaggcacct gtgacactgc 388

ccttttctctg tgcagctgtt tktcttcttc attcttttca ctctctgtta ctcttttttt 448

tttca 453

&lt;210&gt; 784

&lt;211&gt; 587

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 85..168

&lt;221&gt; sig\_peptide

&lt;222&gt; 85..144

&lt;223&gt; Von Heijne matrix

score 5

seq ALLSVCSTDVTTA/HA

&lt;400&gt; 784

ccccctgtgg ccaagcctgg aacatcacat ctgtacgttg caatctgtgg atcagctacg 60

agactgagag aaaggaatga aagg atg gaa gaa tta caa gat cag gca ctg 111

Met Glu Glu Leu Gln Asp Gln Ala Leu

-20

-15

ctg tct gtc tgt tcc acg gat gta acc aca gca cac gcg tgg ctc acg 159

Leu Ser Val Cys Ser Thr Asp Val Thr Thr Ala His Ala Trp Leu Thr

```

      -10          -5          1          5
gta cta gtg tgataaatgc ttgttacatg aaggcgtgaa cagggatgag      208
Val Leu Val
aagagacttc ctggagaaac aaaaggacta acaatcagga aggggaggtg atcggggcag      268
gagtaaagtg gacacctcag caaagccatt cgctgtgatc tctgattgtg cagtgtcatg      328
tcctgtcacc agagccccct cgtgtttgrk gttggccaat gccgccagca tgatctagca      388
ggccaaatcc taatctacca ttctctgaca ccagctggtc ccctgggtcg tccacccgat      448
gtccccatt ctccccactt ggctccccc acaggctctc ggcaaaggac cgtgggaggg      508
acctgtgaca ctgccctttt cctgtgcagc tgtttktctt cttcattctt ttcactctc      568
gttactcttt tttttttca      587

```

&lt;210&gt; 785

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 250..390

&lt;221&gt; sig\_peptide

&lt;222&gt; 250..384

&lt;223&gt; Von Heijne matrix

score 4.80000019073486

seq ICCAAAAAAGS/RI

&lt;221&gt; misc\_feature

&lt;222&gt; 218

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 785

```

agaggcctcg cgaggcaggg ctagaagctg tggcctcacc cttgaggccc gggcacttcc      60
cgtctcctcc cttgctcccc ttctcacc caatccctac agcctcccgc gcasctgagc      120
tctaggattg tgggttttcc atcctccgaa gacatcacct ttgctcatct cccaggagag      180
tctcgtccaa aggagggggg tgctttctgc ttcagcanga tccaccccaac cctgggatcc      240
gaggagagca atg gtg ggg cga gtg agg gtc tgc cgt aaa tat ccc ccg acc      291
      Met Val Gly Arg Val Arg Val Cys Arg Lys Tyr Pro Pro Thr
      -45          -40          -35
acc ctc tgg gaa ggt gct aga ggc cac agg caa att tca gtc tcc cca      339
Thr Leu Trp Glu Gly Ala Arg Gly His Arg Gln Ile Ser Val Ser Pro
      -30          -25          -20
tgg aat atc tgc tgt gct gct gct gct gct gct gct gct gct ggg tca agg      387
Trp Asn Ile Cys Cys Ala Ala Ala Ala Ala Ala Ala Ala Gly Ser Arg
      -15          -10          -5          1
ata tgagcgagcc tcttcyaaa acagccggga agggagagga atccaagagg      440
Ile
aggagcaggt gggaaagaca a      461

```

&lt;210&gt; 786

&lt;211&gt; 489

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 53..463

&lt;221&gt; sig\_peptide

&lt;222&gt; 53..208

&lt;223&gt; Von Heijne matrix

score 3.90000009536743

seq LCCGLSMFEVILT/RI

&lt;400&gt; 786

```

cattttctgc tctgcgactc cttttgcaga gggggagcgc ctggaggtcc gg atg aaa      58
                                     Met Lys
cgt ctg gaa gcc aag tat gcc ccg ctc cac ctg gtc cct ctg atc gag      106
Arg Leu Glu Ala Lys Tyr Ala Pro Leu His Leu Val Pro Leu Ile Glu
-50                               -45                               -40                               -35
cgg ctg ggg acc cct cag caa atc gcc att gct cgc gag ggt gac ctc      154
Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg Glu Gly Asp Leu
                               -30                               -25                               -20
ctg acc aag gag cgg ctg tgc tgt ggc ctg tcc atg ttc gag gtc atc      202
Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met Phe Glu Val Ile
                               -15                               -10                               -5
ctg acc cgc att cgg agc tac ctg cag gac ccc atc tgg cgg ggc cca      250
Leu Thr Arg Ile Arg Ser Tyr Leu Gln Asp Pro Ile Trp Arg Gly Pro
1                               5                               10
ccg ccc acc aat ggc gtc atg cac gtc gat gag tgt gtg gag ttc cac      298
Pro Pro Thr Asn Gly Val Met His Val Asp Glu Cys Val Glu Phe His
15                               20                               25                               30
cgg ctg tgg agc gcc atg cag ttc gtg tac tgc atc cct gtg gga acc      346
Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile Pro Val Gly Thr
                               35                               40                               45
aac gag ttc aca gct gag cag tgt ttc ggc gat ggc ttg aac tgg gct      394
Asn Glu Phe Thr Ala Glu Gln Cys Phe Gly Asp Gly Leu Asn Trp Ala
50                               55                               60
ggg tck ccr kca ttg tcc tgc tsg gcc agc agc gtc gct ttg acc tgt      442
Gly Ser Pro Xaa Leu Ser Cys Xaa Ala Ser Ser Val Ala Leu Thr Cys
65                               70                               75
tcg act tct gtt acc acc tgc taaaagtgc gaggcaggac gggaag      489
Ser Thr Ser Val Thr Thr Cys
80                               85

```

&lt;210&gt; 787

&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 52..354

&lt;221&gt; sig\_peptide

&lt;222&gt; 52..264

&lt;223&gt; Von Heijne matrix

score 3.70000004768372

seq LXMLSSLLTRGSG/NQ

&lt;400&gt; 787

```

ccctcacgcc cgccctcctt gccgcccagc cgggccaggc ctctggcgaa c atg gcg      57
                                     Met Ala
                                     -70
ctt gtc ccc tgc cag gtg ctg cgg atg gca atc ctg ctg tcy tac tgc      105
Leu Val Pro Cys Gln Val Leu Arg Met Ala Ile Leu Leu Ser Tyr Cys
-65                               -60                               -55
tct atc ctg tgt aac tac aag gcc atc gaa atg ccc tca cac cag acc      153
Ser Ile Leu Cys Asn Tyr Lys Ala Ile Glu Met Pro Ser His Gln Thr
-50                               -45                               -40
tac gga ggg agc tgg aaa ttc ctg acg ttc att gat ctg gtt atc cag      201
Tyr Gly Gly Ser Trp Lys Phe Leu Thr Phe Ile Asp Leu Val Ile Gln
-35                               -30                               -25
gct gtc ttt ttt ggc atc tgt gtg ctg amt gat ctt tcc agt ctt ctg      249
Ala Val Phe Phe Gly Ile Cys Val Leu Xaa Asp Leu Ser Ser Leu Leu
-20                               -15                               -10

```

```

act cga gga agt ggg aac cag gar caa gag agg cag ctc aag aag ctc      297
Thr Arg Gly Ser Gly Asn Gln Glu Gln Glu Arg Gln Leu Lys Lys Leu
-5              1              5              10
atc tct ctc cgg gac tgg atg tta gct gtg ttg gct ttc ctg ttg ggg      345
Ile Ser Leu Arg Asp Trp Met Leu Ala Val Leu Ala Phe Leu Leu Gly
              15              20              25
ttt ttg ttg tagcagtgtt ctgggtcatt tatgcctatg acagmgagat gat      397
Phe Leu Leu
              30

```

&lt;210&gt; 788

&lt;211&gt; 595

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 50..286

&lt;221&gt; sig\_peptide

&lt;222&gt; 50..256

&lt;223&gt; Von Heijne matrix

score 3.70000004768372

seq ALTGSQLLGDTIP/RP

&lt;400&gt; 788

```

ctctctgtcc cctccccct cctgtcctt atctttccct tctgtctcc atg gcg act      58
                                   Met Ala Thr
cac cac ctc ggc ttg cct gca tcc cag cct ctg cca ggg att ctg agc      106
His His Leu Gly Leu Pro Ala Ser Gln Pro Leu Pro Gly Ile Leu Ser
-65              -60              -55
cgg gct cca tcc ctc cct cct cgg agc cct gct acc cgc agc cgt gtc      154
Arg Ala Pro Ser Leu Pro Pro Arg Ser Pro Ala Thr Arg Ser Arg Val
-50              -45              -40              -35
tcc tcc ccc tgg ggt gag tcc agc agc agc ctc ctc ttt cct gac tgt      202
Ser Ser Pro Trp Gly Glu Ser Ser Ser Ser Leu Leu Phe Pro Asp Cys
              -30              -25              -20
cac att tct ttt cca gct ctg acc ggg agt cag ctc ctc ggg gat acc      250
His Ile Ser Phe Pro Ala Leu Thr Gly Ser Gln Leu Leu Gly Asp Thr
              -15              -10              -5
atc ccc cga cct cac ctt cca cct acc gca gcc tgc tagcctttcc      296
Ile Pro Arg Pro His Leu Pro Pro Thr Ala Ala Cys
              1              5              10
gggagaaaag gcacccctac ctctggttga aggtctcggg gcctccccct ctgcatccgg      356
accctctccc catccagcc tcccatgcc aggccgcct tgtcagtcac ttccttttgt      416
catcggttg gcaaacggga gagaaaacag agcttcatgg gaaacagcgg caacagtgg      476
cccatacc tttcccaag ttggagctag gcctggggcc ccagcccatg gygccccggg      536
agctccctac ctgctccats tgctggaga ggttgcgaga ccccatctsg ytgaatgt      595

```

&lt;210&gt; 789

&lt;211&gt; 359

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 21..344

&lt;221&gt; sig\_peptide

&lt;222&gt; 21..125

&lt;223&gt; Von Heijne matrix

score 3.70000004768372

seq SPLCHSLRKTSS/SQ

<400> 789  
aggtctgggg agtcggcgcc atg acc cca tcg agg ctt ccc tgg ttg ctt agc 53  
Met Thr Pro Ser Arg Leu Pro Trp Leu Leu Ser  
-35 -30 -25  
tgg gtc tcg gcc acg gcg tgg aga gcg gca aga tca ccc ctt ctg tgt 101  
Trp Val Ser Ala Thr Ala Trp Arg Ala Ala Arg Ser Pro Leu Leu Cys  
-20 -15 -10  
cat tct ctg agg aaa aca agt tct tct caa gga gga aag tct gaa ctt 149  
His Ser Leu Arg Lys Thr Ser Ser Ser Gln Gly Gly Lys Ser Glu Leu  
-5 1 5  
gtc aaa cag tcc ctt aag aag ccg aag tta cca gaa ggt cgt ttt gat 197  
Val Lys Gln Ser Leu Lys Lys Pro Lys Leu Pro Glu Gly Arg Phe Asp  
10 15 20  
gca cca gag gat tcc cat tta gag aaa gaa cca ctg gaa aaa ttt cca 245  
Ala Pro Glu Asp Ser His Leu Glu Lys Glu Pro Leu Glu Lys Phe Pro  
25 30 35 40  
gat gat gtk rat cca gtg acc aaa gaa aaa ggt gga ccc agg ggc cca 293  
Asp Asp Val Xaa Pro Val Thr Lys Glu Lys Gly Gly Pro Arg Gly Pro  
45 50 55  
gaa cct acc cga tat gga gat tgg gaa cga aaa gga cgc tgt att gat 341  
Glu Pro Thr Arg Tyr Gly Asp Trp Glu Arg Lys Gly Arg Cys Ile Asp  
60 65 70  
ttt taagtcgcat attct 359  
Phe

<210> 790  
<211> 836  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 118..360

<221> sig\_peptide  
<222> 118..270  
<223> Von Heijne matrix  
score 3.59999990463257  
seq ICFVCGVFFSILG/TG

<221> misc\_feature  
<222> 7,359  
<223> n=a, g, c or t

<400> 790  
aggaagnsgg cgggaccgga cttccggctg gtctgtgggg ttccgggttc ggggtttcct 60  
gggtgggcgtc aggggcaggc aacagagtgg cgcccgctac ggccctggaa cggggccc 117  
atg gag aag ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag 165  
Met Glu Lys Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln  
-50 -45 -40  
ggc ctg act gcg cag gtc ctg gat gcc tca tcc ctt agt ttc aac acc 213  
Gly Leu Thr Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr  
-35 -30 -25 -20  
aga ttg aaa tgg ttt gcc atc tgc ttc gta tgt ggc gtt ttc ttt tct 261  
Arg Leu Lys Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser  
-15 -10 -5  
att ctt gga act gga ttg ctg tgg ctt ccg ggc ggc ata aag ctt ttt 309  
Ile Leu Gly Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe  
1 5 10  
gca gtg ttt tat acc ctc ggc aat ctt gct gcg tta sca gta cat gct 357  
Ala Val Phe Tyr Thr Leu Gly Asn Leu Ala Ala Leu Xaa Val His Ala

15	20	25	
tnw taatgggacc tgtgaagcaa ctgaagaaaa tgtttgaagc aacaagattg			410
Xaa			
30			
cttgcaacaa ttgttatgct tttgtgtttc gtatttaccc tgtgtgctgc tctttggtgg			470
cataagaagg gactggctgt gttattctgc atattgcagt tcttgtcaat gacctggtat			530
agcctgtcrt acatcccata tgcaagggat gcagttatta aatgctgttc ttctctccta			590
agttgaaaat cagaaacttg tggaaaagag cacttgaatg ttggtactct atgtttggtg			650
aagtttgctt ttccccataa aacactccag gaacaactga cgtgacagtt gaagaccgtt			710
ttgtactaag tctcattttg tatactggta aaaactacat gcttgattaa accattaaat			770
gcttgtaact ttaaattcat tatgtgtcat taatatactt ttccaaagat aagattttta			830
atcact			836

&lt;210&gt; 791

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 6..329

&lt;221&gt; sig\_peptide

&lt;222&gt; 6..284

&lt;223&gt; Von Heijne matrix

score 3.59999990463257

seq LLRLALRSPDVWL/GQ

&lt;221&gt; misc\_feature

&lt;222&gt; 496,536

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 791

tgtgt atg tgt gaa aat cag gaa gag cca gcg ggg agt gtg tgt tgc cat	50
Met Cys Glu Asn Gln Glu Glu Pro Ala Gly Ser Val Cys Cys His	
-90 -85 -80	
cgc gtc tcc gcc tgc agg ggc ggg acc cca gga gga ggg aga gga cag	98
Arg Val Ser Ala Cys Arg Gly Gly Thr Pro Gly Gly Arg Gly Gln	
-75 -70 -65	
agc cac tgc aga gga cca gac tgg gaa aac aac gat atg gca gga gcc	146
Ser His Cys Arg Gly Pro Asp Trp Glu Asn Asn Asp Met Ala Gly Ala	
-60 -55 -50	
agt ctt ggg gcc cgc ttc tac cgg cag atc aaa aga cat ccg ggg atc	194
Ser Leu Gly Ala Arg Phe Tyr Arg Gln Ile Lys Arg His Pro Gly Ile	
-45 -40 -35	
atc ccg atg atc ggc tta atc tgc ctg ggc atg ggc agc gct gcg ctt	242
Ile Pro Met Ile Gly Leu Ile Cys Leu Gly Met Gly Ser Ala Ala Leu	
-30 -25 -20 -15	
tac ttg ctg cga ctc gcc ctt cgc agc ccc gac gtc tgg ctg gga cag	290
Tyr Leu Leu Arg Leu Ala Leu Arg Ser Pro Asp Val Trp Leu Gly Gln	
-10 -5 1	
aaa gaa caa ccc gga gcc ctg gaa ccg cct gag ccc caa tgaccaatac	339
Lys Glu Gln Pro Gly Ala Leu Glu Pro Pro Glu Pro Gln	
5 10 15	
aagttccttg cagtttccac tgactataag aagctgaaga aggaccggcc agactttctaa	399
gccaggctgg gctgccagt ccatgcaagc cacagccagc cagcccatcc actttcttcca	459
ctcctccccg caggccccaa ggcatactc cggccancct gtcccgctac tgcttacaca	519
ggccgggttc caccsanagg ggargctgct cc	551

&lt;210&gt; 792

&lt;211&gt; 437

&lt;212&gt; DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 31..432

<221> sig\_peptide

<222> 31..78

<223> Von Heijne matrix

score 3.5

seq AGLALLXRRVSSA/LK

<400> 792

```

ggaaacgcgt tttgccagtt atgcgaaaac atg gct gcg gcc ggt ttg gcc ctt      54
                               Met Ala Ala Ala Gly Leu Ala Leu
                               -15                               -10
ctt kgt agg aga gtt tca tcc gcc ctg aaa tct tcc cga tcg tta ata      102
Leu Xaa Arg Arg Val Ser Ser Ala Leu Lys Ser Ser Arg Ser Leu Ile
                               -5                               5
act cct cag gtc cct gcc tgc aca ggg ttt ttt ctt agt ttg ttg ctt      150
Thr Pro Gln Val Pro Ala Cys Thr Gly Phe Phe Leu Ser Leu Leu Pro
                               10                               15                               20
aag agt aca cca aat gtg aca tcc ttt cac caa tat aga tta ctt cat      198
Lys Ser Thr Pro Asn Val Thr Ser Phe His Gln Tyr Arg Leu Leu His
25                               30                               35                               40
acc aca ttg tca agg aaa gga cta gaa gaa ttt ttt gat gac cca aaa      246
Thr Thr Leu Ser Arg Lys Gly Leu Glu Glu Phe Phe Asp Asp Pro Lys
                               45                               50                               55
aac tgg ggg caa gaa aaa gta aaa tct gga gca gca tgg acc tgt cag      294
Asn Trp Gly Gln Glu Lys Val Lys Ser Gly Ala Ala Trp Thr Cys Gln
60                               65                               70
caa cta agg aac aaa agt aat gaa gat tta cac aaa ctt tgg tat gtc      342
Gln Leu Arg Asn Lys Ser Asn Glu Asp Leu His Lys Leu Trp Tyr Val
75                               80                               85
tta ctg aaa gaa aga aac atg ctt cta acc cta gag cag gag gcc aag      390
Leu Leu Lys Glu Arg Asn Met Leu Leu Thr Leu Glu Gln Glu Ala Lys
90                               95                               100
cgg car aga ttg cca atg cca agt cca gag cgg tta gat agg tagta      437
Arg Gln Arg Leu Pro Met Pro Ser Pro Glu Arg Leu Asp Arg
105                               110                               115

```

<210> 793

<211> 350

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 130..321

<400> 793

```

ggaagtggac gaatttgaat cctgtgggcc gttgaatgtg gctgctcgcg gtcggcgtgc      60
cccgacgtac agcgggcccgg gaaaagtggc actgaggctc tggaacttct gccagctct
ccttgtaaa atg aat gaa agt aaa cct ggt gac tca cag aac ctt gct tgt      120
                               Met Asn Glu Ser Lys Pro Gly Asp Ser Gln Asn Leu Ala Cys
                               1                               5                               10
gtt ttc tgt cga aaa cat gat gac tgt cct aat aaa tac gga gaa aag      219
Val Phe Cys Arg Lys His Asp Asp Cys Pro Asn Lys Tyr Gly Glu Lys
15                               20                               25                               30
aaa act aag gag aaa tgg aat ctc act gta cat tac tac tgt ttg ttg      267
Lys Thr Lys Glu Lys Trp Asn Leu Thr Val His Tyr Tyr Cys Leu Leu
35                               40                               45
atg tca agt gga att tgg cag aga ggc aaa gaa gaa gaa gga gtt atg      315

```

Met Ser Ser Gly Ile Trp Gln Arg Gly Lys Glu Glu Gly Val Met  
 50 55 60  
 gtt ttc taatagaaga tatcaggaag gaagtgaat 350  
 Val Phe

<210> 794  
 <211> 431  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 37..273

<400> 794  
 ggcgatgtgc agaagggaaa cgtgaagaag gtgaag atg gcg gtg gcc agg gcc 54  
 Met Ala Val Ala Arg Ala  
 1 5  
 ggg gtc ttg gga gtc cag tgg ctg caa agg gca tcc cgg aac gtg atg 102  
 Gly Val Leu Gly Val Gln Trp Leu Gln Arg Ala Ser Arg Asn Val Met  
 10 15 20  
 ccg ctg ggc gca cgg aca gcc tcc cac atg acc aag gac atg ttc ccg 150  
 Pro Leu Gly Ala Arg Thr Ala Ser His Met Thr Lys Asp Met Phe Pro  
 25 30 35  
 ggg ccc tat cct agg acc cca gaa cgg gcc gcc gcc gcc aag aag 198  
 Gly Pro Tyr Pro Arg Thr Pro Glu Glu Arg Ala Ala Ala Ala Lys Lys  
 40 45 50  
 tat aat atg cgt gtg gaa gac tac gaa cct tac ccg gat gat ggc atg 246  
 Tyr Asn Met Arg Val Glu Asp Tyr Glu Pro Tyr Pro Asp Asp Gly Met  
 55 60 65 70  
 ggg tat ggc gac ctt ttc ctg twt gtc tgatttttat tatttaaaaa 293  
 Gly Tyr Gly Asp Leu Phe Leu Xaa Val  
 75  
 aatggaaaaa caaaagtgc tttttcatte aataaatgtt ccatccttat ttagttttgt 353  
 tgaatcaagt cactttttac aagttttgtt tgatatgtat tttcatgctg ttaacacatt 413  
 tttctctgtc attatatt 431

<210> 795  
 <211> 516  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 140..337

<400> 795  
 agagtgcatt ccggaacccg gggcgcgggc cactgcgcag gcggccggac tccgctcagt 60  
 ttccggtgcg gcgaacacca aagtcgggga acttaagcat ttccggtttc tagggttgtt 120  
 acgaagctgc aggagcgag atg gag gtg gac gca ccg ggt gtt gat ggt cga 172  
 Met Glu Val Asp Ala Pro Gly Val Asp Gly Arg  
 1 5 10  
 gat ggt ctc cgg gag cgg cga ggc ttt agc gag gga ggg agg cag aac 220  
 Asp Gly Leu Arg Glu Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln Asn  
 15 20 25  
 ttc gat gtg agg cct cag tct ggg gca aat ggg ctt ccc aaa cac tcc 268  
 Phe Asp Val Arg Pro Gln Ser Gly Ala Asn Gly Leu Pro Lys His Ser  
 30 35 40  
 tac tgg ttg gac ctc tgg ctt ttc atc ctt ttc gat gtg gtg gtg ttt 316  
 Tyr Trp Leu Asp Leu Trp Leu Phe Ile Leu Phe Asp Val Val Val Phe  
 45 50 55  
 ctc ttt gtg tat ttt ttg cca tgacttggtc gctgatatct aaattaagaa 367  
 Leu Phe Val Tyr Phe Leu Pro



&lt;221&gt; CDS

&lt;222&gt; 79..372

&lt;221&gt; misc\_feature

&lt;222&gt; 364..365

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 798

```

atggggacgg ggctgttccc ggggaggctg tgatgggttg acaggtgctg gacagtggga      60
gctgctctcg gcacaagc atg tac ggc aaa ggc aag agt aac agc agc gcc      111
                Met Tyr Gly Lys Lys Gly Lys Ser Asn Ser Ser Ala
                1                5                10
gtc ccg tcc gac agc cag gcc cgg gag aag tta gca ctc tac gta tat      159
Val Pro Ser Asp Ser Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr
                15                20                25
gaa tat ctg ctc cat gta gga gct cag aaa tca gct caa aca ttt tta      207
Glu Tyr Leu Leu His Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu
                30                35                40
tca gag ata aga tgg gaa aaa aac atc aca ttg ggg gaa cca cca gga      255
Ser Glu Ile Arg Trp Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly
                45                50                55
ttc tta cat tct tgg tgg tgt gta ttt tgg gat ctc tac tgt gca gct      303
Phe Leu His Ser Trp Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala
                60                65                70                75
cca gag aga cgt gaa aca tgt gaa cac tca agt gaa gca aaa gcc ttc      351
Pro Glu Arg Arg Glu Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe
                80                85                90
cat gat tac gta nnt aac ata taattttaca aagttacact gtcagttttc      402
His Asp Tyr Val Xaa Asn Ile
                95
tgtttaacca c      413

```

&lt;210&gt; 799

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 46..195

&lt;400&gt; 799

```

actgcagaga accagacaat accaggttgc ttataaaagg atgcc atg tgc ttg ctg      57
                Met Cys Leu Leu
                1
gag gtc cca ggt gca acc aaa ttg ctt gca gct agg agg acc ttg aag      105
Glu Val Pro Gly Ala Thr Lys Leu Leu Ala Ala Arg Arg Thr Leu Lys
                5                10                15                20
aga aat ggg atc agc ccg cca aac caa gaa ggg tta gca ctt ttg cta      153
Arg Asn Gly Ile Ser Pro Pro Asn Gln Glu Gly Leu Ala Leu Leu Leu
                25                30                35
gga gag ctg acc acg cac aaa cag atg aga acc aaa acc gag      195
Gly Glu Leu Thr Thr His Lys Gln Met Arg Thr Lys Thr Glu
                40                45                50
tgaagaggat tgaagatgaa cccacatttt aaaagttctt gtctgctgga ggtggcatta      255
cctgtgacct cgcttcactt ctccatacat ggctgttata gcagaaaatc cagctttctg      315
aagcatattt caccacatat gatgagactt atgtgatgtg agacctgaga aaactatgat      375
agamagaagc aactcaagtt gcaagg      401

```

&lt;210&gt; 800

&lt;211&gt; 465

&lt;212&gt; DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 96..191

<400> 800

```

agagccgccc aagggatggc gatggcgtagc ttggcttgga gactggcgcg gcgttcgtgt      60
ccgaggtcac tagtttcccg gtagttcagc tgcac atg aat aga aca gca atg      113
                               1           5
aga gcc agt cag aag gac ttt gaa aat tca atr aat caa gtg aaa ctc      161
Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Xaa Asn Gln Val Lys Leu
                               10          15          20
ttg aaa aag gat cca gga aac gar tgm agc taaaactcta cgcgctatat      211
Leu Lys Lys Asp Pro Gly Asn Glu Xaa Ser
                               25          30
aagcaggcca ctgaaggacc ttgtaacatg cccaaccag gtgtatttga cttgatcaac      271
aaggccaaat gggacgcatg gaatgccctt ggcagcctgc ccaaggaagc tgccaggcag      331
aactatgtgg atttggtgtc cagtttgagt ccttcattgg aatcctctag tcagggtggag      391
cctggaacag acaggaaatc aactgggttt gaaactctgg tggtagacct cgaagatggc      451
atcacaaaga tcat                                         465

```

<210> 801

<211> 629

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 144..317

<221> misc\_feature

<222> 583..584

<223> n=a, g, c or t

<400> 801

```

agtccatccc ctgtgcccgg gaaccgcggc tctgcccgc aaagggcacg cggactacaa      60
ctcccagagt ccactgcagc ggccaagggc tactgttccc agcgaggccc gssggcgggc      120
accgcgaagg gaggagtggc aac atg gcg tct tgc gga gct ggt gac cct ctg      173
                               1           5          10
gat tct aag cgt gga gag gcc ccg ttc gct cag cgt atc gac ccg act      221
Asp Ser Lys Arg Gly Glu Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr
                               15          20          25
cgg gag aag ctg aca ccc gag caa ctg cat tcc atg cgg cag gcg gag      269
Arg Glu Lys Leu Thr Pro Glu Gln Leu His Ser Met Arg Gln Ala Glu
                               30          35          40
ttg ccc agt ggc aga agg tcc tac cac ggc ggc gaa ccc gga aca tcg      317
Leu Pro Ser Gly Arg Arg Ser Tyr His Gly Gly Glu Pro Gly Thr Ser
                               45          50          55
tgaccggcct aggcacgagg gccctgggtg ttgctattta tggttacacc ttctactcga      377
tttcccagga gcgtttccta gatgagctag aagacgaggc caaagctgcc cgagcccagag      437
ctctggcaag ggcgtcaggg tcctaactctg gatgggtatt gatcatgtcc aacctgctgg      497
agccccttca catggtggat gatgcccacat gaccctgtga gaaattgaat cctgctcaca      557
acattgttgg ccttcttact aacctnngac ctgattgagc ccaagaaacc agggasttac      617
gcatttggcc aa                                         629

```

<210> 802

<211> 477

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 169..462

&lt;400&gt; 802

```

atataagtgg aggtcatttc cctgcccc accccagct tcctcagatc tgggcagagg      60
aaccaaaggg aaaagccacc ttcccaggca cagccataac atccacctca ctcaactgct    120
tgtcaagttc accaccaaca cagagggggc tcagataatc aagaaaca atg tcg agt      177
                                     Met Ser Ser
                                     1
gat gat aaa agt aaa tca aat gac ccc aag act gag ccc aag aac tgc      225
Asp Asp Lys Ser Lys Ser Asn Asp Pro Lys Thr Glu Pro Lys Asn Cys
   5              10              15
gat ccc aag tgt gaa caa aag tgt gag tcc aaa tgc cag ccc agc tgt      273
Asp Pro Lys Cys Glu Gln Lys Cys Glu Ser Lys Cys Gln Pro Ser Cys
  20              25              30              35
tta aag aag ctg ctg caa cgc tgt ttc gaa aag tgc cca tgg gaa aag      321
Leu Lys Lys Leu Leu Gln Arg Cys Phe Glu Lys Cys Pro Trp Glu Lys
              40              45              50
tgt cca gca cca ccc aag tgc ctg ccc tgc ccc tcg cag tct cct tca      369
Cys Pro Ala Pro Pro Lys Cys Leu Pro Cys Pro Ser Gln Ser Pro Ser
              55              60              65
tcc tgc cct ccc cag ccc tgc acc aag ccc tgt cct cct aaa tgc cct      417
Ser Cys Pro Pro Gln Pro Cys Thr Lys Pro Cys Pro Pro Lys Cys Pro
              70              75              80
tca tcc tgc cca cat gct tgc cca mct ccc tgc cct ccc cca gag      462
Ser Ser Cys Pro His Ala Cys Pro Xaa Pro Cys Pro Pro Pro Glu
              85              90              95
tgaggcactg tgggc      477

```

&lt;210&gt; 803

&lt;211&gt; 586

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 179..307

&lt;400&gt; 803

```

cggtagtsag aacccttccg gtgggctagg tactgagcgc gcgaggtgag gagttgtgca      60
gggtwtgggg aaaggaaggc tggcttggcg agagggcagg tttgcgggct ttcgcccct      120
tttccaaaga ccaacaaaga gtccttcccc aactcccaac tcaaccctt ttggaact      178
atg tgt ggt ggt tgg gac cct gtg gcg cat cct tgt cgc tcg tgt cct      226
Met Cys Gly Gly Trp Asp Pro Val Ala His Pro Cys Arg Ser Cys Pro
  1              5              10              15
tct cat gcc cgg cga cgc gtc ttt gtg gta acg ccc tgc tgc cat ctc      274
Ser His Ala Arg Arg Arg Val Phe Val Val Thr Pro Cys Cys His Leu
              20              25              30
ttt tct tct cta tgc gag gat ttg gac tgg cag tgagaataag agacaacgat      327
Phe Ser Ser Leu Cys Glu Asp Leu Asp Trp Gln
              35              40
tcacgtctac tttctaggat gacttccatg tgctccatct cgcgcgctcc tgagcatgtt      387
gaatttccaa atcctaaata agccgcgcgg tgtagtttgt attatgttgc gtttctcttt      447
ctgcttttcc tcgccctttc tccatcatcc tttaggctct acagagtga ggtttaaatc      507
caaggtcatg gcaaaacatc tgaagttcat cgccaggact gtgatgttac aggaagggaa      567
cgtggaaagc gcatacagg      586

```

&lt;210&gt; 804

&lt;211&gt; 559

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 78..548

&lt;400&gt; 804

```

acgtcattca cccgcgccac ccggaagccg cggttcctac cwaccgttct tattgctggc      60
ggcctgagga gcccatc atg gcg acg ccc cct aag cgg cgg gcg gtg gag      110
      Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu
      1          5          10
gcc acg ggg gag aaa gtg ctg cgc tac gag acc ttc atc agt gac gtg      158
Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val
      15          20          25
ctg cag cgg gac ttg cga aag gtg ctg gac cat cga gac aag gta tat      206
Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr
      30          35          40
gag cag ctg gcc aaa tac ctt caa ctg aga aat gtc att gag cga ctc      254
Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu
      45          50          55
cag gaa gct aag cac tcg gag tta tat atg cag gtg gat ttg ggc tgt      302
Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys
      60          65          70          75
aac ttc ttc gtt gac aca gtg gtc cca gat act tca cgc atc tat gtg      350
Asn Phe Phe Val Asp Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val
      80          85          90
gcc ctg gga tat ggt ttt ttc ctg gag ttg aca ctg gca gaa gct ctc      398
Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu
      95          100          105
aag ttc att gat cgt aag agc tct ctc ctc aca gag ctc agc aac agc      446
Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser
      110          115          120
ctc acc aag gac tcc atg aat atc aaa gcc cat atc cac atg ttg cta      494
Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His Met Leu Leu
      125          130          135
gag ggg ctt aga gaa cta caa ggc ctg cag aat ttc cca gag aag cct      542
Glu Gly Leu Arg Glu Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro
      140          145          150          155
cac cat tgacttcttc c
His His

```

&lt;210&gt; 805

&lt;211&gt; 570

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 122..478

&lt;400&gt; 805

```

aaacacatcc aagcttaaga cggtagaggtc agcttcacat tctcaggaac tctccttctt      60
tgggtctggc tgaagttgag gatctcttac tctctaggcc acggaattaa cccgagcagg      120
c atg gag gcc tct gct ctc acc tca tca gca gtg acc agt gtg gcc aaa      169
      Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys
      1          5          10          15
gtg gtc agg gtg gcc tct ggc tct gcc gta gtt ttg ccc ctg gcc agg      217
Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg
      20          25          30
att gct aca gtt gtg att gga gga gtt gtg gct gtg ccc atg gtg ctc      265
Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Val Pro Met Val Leu
      35          40          45
agt gcc atg ggc ttc act gcg gcg gga atc gcc tcg tcc tcc ata gca      313
Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser Ser Ile Ala

```

429

```

      50              55              60
gcc aag atg atg tcc gcg gcg gcc att gcc aat ggg ggt gga gtt gcc      361
Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ala
65              70              75              80
tcg ggc agc ctt gtg gct act ctg cag tca ctg gga gca act gga ctc      409
Ser Gly Ser Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Thr Gly Leu
      85              90              95
tcc gga ttg acc aag tkc atc ctg ggc tcc att ggg tct gcc att gcg      457
Ser Gly Leu Thr Lys Xaa Ile Leu Gly Ser Ile Gly Ser Ala Ile Ala
      100              105              110
gct gtc att gcg agg ttc tac tagctccctg cccctcgccc tgcagagaag      508
Ala Val Ile Ala Arg Phe Tyr
      115
agaaccatgc caggggagaa ggcacccagc catcctgacc cagcgaggrg caactatccc      568
aa                                                                570

```

&lt;210&gt; 806

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 90..332

&lt;400&gt; 806

```

aaacacatcc aagcttaaga cggtagagtc agcttcacat tctcaggaac tctccttctt      60
tgggggctca ccgtgtgggg gagcaaatc atg tat atc cag tgc tgt gag tgg      113
                               Met Tyr Ile Gln Cys Cys Glu Trp
                               1              5
ctc cag tca tgg agg agc aag gat gag ttc tgc ctg gaa gaa tct ggg      161
Leu Gln Ser Trp Arg Ser Lys Asp Glu Phe Cys Leu Glu Glu Ser Gly
      10              15              20
aag gct tcc tgg agg agg gaa caa tgg cat gga cct tgd dga gtc aga      209
Lys Ala Ser Trp Arg Arg Glu Gln Trp His Gly Pro Xaa Xaa Val Arg
      25              30              35              40
agc ttt caa ttc att cca ttc aag cat tgc tct cat gtg gca ttc aag      257
Ser Phe Gln Phe Ile Pro Phe Lys His Cys Ser His Val Ala Phe Lys
      45              50              55
cat tct ata gtg ctt gcc gtg act cag gcg cac agt gca aaa gga agc      305
His Ser Ile Val Leu Ala Val Thr Gln Ala His Ser Ala Lys Gly Ser
      60              65              70
aca tct ttc tct gcc atg agg act tat tagtgtctga agagcttttt      352
Thr Ser Phe Ser Ala Met Arg Thr Tyr
      75              80
ctggactata ggagaaagtc atggtctccc tc      384

```

&lt;210&gt; 807

&lt;211&gt; 371

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 152..346

&lt;221&gt; misc\_feature

&lt;222&gt; 302..303

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 807

```

aagggttactt gactggggagt tctcagacct ccagtttcag ccctgccctc agcctccaat      60

```

430

```

ccgtaagaga caccagcccc cagcaattgg attgggcagc ccgtcttgac acrcastgt      120
gcygagtggc ttgaaggacg tgtttcaaca g atg gtt ggg gtt agt gtg tgt      172
                               1       5
                               Met Val Gly Val Ser Val Cys

cat cac att cga gtg ggg att aag aga agg aag gct gcc ttg ctg gag      220
His His Ile Arg Val Gly Ile Lys Arg Arg Lys Ala Ala Leu Leu Glu
      10       15       20
ctg tgt ggt ctt ctc caa gtg aga gtc gca ggc aat aga act act ttg      268
Leu Cys Gly Leu Leu Gln Val Arg Val Ala Gly Asn Arg Thr Thr Leu
      25       30       35
ctt ttg gag gaa aag mgg aat tca ttt tca gca nnc acr aga aaa gca      316
Leu Leu Glu Glu Lys Arg Asn Ser Phe Ser Ala Xaa Thr Arg Lys Ala
      40       45       50       55
gtt ttt ttt tca ggg gat ctt cac ttc tct tgaacaagga actcactcag      366
Val Phe Phe Ser Gly Asp Leu His Phe Ser
      60       65

agact                                                                    371

```

<210> 808  
 <211> 435  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 98..430

```

<400> 808
cgacaggagc cctcaagctg atctgggtcgg gaccggatac attattaacc ccagtgcagt      60
agggtcccca ggggcaacct gccccacagc gcccaag atg cct agc aga act gcc      115
                               1       5
                               Met Pro Ser Arg Thr Ala

cgc tat gcc cgc tac agc cca cgg cag cgg cgg cgg atg ctg gct      163
Arg Tyr Ala Arg Tyr Ser Pro Arg Gln Arg Arg Arg Met Leu Ala
      10       15       20
gat cgc agc gtg cgt ttc cct aat gat gtc ctg ttc ttg gac cac atc      211
Asp Arg Ser Val Arg Phe Pro Asn Asp Val Leu Phe Leu Asp His Ile
      25       30       35
cgg cag ggt gac ctg gag cag gtg ggg cgc ttc atc cgg act cgg aaa      259
Arg Gln Gly Asp Leu Glu Val Gly Arg Phe Ile Arg Thr Arg Lys
      40       45       50
gtc tcc ctg gcc acc atc cac ccc tca ggc ctg gcc gcc ttg cat gaa      307
Val Ser Leu Ala Thr Ile His Pro Ser Gly Leu Ala Ala Leu His Glu
      55       60       65       70
gcc gtg ctc tct gga aac ctg gaa tgc gtg aag ctg ctg gtc aaa tac      355
Ala Val Leu Ser Gly Asn Leu Glu Cys Val Lys Leu Leu Val Lys Tyr
      75       80       85
ggg gct gac att cac cag cga gat gag gcg ggc tgg aca ccc ctg cac      403
Gly Ala Asp Ile His Gln Arg Asp Glu Ala Gly Trp Thr Pro Leu His
      90       95       100
att gcc tgc agc gat ggg tac ctg aca tagcc      435
Ile Ala Cys Ser Asp Gly Tyr Leu Thr
      105       110

```

<210> 809  
 <211> 394  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 149..247

```
<221> misc_feature
<222> 375
<223> n=a, q, c or t
```

```

<400> 809
attcatttgg tgggcacttc ctgggtgcct gctctgggtc aggcctgtgg ggkggaccac      60
tgagggcagg aaacctggcc tgccctcca ggaagcgaag tcaacactgg cacctgcaga      120
tgaagtggca gagcagcccc cagctttg atg gca tgg ggt ggt tgg ggg gca      172
                               Met Ala Trp Gly Gly Trp Gly Ala
                               1                               5
cat tct gca tgc tca gaa gag aga gca act cgc cct gtg gaa gga gca      220
His Ser Ala Cys Ser Glu Glu Arg Ala Thr Arg Pro Val Glu Gly Ala
      10                               15                               20
tac agt ggg aga tgg gga cag gcc cag tgacgagcac catccggaag      267
Tyr Ser Gly Arg Trp Gly Gln Ala Gln
25                               30
tgagggtgta tgggtacgtg gacaacctcg cagagcagtg gacctgctgc tgcagcacgc      327
cgacaagtga tggcctcctg ggagagcccc gctcctccac ccttgccnct cctccacctg      387
ccccctg                                           394

```

```
<210> 810
<211> 835
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 198..536
```

```
<221> misc_feature
<222> 511,749..750,790..791,807
<223> n=a, q, c or t
```

<400>	810
agacttgggt tgtgggacac acttggtttc agggaagggg aaagaggtca ccaaggggcag	60
agggtgtccag gcccgagcca ggggcccccac tggttgggatg ctggctgcag tggggcgccc	120
caagccccagg tccccctctgt cttctctttc gactttgcag ctgtacttgt tttgtctctc	180
taccgcgcagg agctgac atg gac ccaaat cct cgGCC GCC CTG gag CGC	230
Met Asp Pro Asn Pro Arg Ala Ala Leu Glu Arg	
1 5 10	
cag cag CTC CGC CTT CGG GAG CGG caa aaa TTC TTC gag gac att TTA	278
Gln Gln Leu Arg Leu Arg Glu Arg Gln Lys Phe Phe Glu Asp Ile Leu	
15 20 25	
CAG CCA GAG ACA GAG TTT GTC TTT CCT CTG TCC CAT CTG CAT CTC GAG	326
Gln Pro Glu Thr Glu Phe Val Phe Pro Leu Ser His Leu His Leu Glu	
30 35 40	
TCG CAG AGA CCC CCC ATA GGT AGT ATC TCA TCC ATG GAA GTG AAT GTG	374
Ser Gln Arg Pro Pro Ile Gly Ser Ile Ser Ser Met Glu Val Asn Val	
45 50 55	
GAC ACA CTG GAG CAAGTA GAAC TT ATT GAC CTT GGG GAC CCG GAT GCA	422
Asp Thr Leu Glu Gln Val Glu Leu Ile Asp Leu Gly Asp Pro Asp Ala	
60 65 70 75	
GCA GAT GTG TTC TTG CCT TGC GAA GAT CCT CCA CCA ACC CCC CAG TCG	470
Ala Asp Val Phe Leu Pro Cys Glu Asp Pro Pro Thr Pro Gln Ser	
80 85 90	
TCT GGG GTG GAC AAC CAT TTG GAG GAG CTG AGC CTG CCG GNT GCC TAC	518
Ser Gly Val Asp Asn His Leu Glu Glu Leu Ser Leu Pro Xaa Ala Tyr	
95 100 105	
ATC AGA CAG GAC CAC ATC TAGGACTCC TCCTCCTCCT CTCCTCGACTC	566
Ile Arg Gln Asp His Ile	
110	

432

```

ctccaccaac ctgcataggc caaatccaag tgatgatgga gcagatacgc ccttggcaca 626
gtcggatgaa gaggaggaaa ggggtgatgg aggggcagag cctggagcct gcagctagca 686
gtgggcccct gcctacagac tgaccacgct ggctattctc cacatgagac cackagccca 746
mknnagagcc tgcggggaga agaccagact ctttacttgc agtnnracca gaggtgggaa 806
ngatggtggg attgtgtacc tttctaaga 835

```

<210> 811  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 21..194

<221> misc\_feature  
 <222> 373  
 <223> n=a, g, c or t

```

<400> 811
aagtcacatg agccaccaa atg gtg gtg ttc ggg tat gag gct ggg act aag 53
                Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys
                1          5          10
cca agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag 101
Pro Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys
                15          20          25
gac aca aaa tat ata tca aat ggc gac att tgg aac aac agc tgg ttt 149
Asp Thr Lys Tyr Ile Ser Asn Gly Asp Ile Trp Asn Asn Ser Trp Phe
                30          35          40
ctc tgg aat att ctc aaa ctt cct gtt cag acg ctg ctt caa ggt 194
Leu Trp Asn Ile Leu Lys Leu Pro Val Gln Thr Leu Leu Gln Gly
                45          50          55
taaacatgat gctttgaaga catatgcatac attggctaca cttccatttt tgtctactgt 254
tggtactgac aagctttttg taattgatgc tttgtattca gataatataa gcaaggaaaa 314
ctgtgttttc agaagctcac tgattggcat agtttgtggw gttttctatc ccagttctnt 374
ggcttttact a 385

```

<210> 812  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14..-1

```

<400> 812
Met Leu Leu Pro Leu Leu Leu Leu Leu Pro Met Cys Trp Ala Val Glu
                -10          -5          1
Val Lys Arg Pro Arg Gly Val Ser Leu Thr Asn His His Phe Tyr Asp
                5          10          15
Glu Ser Lys Pro Phe Thr Cys Leu Asp Gly Ser Ala Thr Ile Pro Phe
                20          25          30
Asp Gln Val Asn Asp Asp Tyr Cys Asp Cys Lys Asp Gly Ser Asp Glu
35          40          45          50
Pro Gly Thr Ala Ala Cys Pro Asn Gly Ser Phe His Cys Thr Asn Thr
                55          60          65
Gly Tyr Lys Pro Leu Tyr Ile Pro Ser Asn
                70          75

```

<210> 813  
 <211> 80

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16..-1

&lt;400&gt; 813

```

Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala
  -15          -10          -5
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
 1          5          10          15
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
          20          25          30
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Val Ser Pro Ser Pro
          35          40          45
Leu Ser Pro Ala Leu Leu Thr Pro Leu Leu Lys Pro Ala Pro Thr Gly
 50          55          60

```

&lt;210&gt; 814

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -22..-1

&lt;400&gt; 814

```

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
  -20          -15          -10
Leu Arg Gly Ala Arg Cys Gly Val Gln Met Thr Gln Phe Pro Leu Ser
  -5          1          5          10
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser
          15          20          25
His Ile Ile Asn Ile Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
          30          35          40
Ala Pro Trp
      45

```

&lt;210&gt; 815

&lt;211&gt; 50

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -23..-1

&lt;400&gt; 815

```

Met Ala Ala Ala Leu Trp Gly Phe Phe Pro Val Leu Leu Leu Leu
  -20          -15          -10
Leu Ser Gly Asp Val Gln Ser Ser Glu Val Pro Gly Ala Ala Ala Glu
  -5          1          5
Gly Ser Gly Gly Ser Gly Val Gly Ile Gly Xaa Arg Phe Lys Ile Glu
10          15          20          25
Gly Leu

```

&lt;210&gt; 816

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -22...-1

&lt;400&gt; 816

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 -20 -15 -10  
 Leu Xaa Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Val Leu  
 -5 1 5 10  
 Pro Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln  
 15 20 25  
 Ser Ile Gly Ser Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly His Ala  
 30 35 40  
 Pro Arg Leu Leu Ile Tyr Ala Ala Thr Thr Leu Ser Arg Gly Gly Pro  
 45 50 55  
 Ala Arg Phe Ser  
 60

&lt;210&gt; 817

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -32...-1

&lt;400&gt; 817

Met Ala Ala Ser Arg Trp Ala Arg Lys Ala Val Val Leu Leu Cys Ala  
 -30 -25 -20  
 Ser Asp Leu Leu Leu Leu Leu Leu Leu Pro Pro Pro Gly Ser Cys  
 -15 -10 -5  
 Ala Gly Arg Arg Ser Pro Xaa Thr Pro Asp Glu Ser Thr Pro Pro Pro  
 1 5 10 15  
 Arg Lys Lys Lys Lys Asp Ile Arg Asp Tyr Asn Asp Ala Asp Met Ala  
 20 25 30  
 Arg Leu Leu Glu Gln Gly Glu Gly  
 35 40

&lt;210&gt; 818

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 818

Met Glu Leu Gly Leu Cys Trp Val Leu Leu Leu Ala Leu Leu Glu Gly  
 -15 -10 -5  
 Val Gln Cys Asp Val Glu Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
 1 5 10  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe  
 15 20 25  
 Ser Thr Tyr Glu Met His Trp Ile Arg Gln Ala Pro Gly Lys Gly Pro  
 30 35 40 45  
 Glu Trp Val Xaa Tyr Val Ser Gly Gly Gly Gly Thr Xaa Xaa Asn Ala  
 50 55 60  
 Xaa Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Asn Ser  
 65 70 75  
 Phe Val Tyr Leu Gln Met Asp Ser Leu Arg Val Glu Asp Thr Ala Leu  
 80 85 90

Tyr Tyr Cys Ala Arg Xaa Asp Tyr Asp Phe Trp Ser Gly Tyr Tyr  
 95 100 105

<210> 819  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 819  
 Met Ala Trp Thr Pro Leu Leu Leu Leu Leu Ser His Cys Thr Gly  
 -15 -10 -5  
 Ser Leu Ser Gln Pro Val Leu Thr Gln Pro Arg Gly  
 1 5

<210> 820  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 820  
 Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val Ala Leu Leu Arg Gly  
 -15 -10 -5  
 Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln  
 1 5 10  
 Pro Gly Thr Ser Leu Thr Leu Ser Cys Ala Gly Ser Gly Phe Ser Phe  
 15 20 25  
 Ser Asp Tyr Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 30 35 40 45  
 Glu Trp Val Ala Val Ile Ser His Asp Gly Asn Asn Lys Tyr Tyr Gly  
 50 55 60  
 Gly Ser Met Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ser Arg His  
 65 70 75  
 Thr Val Ser Leu Gln Met Ser Ser Leu Gly Pro Glu Asp Thr Ala Val  
 80 85 90  
 Tyr Tyr Cys Ala Lys Asp Arg Thr Gly Gly  
 95 100

<210> 821  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 821  
 Met Lys Leu Leu Trp Phe Phe Leu Leu Leu Leu Ala Ala Pro Arg Trp  
 -15 -10 -5  
 Val Leu Ser Gln Val Gln Leu Val Xaa Ser Gly Pro Gly Leu Val Lys  
 1 5 10  
 Pro Ser Gly Thr Leu Ser Leu Thr Cys Thr Val Xaa Gly Xaa Xaa Ile  
 15 20 25  
 Thr Asn Tyr Tyr Trp Ser Xaa Ile Arg Gln Ser Pro Gly Lys Gly Leu  
 30 35 40 45

Glu Trp Ile Gly Thr Ile Tyr Tyr Ser Gly Ser Ala Asp His Asn Pro  
50 55 60  
Ser Leu Arg Ser Arg Ala Thr Ile Ser Leu Asp Thr Arg  
65 70

```
<210> 822
<211> 48
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -20..-1
```

<400> 822  
Met Ala Ser Leu Gly Leu Leu Leu Leu Xaa Leu Leu Thr Ala Leu Pro  
-20 -15 -10 -5  
Pro Leu Trp Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys  
1 5 10  
Ala Thr Xaa Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Gly  
15 20 25

```
<210> 823
<211> 96
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -28..-1
```

<400> 823															
Met	Asp	Val	Gly	Pro	Ser	Ser	Leu	Pro	His	Leu	Gly	Leu	Lys	Leu	Leu
			-25					-20					-15		
Leu	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Arg	Gly	Gln	Ala	Asn	Thr	Gly	Cys
		-10					-5					1			
Tyr	Gly	Ile	Pro	Gly	Met	Pro	Gly	Leu	Pro	Gly	Ala	Pro	Gly	Lys	Asp
5					10					15					20
Gly	Tyr	Asp	Gly	Leu	Pro	Gly	Pro	Lys	Gly	Glu	Pro	Gly	Ile	Pro	Ala
			25						30					35	
Ile	Pro	Gly	Ile	Arg	Gly	Pro	Lys	Gly	Gln	Lys	Gly	Glu	Pro	Gly	Leu
		40						45					50		
Pro	Gly	His	Pro	Gly	Lys	Asn	Gly	Pro	Met	Gly	Pro	Pro	Gly	Met	Pro
		55					60					65			

```
<210> 824
<211> 143
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -19...-1
```

```

<400> 824
Met Asp Cys Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Gly
          -15                      -10                      -5
Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
          1                      5                      10
Pro Gly Ala Ser Val Lys Val Ser Cys Gln Val Ser Gly Tyr Asn Val
          15                      20                      25
Val Glu Leu Ser Ile His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
30                      35                      40                      45

```

Glu	Trp	Met	Gly	Gly	Phe	Asp	Leu	Glu	Ser	Gly	Glu	Thr	Ile	Tyr	Ala
				50					55					60	
Gln	Arg	Phe	Gln	Gly	Arg	Ile	Thr	Met	Thr	Glu	Asp	Ser	Ser	Ser	Asp
			65					70					75		
Thr	Ala	Phe	Met	Glu	Leu	Ile	Ser	Leu	Arg	Pro	Glu	Asp	Ala	Ala	Val
		80					85					90			
Tyr	Tyr	Cys	Ala	Thr	Ile	Arg	Leu	Pro	Val	Val	Leu	Phe	Phe	Ala	Ala
	95					100					105				
Ser	Gly	Ala	Arg	Glu	Pro	Trp	Ser	Pro	Ser	Pro	Gln	Xaa	Pro	Arg	
110					115					120					

```
<220>
<221> SIGNAL
<222> -18...-1
```

```

<400> 825
Met Trp Leu Pro Leu Val Leu Leu Leu Ala Val Leu Leu Leu Ala Val
      -15                      -10                      -5
Leu Cys Lys Val Tyr Leu Gly Leu Phe Ser Gly Ser Ser Pro Asn Pro
      1                      5                      10
Phe Ser Glu Glu Arg
15

```

```
<210> 826
<211> 51
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -25..-1
```

```

<400> 826
Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu Leu
-25          -20          -15          -10
Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp Trp Pro
          -5          1          5
Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
          10          15          20
Ala Tyr Met
          25

```

```
<210> 827
<211> 131
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -19..-1
```

```

<400> 827
Met Ala Trp  Thr  Pro  Leu  Phe  Leu  Phe  Leu  Leu  Thr  Cys  Cys  Pro  Gly
              -15              -10              -5
Ser Asn Ser  Gln  Ala  Val  Xaa  Thr  Gln  Glu  Pro  Leu  Thr  Asp  Cys  Val
              1              5              10
Pro Arg  Xaa  Thr  Val  Thr  Leu  Thr  Cys  Gly  Ser  Ser  Ile  Gly  Ala  Val
              15              20              25

```

Thr Asn Gly His Phe Pro Tyr Trp Phe Gln Gln Lys Pro Gly Gln Ala  
 30 35 40 45  
 Pro Arg Thr Leu Ile Ser Asp Thr Phe Asn Arg Gln Ser Ser Thr Pro  
 50 55 60  
 Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Val Leu Thr Leu  
 65 70 75  
 Ser Asp Ala Gln Pro Asp Asp Glu Ala Glu Tyr Tyr Cys Val Leu Ser  
 80 85 90  
 Tyr Ser Gly Gly Arg Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val  
 95 100 105  
 Leu Ser Gln  
 110

&lt;210&gt; 828

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -21...-1

&lt;400&gt; 828

Met Gln Ala Cys Met Val Pro Gly Leu Ala Leu Cys Leu Leu Leu Gly  
 -20 -15 -10  
 Pro Leu Ala Gly Ala Lys Pro Val Gln  
 -5 1

&lt;210&gt; 829

&lt;211&gt; 79

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -23...-1

&lt;400&gt; 829

Met Pro Ser Tyr Lys Val Cys Gly Val Phe Cys Leu Phe Val Cys Leu  
 -20 -15 -10  
 Phe Leu Ser Gln Ser Phe Ala Phe Val Leu Gln Ala Gly Val Gln Trp  
 -5 1 5  
 Arg Asp Leu Cys Ser Leu Gln Pro Gln Leu Pro Arg Phe Gly Pro Ser  
 10 15 20 25  
 Ser Cys Leu Ser Leu Pro Ser Gly Trp Asp Cys Arg Arg Pro Pro Pro  
 30 35 40  
 Arg Leu Ala Asn Ser Cys Val Phe Gly Gly Asp Gly Val Ser Pro  
 45 50 55

&lt;210&gt; 830

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -21...-1

&lt;400&gt; 830

Met Gly Thr Gln Glu Gly Trp Xaa Leu Leu Leu Cys Leu Ala Leu Ser  
 -20 -15 -10  
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala  
 -5 1 5 10

439

Val Xaa Val Val Leu Asp Xaa Phe Leu Val Lys Asp Xaa Ala His Arg  
                   15                  20                  25  
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg  
                   30                  35

<210> 831  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 831  
 Met Ser Met Leu Val Val Phe Leu Leu Leu Trp Gly Val Thr Trp Gly  
           -15                  -10                  -5  
 Pro Val Thr Glu Ala Ala Ile Phe Tyr Glu Thr Gln Xaa Ser Leu Trp  
 1                  5                  10                  15  
 Ala Glu Ser Glu His Xaa Leu Lys Thr Leu Gly Gln Cys Asp Ala Asp  
                   20                  25                  30  
 Val Pro Gly Pro Pro Gly Asp Ser Arg Leu Pro Ala Val Gln Glu Trp  
           35                  40                  45  
 Gly Ala Gln Glu Pro Val His Leu Asp Ser Pro Ala Ile Lys His Gln  
           50                  55                  60  
 Phe Leu Leu Thr Gly Asp Thr Gln Gly Arg Tyr Arg Cys Arg Ser Gly  
 65                  70                  75                  80  
 Leu Ser Thr Gly Trp Xaa Gln Leu Ser Lys Leu Leu Glu Leu Thr Gly  
                   85                  90                  95  
 Pro Lys Val Leu Ala Cys Ser Leu Ala Leu Asp Gly Ala Ser  
                   100                  105                  110

<210> 832  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 832  
 Met Leu Pro Ser Gln Leu Ile Gly Phe Leu Leu Leu Trp Val Pro Ala  
                   -15                  -10                  -5  
 Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Leu Ser Val  
                   1                  5                  10  
 Thr Pro Lys Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Xaa Ser Ile  
           15                  20                  25  
 Gly Ser Ser Leu Tyr Trp Tyr Gln Gln Lys Pro His Gln Ser Pro Lys  
 30                  35                  40                  45  
 Leu Val Ile Lys Tyr Ala Ser Gln Ser Phe Ser Gly Val Ser Ser Arg  
                   50                  55                  60  
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser  
           65                  70                  75  
 Leu Glu Pro Gly  
           80

<210> 833  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<220>

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 833

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser  
 -20 -15 -10 -5  
 Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp  
 1 5 10  
 Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp  
 15 20 25  
 Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys  
 30 35 40  
 Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu  
 45 50 55 60  
 Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu  
 65 70 75  
 Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu  
 80 85 90  
 Thr Thr Asp  
 95

&lt;210&gt; 834

&lt;211&gt; 119

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 834

Met Arg Pro Gly Leu Ser Phe Leu Leu Ala Leu Leu Phe Phe Leu Gly  
 -20 -15 -10 -5  
 Gln Ala Ala Gly Asp Leu Gly Asp Val Gly Pro Pro Ile Pro Ser Pro  
 1 5 10  
 Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser Phe Ser Ser  
 15 20 25  
 Ser Ser Arg Ser Gly Ser Ser Ser Arg Ser Leu Gly Ser Gly Gly  
 30 35 40  
 Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly Ser Val Asp Asp Arg  
 45 50 55 60  
 Gly Thr Cys Gln Cys Ser Val Ser Leu Pro Asp Thr Thr Phe Pro Val  
 65 70 75  
 Asp Arg Val Glu Arg Leu Glu Phe Thr Ala His Val Leu Ser Gln Lys  
 80 85 90  
 Phe Glu Lys Glu Leu Ser Lys  
 95

&lt;210&gt; 835

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 835

Met Asp Leu Leu His Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu  
 -25 -20 -15  
 Leu Val Ala Ala Pro Arg Trp Val Arg Ser Gln Val Gln Leu Xaa Glu  
 -10 -5 1 5  
 Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu Ser Leu Ile Cys

```

      10      15      20
Gly Val Ser Gly Asp Ser Val Thr Ile Ser Gly Trp Trp Ser Trp Val
      25      30      35
Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Ser Glu Ile Asp His
      40      45      50
Gly Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Xaa Ile
55      60      65      70
Ser Leu Asp Lys Ser Lys Asn Lys Phe Ser Leu Arg Leu Thr Ser Val
      75      80      85
Thr Ala Ala Asp Thr Ala Met Tyr Xaa Cys Ala Arg Gly Gly Ala Xaa
      90      95      100
Ser Ser Ser Ala Phe Asp Val Trp Gly Leu Xaa Thr Met Val Ile Ile
      105      110      115
Ser Ser Ala
      120

```

&lt;210&gt; 836

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 836

```

Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu Thr Val Pro Ser Trp
      -15      -10      -5
Val Leu Ser Gln Val Thr Leu Xaa Glu Ser Gly Pro Ala Leu Val Lys
      1      5      10
Ala Thr Gln Thr Leu Arg Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
15      20      25
Ser Thr Asn Arg Met Arg Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
30      35      40      45
Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp Asp Tyr Lys Arg Tyr
      50      55      60
Ser Thr Ser Leu Lys Thr Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
      65      70      75
Asn Gln Val Ile Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala
      80      85      90
Thr Tyr Tyr Cys Ala Arg Leu Ser Thr Ala Ala Thr Pro Gln Phe Phe
95      100      105
Asp Phe Trp Gly Gln Gly Val Leu Val Ser Val
110      115      120

```

&lt;210&gt; 837

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 837

```

Met Xaa His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
      -15      -10      -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
      1      5      10
Pro Ser Xaa Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile
15      20      25
Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
30      35      40      45

```

442

Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Asn	Tyr	Asn	Pro
			50						55					60	
Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln
			65					70					75		
Phe	Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr
			80				85					90			
Tyr	Cys	Ala	Arg	Xaa	Leu	Xaa	Tyr	Tyr	Asp	Arg	Ser	Gly	Tyr	Phe	Arg
			95			100					105				
Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Trp	Ser					
110					115					120					

```
<210> 838
<211> 136
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -19..-1
```

```

<400> 838
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
          -15                      -10                      -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
          1                      5                      10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
          15                      20                      25
Asp Ser Gly Asn Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys
30          35          40          45
Gly Leu Glu Trp Ile Gly Arg Ile Tyr Ser Thr Gly Ser Thr Asn Tyr
          50          55          60
Asn Pro Ser Leu Ser Ser Arg Val Gln Ile Ser Leu Asp Thr Ser Lys
          65          70          75
Asn Leu Leu Ser Leu Asn Leu Thr Ser Val Thr Ala Ala Asp Thr Ala
          80          85          90
Val Tyr Phe Cys Ala Arg Thr Phe Pro Phe Tyr Trp Tyr Leu Asp Leu
          95          100          105
Trp Gly Arg Gly Ile Leu Val Thr
110          115

```

```
<210> 839
<211> 143
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -19..-1
```

<400> 839																
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
				-15					-10					-5		
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Arg	Leu	Val	Lys	
		1				5					10					
Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	
	15					20					25					
Ser	Ser	Gly	Gly	Tyr	Phe	Trp	Ser	Trp	Ile	Arg	Gln	His	Pro	Gly	Arg	
30					35					40					45	
Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Tyr	Asn	Trp	Ser	Thr	Tyr	Tyr	
			50					55					60			
Asn	Pro	Ser	Leu	Arg	Ser	Arg	Val	Thr	Met	Ser	Met	Asp	Thr	Ser	Lys	
			65					70					75			
Asn	Gln	Phe	Ser	Leu	Asn	Leu	Asn	Ser	Val	Thr	Ala	Ala	Asp	Thr	Xaa	

80 85 90  
 Met Tyr Tyr Cys Ala Arg Gly Arg Gly Arg Leu Gly Trp Phe Xaa Xaa  
 95 100 105  
 Xaa Gly Xaa Gly Xaa Pro Gly His Arg Leu Ile Ser Arg Pro Gly  
 110 115 120

<210> 840  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 840  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 -15 -10 -5  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
 1 5 10  
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile  
 15 20 25  
 Arg Thr Gly Ser Tyr Tyr Trp Thr Trp Val Arg Gln Pro Pro Gly Lys  
 30 35 40 45  
 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Thr Gly Asp Thr Tyr Tyr  
 50 55 60  
 Asn Pro Ser Leu Lys Ser Arg Ile Thr Met Ser Leu Asp Thr Xaa Xaa  
 65 70 75  
 Asn Gln Phe Xaa Leu Ser Leu Thr Ser Val Thr Val Ala Asp Thr  
 80 85 90

<210> 841  
 <211> 53  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 841  
 Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu Ala Leu Cys Cys  
 -15 -10 -5 1  
 Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val Ser Glu Leu Leu  
 5 10 15  
 Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu Ser Leu Ala Lys  
 20 25 30  
 Phe Asp Ala Pro Arg  
 35

<210> 842  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 842  
 Met Ser Pro Val Leu Leu Val Leu Ser Leu Ser Gln Cys Leu Leu Ser  
 -15 -10 -5  
 Asp Pro Val Ile Pro Gly Leu

1 5  
 <210> 843  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 843  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 -15 -10 -5  
 Val Leu Ser Gln Val Arg Leu Gln Glu Ser Gly Pro Arg Leu Val Lys  
 1 5 10  
 Pro Ser Glu Xaa Leu Ser Leu Thr Cys Ser Val Ser Gly Val Ser Val  
 15 20 25  
 Thr Asn Phe Phe Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu  
 30 35 40 45  
 Glu Trp Leu Gly Tyr Met Ser Tyr Gly Val Ser Thr Asn Tyr His Pro  
 50 55 60  
 Ala Tyr Gln Ser Arg Val Ser Ile Ser Ile Asp Thr Trp  
 65 70

<210> 844  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 844  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 -15 -10 -5  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Arg Leu Val Lys  
 1 5 10  
 Pro Ser Glu Ala Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Ser  
 15 20 25  
 Ser Asn Tyr Asp Trp Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu  
 30 35 40 45  
 Glu Trp Ile Gly Tyr Ile Asp Asp Ser Lys Asn Arg Gly Ser Thr Thr  
 50 55 60  
 Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Xaa Asp Thr Ser  
 65 70 75  
 Lys Xaa Gln Leu Ser Leu Arg Leu Thr Ser Val Thr Xaa Ala Asp Thr  
 80 85 90  
 Ala Val Tyr Tyr Cys Ala Arg Lys Ser Ser Met His Ser Ser Gly Trp  
 95 100 105  
 His Asn Arg Ser Leu Tyr Trp Tyr Phe Asp Pro  
 110 115 120

<210> 845  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

&lt;400&gt; 845

Met Asp Leu Leu His Lys Asn Met Lys Asp Leu Trp Phe Phe Leu Leu  
 -25 -20 -15  
 Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Leu Gln Glu Ser  
 -10 -5 1 5  
 Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu Ser Leu Thr Cys Ala  
 10 15 20  
 Val Ser Gly Gly Ser Ile Ile Ser Ser Asn Trp Trp Ser Trp Val Arg  
 25 30 35  
 Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Tyr Glu Asp  
 40 45 50  
 Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser  
 55 60 65 70  
 Val Asp Lys Ala Lys Asn Gln Phe Ser Leu Lys Met Arg Ser Val Thr  
 75 80 85  
 Ala Ser Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser Ser Ser Val  
 90 95 100  
 Arg Thr Asp Tyr Trp Gly  
 105

&lt;210&gt; 846

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 846

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 -15 -10 -5  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Ser Gly Pro Val Asp  
 1 5 10  
 Xaa Xaa Gln Thr Leu Xaa Leu Thr Cys Thr Xaa Ser Gly Val Ser Ile  
 15 20 25  
 Ser Ser Ser Asp Asn Cys Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys  
 30 35 40 45  
 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr His Ser Gly Gly Thr Tyr Tyr  
 50 55 60  
 Asn Pro Thr Leu Lys Ser Arg Val Thr Ile Ser Xaa Asp Arg Ile Arg  
 65 70 75  
 Asn Gln Phe Ser Leu Lys Leu Ser Val Thr Ala Xaa Asp Thr Ala  
 80 85 90  
 Val Tyr Xaa Cys Gly Arg Ala Gln Gly Arg Met Gly Ile Gly Thr Thr  
 95 100 105  
 Ile Phe Asp Leu Trp Gly Gly Gly Gln Trp Ser Pro Ser Leu Gln Pro  
 110 115 120 125

&lt;210&gt; 847

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 847

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
 -15 -10 -5  
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 1 5 10

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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Xaa Phe  
 15 20 25  
 Thr Xaa Xaa Ala Xaa His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu  
 30 35 40 45  
 Glu Trp Met Gly Trp Ile Asn Ala Ala Xaa Gly Xaa Thr Xaa Tyr Ser  
 50 55 60  
 Gln Xaa Phe Gln Xaa Arg Val Thr Xaa Thr Arg Asp Thr Ser Ala Ser  
 65 70 75  
 Thr Val Ser Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 80 85 90  
 Tyr Phe Cys Ala Arg Asp Trp Glu Ile Ala Val Val Pro Thr Ala Ile  
 95 100 105  
 Asn Ser Tyr Gly Phe Asp Pro Gly Ala Arg Glu Pro  
 110 115 120

&lt;210&gt; 848

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 848

Met Glu Ala Arg Val Glu Arg Ala Val Gln Lys Arg Gln Val Leu Phe  
 -25 -20 -15  
 Leu Cys Val Phe Leu Gly Met Ser Trp Ala Gly Ala Glu Pro Leu Arg  
 -10 -5 1 5  
 Tyr Phe Val Ala Glu Glu Thr Glu Arg Gly Thr Xaa Leu Thr Asn Leu  
 10 15 20  
 Ala Lys Asp Leu  
 25

&lt;210&gt; 849

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 849

Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
 -15 -10 -5  
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys  
 1 5 10  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 15 20 25  
 Thr Arg Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 30 35 40 45  
 Glu Trp Met Gly Trp Ile Ser Ala Xaa Asn Gly Asn Thr Asn Tyr Ala  
 50 55 60  
 Gln Xaa Val Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Arg  
 65 70 75  
 Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile  
 80 85 90  
 Tyr Tyr Cys Ala Arg Glu Ile Xaa Val Xaa Xaa Cys Asp Gly Gln Leu  
 95 100 105  
 Gly Pro Gly Asn Leu Val  
 110 115

<210> 850  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 850  
 Met Asp Val Leu His Lys His Met Lys His Leu Trp Phe Phe Leu Leu  
       -25                  -20                  -15  
 Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Glu Gln Leu Arg Gln  
       -10                  -5                  1                  5  
 Trp Gly Ala Xaa Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys  
               10                  15                  20  
 Ser Val Tyr Gly Gly Ser Phe Asn Gly Tyr Tyr Trp Ser Trp Ile Arg  
           25                  30                  35  
 Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile Gly Gly Ile Asn His Ser  
       40                  45                  50  
 Gly Ser Thr Leu Ser Asn Pro Ser Leu Lys Ser Arg Val Asp Leu Ser  
       55                  60                  65                  70  
 Val Asp Ala Ser Lys Asp Gln Val Ser Leu Arg Leu Lys Leu Val Thr  
               75                  80                  85  
 Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg Pro His Tyr Asp Met  
           90                  95                  100  
 Ser Thr Asp Ser Ser Phe Asp Gly Phe Asp Leu Trp  
       105                  110

<210> 851  
 <211> 44  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 851  
 Met Met Leu Leu Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser  
       -15                  -10                  -5                  1  
 Gln Gly Leu Leu Trp Phe His Thr Asn Phe Lys Val Phe Val Val Ser  
           5                  10                  15  
 Ile Cys Val Lys Thr Ile Ile Gly Ile Ser Gly Gly  
       20                  25

<210> 852  
 <211> 78  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 852  
 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
               -15                  -10                  -5  
 Ala Leu Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys  
           1                  5                  10  
 Pro Gly Ala Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe  
       15                  20                  25  
 Ile Gly Tyr Tyr Val His Trp Ile Arg Gln Thr Pro Gly Arg Xaa Leu

30 35 40 45  
 Glu Trp Met Gly Trp Val Asn Pro Xaa Thr Gly Asp Asn Gly  
 50 55

<210> 853  
 <211> 44  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -37...-1

<400> 853  
 Met Phe Phe Gln Phe Trp Lys Ser Ser Ala Tyr Leu Ile Phe Val Ser  
 -35 -30 -25  
 Ile Cys Lys Gly Phe Leu Pro Val Tyr Leu Leu Leu Val Leu Ser Leu  
 -20 -15 -10  
 Ser Leu Ser Leu Cys Cys Ser Leu Leu Leu Ser Leu  
 -5 1 5

<210> 854  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 854  
 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
 -15 -10 -5  
 Val His Ser Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 1 5 10  
 Pro Gly Thr Pro Val Asn Ile Ser Cys Lys Ala Phe Gly Tyr Thr Phe  
 15 20 25  
 Pro Ala Phe Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Ser Leu  
 30 35 40 45  
 Glu Trp Met Gly Trp Val Asn Ile Gly His Gly Asn Thr Lys Tyr Ser  
 50 55 60  
 Gln Lys Phe Gln Gly Arg Leu Ala Ile Ser Arg Asp Thr Ser Ala Asn  
 65 70 75  
 Ile Val Tyr Xaa Glu Leu Ser Gly Leu Arg Ser Glu Asp Thr Ala Val  
 80 85 90  
 Tyr Tyr Cys Ala Arg Asp Asn Leu Phe Phe Gly Ser Met Gly Phe Asp  
 95 100 105

<210> 855  
 <211> 152  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 855  
 Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly  
 -15 -10 -5  
 Ser Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala  
 1 5 10 15  
 Pro Gly Lys Thr Ala Ser Ile Thr Cys Gly Gly Asp Asn Ile Glu Ser

```

      20      25      30
Gln Val Val His Trp His Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu
      35      40      45
Val Ile Tyr Asp Asp Thr Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe
      50      55      60
Ser Gly Ser Asn Ser Gly His Thr Ala Thr Leu Thr Ile Ser Arg Val
      65      70      75      80
Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg Ser
      85      90      95
Ser Gly Gln Gly Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg
      100      105      110
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
      115      120      125
Glu Leu Gln Ala Asn Lys Ala Thr
      130      135

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&lt;210&gt; 856

&lt;211&gt; 48

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15..-1

&lt;400&gt; 856

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Met Arg Leu Leu Phe Leu Leu Leu Phe Val Cys Phe Ser Arg Gln Gly
-15      -10      -5      1
Leu Ala Leu Ser Leu Arg Leu Glu Cys Ser Gly Met Ile Met Ala Tyr
      5      10      15
Cys Ser Ile Ser Leu Pro Gly Ser Ser Ser Pro Leu Thr Ser Ala Ser
      20      25      30

```

&lt;210&gt; 857

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19..-1

&lt;400&gt; 857

```

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ser Ala Pro Arg Trp
      -15      -10      -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
      1      5      10
Pro Ser Gly Arg Leu Ser Leu Ala Cys Asp Val Val Glu Leu Ser Pro
      15      20      25
Pro Ala Pro Arg Gly Gly Ser Ala Val His Leu Arg Asn Leu Ser Ser
      30      35      40      45
Trp Glu Pro His Leu Gln Pro Val Ser Gly
      50      55

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&lt;210&gt; 858

&lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -32..-1

&lt;400&gt; 858

Met Thr Tyr Phe Pro Leu Gly Arg Tyr Pro Val Met Gly Leu Leu Asp  
 -30 -25 -20  
 Gln Met Val Val Val Phe Leu Leu Leu Leu Val Ser Thr Leu Ser Ser  
 -15 -10 -5  
 Val Val Val Leu Leu Val Cys Ile Pro Thr Ser Ser Val Lys Leu Phe  
 1 5 10 15  
 Pro Phe His His Ile His Thr Asn Trp  
 20 25

&lt;210&gt; 859

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 859

Met Glu Phe Gly Leu Ser Trp Val Leu Leu Val Ala Met Leu Arg Gly  
 -15 -10 -5  
 Leu Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Thr Ala  
 1 5 10

&lt;210&gt; 860

&lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 860

Met Tyr Leu Ser Leu Leu Ile Leu Leu Leu Glu Asn Val Ser Gly Phe  
 -15 -10 -5 1  
 Pro Phe Pro Leu Ile Phe Gln Leu His Ala Ser Pro Gly His Lys Ile  
 5 10 15  
 Leu Pro Asp Cys Met Ile Tyr Ser Ile Thr Val Ser Leu Met Phe Pro  
 20 25 30  
 Val Val Asp Tyr Ile Ser Thr Gln Gly  
 35 40

&lt;210&gt; 861

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -28...-1

&lt;400&gt; 861

Met Met Arg Ala Phe Tyr Leu Ala Ile Leu Phe Cys Leu Ser Leu Ser  
 -25 -20 -15  
 Leu Trp Phe Xaa Cys Leu Leu Phe Leu Leu Phe Ala Trp Pro Gly  
 -10 -5 1

&lt;210&gt; 862

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 862

Met Ala Trp Thr Pro Leu Leu Phe Leu Thr Leu Leu His Cys Thr  
 -20 -15 -10 -5  
 Gly Ser Leu Ala Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala  
 1 5 10  
 Ser Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gly His  
 15 20 25  
 Ser Asn Tyr Gly Ile Ala Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro  
 30 35 40  
 Arg Phe Leu Met Lys Val Asn Ser Asp Gly Ser His Met Lys Ala Asp  
 45 50 55 60  
 Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr  
 65 70 75  
 Leu Ser Ile Ser Ser Leu  
 80

&lt;210&gt; 863

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 863

Met Pro Leu Ala Leu Phe Phe Leu Leu Ser Val Ala Leu Ala Ile Gln  
 -10 -5 1  
 Gly Gln

&lt;210&gt; 864

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 864

Met Asp Trp Thr Trp Arg Xaa Phe Cys Leu Leu Ala Val Ala Pro Gly  
 -15 -10 -5  
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 1 5 10  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 15 20 25  
 Thr Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 30 35 40 45  
 Glu Trp Met Gly Ile Ile Tyr Pro Asp Ser Asp Thr Thr Lys Tyr Xaa  
 50 55 60  
 Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser  
 65 70 75  
 Thr Val Tyr Met Glu Leu Ser Ser Leu Thr Ser Asp Asp Thr Ala Val  
 80 85 90  
 Tyr Tyr Cys Ala Arg Glu Ala Tyr Ser Gly Ser Tyr Arg Phe Asp Tyr  
 95 100 105  
 Trp  
 110

<210> 865  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 865  
 Met Asp Leu Met Cys Lys Lys Met Arg His Leu Trp Phe Leu Leu Leu  
       -25                      -20                      -15  
 Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Leu Gln Leu Gln Glu  
       -10                      -5                      1                      5  
 Ser Gly Pro Gly Leu Val Lys Ala Ser Glu Thr Leu Ser Leu Ala Cys  
                       10                      15                      20  
 Ser Val Ser Gly Asp Ser Ile Ser Ser Gly Asn Tyr Tyr Trp Gly Trp  
                       25                      30                      35  
 Ile Arg Gln Pro Pro Gly Lys Gly Leu Gln Trp Leu Gly Ser Leu Trp  
                       40                      45                      50  
 Asn Arg Gly Gly Pro Gln Tyr Asn Xaa Ser Leu Lys Asn Arg Val Thr  
       55                      60                      65                      70  
 Val Ser Val Asp Thr Ser Thr Asn His Phe Phe Leu Arg Leu Asn Ser  
                       75                      80                      85  
 Val Asn Xaa Gly His Gly Asn Leu Leu Leu Cys Ala  
                       90                      95

<210> 866  
 <211> 32  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 866  
 Met Arg Xaa Xaa Leu Xaa Leu Ser Val Leu Leu Gly Xaa Xaa Xaa Xaa  
       -15                      -10                      -5  
 Lys Xaa Asp Phe Val Gly His Gln Val Leu Arg Ile Ser Val Ala Asp  
       1                      5                      10                      15

<210> 867  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -36...-1

<400> 867  
 Met Ala Glu Ser Arg Glu Glu Gly Glu Ser Cys Val Glu Ser His Cys  
       -35                      -30                      -25  
 Val Leu Phe Phe Thr Leu Phe Phe Leu Leu Phe Phe Cys Phe Val Phe  
       -20                      -15                      -10                      -5  
 Cys Leu Arg Gly Gln Gly  
                       1

<210> 868  
 <211> 110  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 868

```

Met Glu Leu Gly Leu Ser Trp Leu Phe Leu Val Ala Phe Leu Lys Gly
      -15                      -10                      -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
      1                      5                      10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
      15                      20                      25
Ser Ser Tyr Ala Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30                      35                      40                      45
Glu Trp Val Ser Gly Ile Ser Ala Gly Ala Asp Asp Thr Tyr Asp Ala
      50                      55                      60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Lys
      65                      70                      75
Ile Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Arg
      80                      85                      90

```

&lt;210&gt; 869

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -23...-1

&lt;400&gt; 869

```

Met Ala Val Ser Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
      -20                      -15                      -10
Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
      -5                      1                      5
Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
10                      15                      20                      25
Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala
      30                      35

```

&lt;210&gt; 870

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 870

```

Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala Leu Leu Leu Leu Gln
      -20                      -15                      -10
Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu Pro Pro Gln Asp Lys
      -5                      1                      5
Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly
10                      15                      20
His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr Tyr Glu Leu Trp
25                      30                      35                      40
Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys
      45                      50                      55
Val Cys His His Arg Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg
      60                      65                      70

```

Gln His Glu Ile Asn Leu Ile Ala Tyr Arg  
75 80

<210> 871  
<211> 37  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -27...-1

<400> 871  
Met Val Val Ala Asp Arg Asn Arg Ala Ser Ser Ser Ser Tyr Leu Cys  
-25 -20 -15  
Leu Leu Leu Phe Ser Leu Ser Leu Phe Leu Cys His Glu Thr Val Cys  
-10 -5 1 5  
Asp Arg Ala Thr Cys  
10

<210> 872  
<211> 142  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -19...-1

<400> 872  
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly  
-15 -10 -5  
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
1 5 10  
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe  
15 20 25  
Ser Xaa Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
30 35 40 45  
Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Xaa Tyr Ala  
50 55 60  
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Xaa Ser Thr Xaa  
65 70 75  
Thr Xaa Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Xaa  
80 85 90  
Tyr Tyr Cys Ala Arg Gly Gln Ala Pro Gly Arg Val Val Val Pro Leu  
95 100 105  
Phe Leu Trp Gly Gln Gly Thr Trp Ser Pro Ser Pro Gln Pro  
110 115 120

<210> 873  
<211> 87  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -45...-1

<400> 873  
Met Thr Tyr Ser Tyr Ser Phe Phe Arg Pro Glu Leu Ile Val Asn His  
-45 -40 -35 -30  
Leu Asn Tyr Val His Ser Glu Ala Asn Arg Arg Thr Lys Thr Lys Thr  
-25 -20 -15

455

```

<400> 876
Met Trp Lys Glu Ser Ser His Gly Cys Asn Asn Leu Gly Ser Ser Tyr
      -35      -30      -25
Leu Asp Asp Thr Gly Val Gly Ser Phe Leu Phe Val Leu Phe Cys Phe
      -20      -15      -10

```

Gly Gly Ser Arg Ala Leu Leu Leu Pro Gly Ser Gly  
 -5 1 5

<210> 877  
 <211> 26  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 877  
 Met His Thr Phe Leu Cys Leu Leu Phe Tyr Leu Ile Val Ser Cys Gly  
 -15 -10 -5  
 Ala Val Phe Leu Thr Val Pro Ser Pro Gln  
 1 5 10

<210> 878  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -39...-1

<400> 878  
 Met Ala Trp His Pro Thr Pro Pro Pro Leu Xaa Xaa Pro Pro Pro Leu  
 -35 -30 -25  
 Xaa Arg Xaa Ser Leu Pro Ala Cys Ala Asp Ser Ile Ile Leu Xaa Leu  
 -20 -15 -10  
 Xaa Phe Pro Gly Ile Leu Gly Gln Ala His Leu Xaa Ser Glu Gln Trp  
 -5 1 5  
 Thr Gln Tyr Leu  
 10

<210> 879  
 <211> 37  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 879  
 Met Pro Ile Leu Pro Gln Asp Ile Leu His Leu Leu Ile Leu Leu Ser  
 -20 -15 -10  
 Gly Thr Cys Phe Thr Trp Ile Leu Leu Trp Leu Pro Leu Ser Pro Leu  
 -5 1 5 10  
 Leu Gly Leu Lys Cys  
 15

<210> 880  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

&lt;400&gt; 880

Met Lys Ala Leu Gly Ala Val Leu Leu Ala Leu Leu Leu Cys Gly Arg  
 -20 -15 -10 -5  
 Pro Gly Arg Gly Gln Thr Gln Gln Glu Glu Glu Glu Asp Glu Asp  
 1 5 10  
 His Gly Pro Asp Asp Tyr Asp Glu Asp Glu Asp Glu Val Glu Glu  
 15 20 25  
 Glu Glu Thr Asn Arg Leu Pro Gly Gly Arg Ser Arg Val Leu Leu Arg  
 30 35 40  
 Cys Tyr Thr Xaa Xaa Ser Leu Pro Arg Asp Glu Arg Cys Asn Leu Thr  
 45 50 55 60  
 Gln Asn Cys Ser His  
 65

&lt;210&gt; 881

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 881

Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala Lys  
 -15 -10 -5 1  
 Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met Leu Lys  
 5 10 15  
 Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp Asp Asp  
 20 25 30  
 Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu Pro Arg Ser His  
 35 40 45  
 Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro Phe Gly Cys Gln Cys  
 50 55 60 65  
 Tyr Ser Arg Val Val His Cys Ser  
 70

&lt;210&gt; 882

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 882

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 -15 -10 -5  
 Ala Met Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Arg Leu Val Lys  
 1 5 10  
 Pro Ser Gly Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Met  
 15 20 25  
 Ala Thr Ser Asp Trp Trp Ser Trp Phe Arg Gln Thr Pro Glu Lys Gly  
 30 35 40 45  
 Leu Glu Trp Ile Gly Glu Ile Phe Gln Thr Gly Pro Thr Asn Tyr Asn  
 50 55 60  
 Pro Ser Leu Lys Ser Arg Val Ser Met Ser Val Asp Met Ser Lys  
 65 70 75

&lt;210&gt; 883

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 883

```

Met Asp Leu Thr Cys Lys Lys Met Lys His Leu Trp Phe Phe Leu Leu
  -25          -20          -15
Leu Val Ala Ala Pro Arg Trp Ala Leu Ser Gln Leu Gln Leu Gln Glu
-10          -5          1          5
Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
      10          15          20
Thr Val Ser Gly Glu Ser Ile Thr Thr Asn Ser Phe Cys Trp Ala Trp
      25          30          35
Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Thr Val Cys
  40          45          50
Tyr Gly Gly Thr Thr Tyr Xaa Asn Xaa Ser Leu Lys Ser Arg Val Lys
55          60          65          70
Leu Ser Leu Asp Thr Ser Thr Asn Gln Phe Ser Leu Lys Val Thr Ser
      75          80          85
Met Thr Ala Gly Asp Ala Ala Val His Tyr Cys Ala Gly Leu Arg Val
      90          95          100
Ser

```

&lt;210&gt; 884

&lt;211&gt; 66

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -63...-1

&lt;400&gt; 884

```

Met Ala Asn Gly Thr Asn Ala Ser Ala Pro Tyr Tyr Ser Tyr Glu Tyr
      -60          -55          -50
Tyr Leu Asp Tyr Leu Asp Leu Ile Pro Val Asp Glu Lys Lys Leu Lys
      -45          -40          -35
Ala His Lys His Ser Ile Val Ile Ala Phe Trp Val Ser Leu Ala Ala
      -30          -25          -20
Phe Val Val Leu Leu Phe Leu Ile Leu Leu Tyr Met Ser Trp Ser Ala
-15          -10          -5          1
Ser Pro

```

&lt;210&gt; 885

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 885

```

Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
      -15          -10          -5
Val Gln Ser Gln Xaa Xaa Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
      1          5          10
Pro Gly Ser Ser Val Lys Val Ser Cys Xaa Ala Ser Gly Gly Ile Xaa
      15          20          25
Ser Xaa Tyr Ser Phe Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
30          35          40          45

```

459

Glu Trp Leu Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala  
                           50                          55                          60  
 Glu Lys Phe Arg Gly Arg Leu Thr Ile Thr Val Asp Lys Ser Thr Arg  
                           65                          70                          75  
 Val Val Tyr Met Glu Gln Ser Ser Leu Thr Ser Ala Asp Thr Ala Val  
                           80                          85                          90  
 Tyr Tyr Cys Ala Lys Pro Thr Met Thr Ser Glu Leu Arg Val Tyr Tyr  
                           95                          100                          105  
 Gln Xaa Thr Leu Trp  
 110

<210> 886  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 886  
 Met Trp Asn Arg Tyr Phe Val Phe Tyr Leu Leu Leu Leu Ser Ala Phe  
                           -20                          -15                          -10  
 Thr Ser Gln Thr Val Ser Gly Gln Arg Lys Lys Gly Pro Arg  
                           -5                          1                          5

<210> 887  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 887  
 Met Lys His Leu Gly Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
                           -15                          -10                          -5  
 Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Ser Gly Leu Glu Lys  
                           1                          5                          10  
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
                           15                          20                          25  
 Ser Ser Asp Asp Leu Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys  
 30                          35                          40                          45  
 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gln Asn Glu Arg Thr Leu Tyr  
                           50                          55                          60  
 Asn Pro Ser Leu Lys Ser Arg Ala Ala Ile Ser Val Asp Arg Ser Lys  
                           65                          70                          75  
 Asn Gln Phe Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Met Ala  
                           80                          85                          90  
 Val Tyr Tyr Cys Ala Thr Ser Val Met Xaa Ser Phe Gly Gly Val Leu  
                           95                          100                          105  
 Val Pro Asn Leu Phe Leu Thr Thr Gly Ala Arg Glu Ser Arg  
 110                          115                          120

<210> 888  
 <211> 155  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

&lt;400&gt; 888

```

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Gly Pro Arg Trp
      -15      -10      -5
Val Leu Ser Gln Val Gln Leu Xaa Glu Ser Gly Pro Arg Leu Val Lys
      1      5      10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Val
      15      20      25
Ser Ser Arg Gly Tyr Tyr Trp Thr Trp Ile Arg Gln Leu Pro Gly Lys
      30      35      40      45
Gly Leu Glu Trp Ile Gly Tyr Ile Xaa Tyr Thr Gly Ser Thr Phe Tyr
      50      55      60
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Ile Asp Thr Ser Lys
      65      70      75
Asn Gln Phe Ser Leu Asn Leu Arg Ser Val Thr Thr Ala Asp Thr Ala
      80      85      90
Val Tyr Tyr Cys Ala Arg Asp His Phe Asp Leu Leu Phe Asp Pro Trp
      95      100      105
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
      110      115      120      125
Ser Val Phe Pro Leu Ala Xaa Ser Ser Lys Ser
      130      135

```

&lt;210&gt; 889

&lt;211&gt; 63

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -41...-1

&lt;400&gt; 889

```

Met Ala Cys Arg Glu Arg Pro Arg Pro Leu Leu Trp Arg Ser Arg Gly
      -40      -35      -30
Arg Phe Phe Asn Trp Gly Lys Leu Phe Phe Cys Phe Val Leu Xaa Leu
      -25      -20      -15      -10
Phe Cys Phe Val Phe Glu Ala Glu Ser Arg Ser Val Ala Gln Ala Gly
      -5      1      5
Val Gln Trp Arg Tyr Phe Gly Ser Leu Gln Ala Leu Pro Pro Trp
      10      15      20

```

&lt;210&gt; 890

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -21...-1

&lt;400&gt; 890

```

Met His Glu Phe Ile Ser Gly Phe Phe Ile Leu Phe His Trp Ser Leu
      -20      -15      -10
Cys Leu Cys Leu Cys Gln Tyr His Ala
      -5      1

```

&lt;210&gt; 891

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> SIGNAL  
 <222> -42...-1

<400> 891  
 Met Ala Tyr Ala Ile Ser Pro Phe His Ser Ser Trp Asn Pro Leu Phe  
           -40                          -35                          -30  
 Thr Ser His Lys Ala Ser Ala Ser His Ser His Leu Gly Leu Leu Val  
           -25                          -20                          -15  
 Cys Leu Phe Ala Val Thr Ser Ile Leu Cys Ser Ser  
           -10                          -5                          1

<210> 892  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 892  
 Met Ser Pro Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro Leu  
           -15                          -10                          -5                          1  
 Pro Gly Ser Ala Xaa Ala Xaa Ser Ala Ser Leu Gly Gln Phe Ser Met  
                           5                          10                          15  
 Cys Gly Arg Cys Pro Thr Cys Pro Gly Asn Gly Pro Leu Arg Thr Pro  
           20                          25                          30  
 Ala Ala Thr Xaa Xaa Xaa Val Pro Gly His Val Asp  
           35                          40                          45

<210> 893  
 <211> 154  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 893  
 Met Ala Thr Ala Met Asp Trp Leu Pro Trp Ser Leu Leu Leu Phe Ser  
           -20                          -15                          -10  
 Leu Met Cys Glu Thr Ser Ala Phe Tyr Val Pro Gly Val Ala Pro Ile  
           -5                          1                          5  
 Asn Phe His Gln Asn Asp Pro Val Glu Ile Lys Ala Val Lys Leu Thr  
   10                          15                          20                          25  
 Ser Ser Arg Thr Gln Leu Pro Tyr Glu Tyr Tyr Ser Leu Pro Phe Cys  
           30                          35                          40  
 Gln Pro Ser Lys Ile Thr Tyr Lys Ala Glu Asn Leu Gly Glu Val Leu  
           45                          50                          55  
 Arg Gly Asp Arg Ile Val Asn Thr Pro Phe Gln Val Leu Met Asn Ser  
           60                          65                          70  
 Glu Lys Lys Cys Glu Val Leu Cys Ser Gln Ser Asn Lys Pro Val Thr  
           75                          80                          85  
 Leu Thr Val Glu Gln Ser Arg Leu Val Ala Glu Arg Ile Thr Glu Asp  
   90                          95                          100                          105  
 Tyr Tyr Val His Leu Ile Ala Asp Asn Leu Pro Val Ala Thr Gly Trp  
           110                          115                          120  
 Ser Ser Thr Pro Thr Glu Thr Ala Met Thr  
           125                          130

<210> 894  
 <211> 28

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 894

Met	Pro	Ser	Pro	Cys	Leu	Ile	Ser	Leu	Leu	Gln	Cys	Ala	His	Val	Ser
			-15					-10					-5		
Leu	Gly	Leu	Gln	Tyr	Pro	Cys	Xaa	Leu	Leu	Leu	Pro				
	1					5					10				

&lt;210&gt; 895

&lt;211&gt; 53

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 895

Met	Asn	Leu	Ser	Leu	Val	Leu	Ala	Ala	Phe	Cys	Leu	Gly	Ile	Ala	Ser
		-15					-10				-5				
Ala	Val	Pro	Lys	Phe	Asp	Gln	Asn	Leu	Asp	Thr	Lys	Trp	Tyr	Gln	Trp
	1			5					10					15	
Lys	Ala	Thr	His	Arg	Arg	Leu	Tyr	Gly	Ala	Asn	Glu	Glu	Gly	Trp	Arg
			20					25						30	
Arg	Ala	Ala	Trp	Glu											
			35												

&lt;210&gt; 896

&lt;211&gt; 85

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 896

Met	Glu	Phe	Gly	Leu	Asn	Trp	Val	Phe	Leu	Val	Ala	Ile	Phe	Thr	Gly
			-15						-10				-5		
Val	His	Cys	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu	Val	Gln
		1				5					10				
Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Thr	Phe
	15				20					25					
Gly	Asp	Tyr	Ala	Met	Thr	Trp	Phe	Arg	Gln	Ala	Ser	Gly	Lys	Arg	Leu
	30				35					40				45	
Glu	Trp	Leu	Gly	Phe	Ile	Arg	Asn	Arg	Gly	Ser	Gly	Gly	Ser	Ala	Glu
			50					55						60	
Tyr	Gly	Ala	Ser	Val											
			65												

&lt;210&gt; 897

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 897

Met Lys Asn Cys Leu Leu Ile Leu Leu Met Leu Leu Leu Phe Ala Ile  
 -15 -10 -5  
 His Ile Asn Arg Met Asn Val Arg Asn Val Gly Asn Thr Leu Val Val  
 1 5 10 15  
 Val Gln Ile Leu Phe Ser Ile Arg Val Phe Ile Leu Glu Arg Asn Pro  
 20 25 30  
 Leu Asn Val

&lt;210&gt; 898

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 898

Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu Ala Ile Leu Lys Gly  
 -15 -10 -5  
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln  
 1 5 10  
 Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 15 20 25  
 Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 30 35 40 45  
 Glu Trp Val Ser Gly Ile Thr Trp Asn Ser Gly Xaa Ile Gly Tyr Ala  
 50 55 60  
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 65 70 75  
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Phe  
 80 85 90  
 Tyr Phe Cys Ala Lys Ala Arg Gly Leu Phe Ser Asp Thr Trp Pro Tyr  
 95 100 105  
 Xaa His Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val  
 110 115 120 125  
 Ser Ser Ala Ser Thr  
 130

&lt;210&gt; 899

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 899

Met Leu Leu Val Phe Phe Val Leu Trp Thr Cys Ser Leu Ala Leu Leu  
 -10 -5 1  
 Ala Ser Ser Pro Ile Ala Ala Xaa Pro  
 5 10

&lt;210&gt; 900

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19..-1

&lt;400&gt; 900

```

Met Asp Trp Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Asp
      -15                      -10                      -5
Ala Ser Ser Gln Met Gln Leu Leu Gln Ser Gly Pro Glu Val Lys Lys
      1          5          10
Thr Gly Ser Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Asp Thr Leu
      15          20          25
Ala Tyr His Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Ala Leu
      30          35          40          45
Glu Trp Met Gly Trp Ile Thr Pro Phe Ser Gly Asp Thr Asn Phe Ala
      50          55          60
Gln Arg Phe Gln Asp Arg Leu Thr Phe Thr Arg Asp Arg Ser Met Ser
      65          70          75
Thr Val Tyr Met Thr Leu Thr Ser Leu Ile Ser Glu Asp Thr Ala Met
      80          85          90
Tyr Tyr Cys Ala Thr Asp Gly Arg Arg Thr Asn Arg Leu Phe Glu
      95          100          105

```

&lt;210&gt; 901

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18..-1

&lt;400&gt; 901

```

Met Ala Gly Gln Leu Leu Gly Cys Leu Leu Trp Leu Leu Thr His Ile
      -15                      -10                      -5
Lys Ala Gln Asp Ser Val Arg Asp Ala Tyr Trp Lys Thr Gly Ser Cys
      1          5          10
Pro Pro Pro Phe Leu His Val Ser Thr Phe Xaa Xaa Lys Leu Thr Phe
      15          20          25          30
Ser Thr Lys Gly Asn Leu Leu His Ser Ile Pro Leu Ser Ser Pro Leu
      35          40          45
Ala Cys Val Leu
      50

```

&lt;210&gt; 902

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -91..-1

&lt;400&gt; 902

```

Met Lys Glu Ala Val Pro Pro Gly Cys Thr Lys Ser Pro Ser His Phe
      -90          -85          -80
Ser Glu Gly Phe Asp Arg Trp Ala Leu Glu Glu Thr Pro Pro Glu Asn
      -75          -70          -65          -60
Leu Ile Gly Ala Leu Leu Ala Ile Phe Gly His Leu Val Val Ser Ile
      -55          -50          -45
Ala Leu Asn Leu Gln Lys Tyr Cys His Ile Arg Leu Ala Gly Ser Lys
      -40          -35          -30
Asp Pro Arg Ala Tyr Phe Lys Thr Lys Thr Trp Trp Leu Gly Leu Phe
      -25          -20          -15
Leu Met Leu Leu Gly Glu Leu Gly Val Phe Ala Ser Tyr Ala Phe Ala
      -10          -5          1          5

```

Pro Leu Ser Leu Ile Val Pro Leu Ser  
10

<210> 903  
<211> 44  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -18...-1

<400> 903  
Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr  
-15 -10 -5  
Phe Gly Cys Gly Val Pro Ala Ile His Pro Gly Cys Gln Leu Ser Pro  
1 5 10  
Arg Leu Pro Pro Thr Leu Leu Pro Thr Glu Arg Gly  
15 20 25

<210> 904  
<211> 82  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -20...-1

<400> 904  
Met Ala Pro Phe Gln Asn Phe Leu Trp Leu Phe Phe Val Leu Asn Leu  
-20 -15 -10 -5  
Gly Ser Phe Ala Phe Ser Ser Xaa Pro Asn Ser Leu Phe Tyr Thr Ile  
1 5 10  
His Phe Gly Pro Asn Phe Phe Thr Leu Leu Tyr Lys Gln Gly Ala Glu  
15 20 25  
Met Cys Val Tyr Val Phe Asn Phe Leu Tyr Pro Phe Ala Leu Gly Tyr  
30 35 40  
Phe Phe Ser Tyr Asp Ile Leu Asp Leu Pro Val Xaa Val Arg Pro Pro  
45 50 55 60  
Ser Gly

<210> 905  
<211> 54  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -35...-1

<400> 905  
Met Asp Phe Thr Gln Cys His Ser Leu Leu Leu Arg Val Glu Tyr Ser  
-35 -30 -25 -20  
Pro Val Ser Val Cys Phe Leu Leu Leu Ser Val Ala Phe Asn Gln Leu  
-15 -10 -5  
Val Phe Ala Leu Tyr Pro Ile Gln Ala Thr Xaa Cys Phe Ser Xaa Val  
1 5 10  
Ser Leu Pro Phe Pro Ala  
15

<210> 906  
<211> 23

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 906

Met Leu Leu Leu Leu Leu Ala Cys Gly Val Pro Ser Leu Trp Pro Phe  
 -15 -10 -5 1  
 Ala Leu Ala Leu Leu Lys Thr  
 5

&lt;210&gt; 907

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -23...-1

&lt;400&gt; 907

Met Phe Ile Glu Asn Ile Gly Leu Lys Phe Ser Phe Leu Leu Leu His  
 -20 -15 -10  
 Leu Cys Gln Val Leu Leu Ser Arg Arg Ala Gly Thr Ile Pro Thr Glu  
 -5 1 5  
 Thr Ile Pro Lys Lys Leu Arg Arg Arg Asp Gly  
 10 15 20

&lt;210&gt; 908

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 908

Met Gln Asn Arg Thr Gly Leu Ile Leu Cys Ala Xaa Ala Leu Leu Met  
 -20 -15 -10  
 Gly Phe Leu Met Val Cys Leu Gly Ala Phe Phe Ile Ser Trp Gly Ser  
 -5 1 5  
 Ile Phe Asp Cys Gln Gly Ser Leu Ile Ala Ala Tyr Leu Leu Leu Pro  
 10 15 20  
 Leu Gly Phe Val Ile Leu Leu Ser Gly Ile Phe Trp Ser Asn Tyr Arg  
 25 30 35 40  
 Gln Val Thr Glu Ser Lys Gly Val Leu Arg His Met Leu Arg Gln His  
 45 50 55  
 Leu Ala His Gly Ala Leu Pro Val Ala Thr Val Asp Ser Ala Ala Leu  
 60 65 70  
 Leu Lys Ile Met Cys Lys Gln Leu Leu  
 75 80

&lt;210&gt; 909

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -44...-1

&lt;400&gt; 909

```

Met Lys Val Glu Gly Glu Glu Lys Leu Tyr Arg Leu Leu Arg Ser Gly
              -40                      -35                      -30
Asp Leu Phe Lys Phe His Gln Pro His Phe Tyr Glu Leu Ser Gly Leu
              -25                      -20                      -15
Thr Cys Thr Ser Ser Leu Leu Ser Phe Ala Leu Gly Arg Ser Ile Pro
              -10                      -5                      1
Gly Ser Phe Pro
5

```

&lt;210&gt; 910

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 910

```

Met Glu Ser Arg Thr Leu Leu Leu Leu Phe Ser Gly Ala Val Ala Leu
              -15                      -10                      -5
Ile Gln Thr Trp Ala Gly Glu Cys Gly Val Gly Arg Glu Lys Ala Ser
              1                      5                      10
Ala Gly Arg Ser Glu Gly Pro Ala Arg Arg Ser Lys Ser Ala His Ile
              15                      20                      25
Xaa Asn Tyr Arg Leu Gln Leu Gln Ser Arg Gln Gly
30                      35                      40

```

&lt;210&gt; 911

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 911

```

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
              -15                      -10                      -5
Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
1                      5                      10                      15
Asp Lys Leu

```

&lt;210&gt; 912

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 912

```

Met Pro Trp Thr Ile Leu Leu Phe Ala Ala Gly Ser Leu Ala Ile Pro
              -10                      -5                      1
Ala Pro Ser Ile Arg Val Val Pro Pro Tyr Pro Ser Ser Gln Glu Asp
              5                      10                      15
Pro Ile His Ile Ala Cys Met Ala Ala Gly Asn Phe Pro Gly Ala Asn
              20                      25                      30
Phe Thr Leu Tyr

```

35

&lt;210&gt; 913

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -64...-1

&lt;400&gt; 913

```

Met Ala Glu Gly Glu Arg Val Cys Ala Ser Val Val Pro Ser Ala Leu
      -60      -55      -50
Arg Thr Leu Lys Arg Arg Ser Asn Leu Ser Arg Ile Pro Ala Gly Gln
      -45      -40      -35
Glu Lys Glu Gly Lys Ser Arg His Val Ala Pro Pro Phe Arg Phe Phe
      -30      -25      -20
Pro Phe Ser Gly Phe Leu Phe Phe Gly Phe Leu Phe Pro Val Phe Ser
      -15      -10      -5
Phe Pro Ser
1

```

&lt;210&gt; 914

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -13...-1

&lt;400&gt; 914

```

Met Phe Cys Leu Ala Ala Ile Leu Ala Ser Ala Ser Ala Gln Arg Phe
      -10      -5      1
Pro Ser Ala Phe Ser Pro Ser Pro Phe Xaa Trp Leu Xaa Gln Cys Xaa
      5      10      15
Thr Ala Thr Ser Leu Gly Phe Xaa Thr Val Cys Xaa Asn Ser Ile Ile
20      25      30      35
Ser Leu Trp Tyr Leu Xaa Gly Val Pro Pro Glu Val Xaa Glu Leu Pro
      40      45      50
Phe Phe Pro Tyr Cys Ser Met
      55

```

&lt;210&gt; 915

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 915

```

Met Val Asp Gly Thr Leu Leu Leu Leu Leu Ser Glu Ala Leu Ala Leu
      -15      -10      -5
Thr Gln Thr Trp Ala Gly Ser His Ser Xaa Lys Tyr Phe His Thr Ser
      1      5      10      15
Val Ser Arg Xaa Gly Arg Gly Glu Pro Arg Phe Ile Ser Val Gly Tyr
      20      25      30
Val Asp Asp Thr Arg Ser Glu Tyr Trp Asp Arg Glu Thr Arg Ser Ala
      35      40      45
Arg Asp Thr Ala Gln Ile Phe Arg Val Asn Leu Arg Thr Leu Arg Gly

```

50                      55                      60  
 Tyr Tyr Asn Gln Ser Glu Ala Gly Ser Xaa Thr Leu Gln  
      65                      70                      75

<210> 916  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 916  
 Met Asn Phe Arg Gly Pro Gln Thr Phe Ser Leu Ser His Ser Leu Val  
      -25                      -20                      -15  
 Leu Ser Leu Ile Ser Leu Ser Ile Ala Trp Ser Met Val Glu Met Xaa  
      -10                      -5                      1                      5  
 Thr Ser Ala Ser Tyr Lys Gln Lys Phe Ala Leu Arg Ile Leu Val Val  
                          10                      15                      20  
 Gln Leu Pro Thr Trp Val Glu Cys Pro Val Asn His Arg Cys Ala Leu  
                          25                      30                      35  
 Gly Arg Lys Asn Cys Ser Ile Arg Thr Gln Pro  
          40                      45

<210> 917  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 917  
 Met Thr Gly Ile Ser Ile Cys Ser Cys Ile Cys Leu Phe Leu Pro Ser  
      -20                      -15                      -10                      -5  
 Leu Ile His Ser Phe Pro Pro Pro Cys  
                          1                      5

<210> 918  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 918  
 Met Asp Leu Leu Cys Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu  
      -25                      -20                      -15  
 Leu Val Ala Ala Pro Arg Trp Val Gln Leu Gln Glu Ser Gly Pro Arg  
      -10                      -5                      1                      5  
 Leu Val Arg Pro Pro Glu Thr Leu Lys Pro Ser Glu Thr Leu Ser Leu  
                          10                      15                      20  
 Thr Cys Thr Ile Ser Gly Asp Ser Met Ser Ser Ala Ser Tyr Tyr Trp  
                          25                      30                      35  
 Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Phe Ile Gly Arg  
          40                      45                      50  
 Ala Leu Tyr Ser Gly Thr Thr Asp Tyr Asn Pro Ser Leu Ser Ser Arg  
      55                      60                      65                      70  
 Ile Thr

<210> 919  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -45..-1

<400> 919  
 Met Ser Ser Glu Lys Ser Gly Leu Pro Asp Ser Val Pro His Thr Ser  
 -45 -40 -35 -30  
 Pro Pro Pro Tyr Asn Ala Pro Gln Pro Pro Ala Glu Pro Pro Ala Pro  
 -25 -20 -15  
 Pro Leu Ser Leu Ser Leu Cys Leu Ser Leu Cys His Thr His Thr His  
 -10 -5 1  
 Thr His Thr His  
 5

<210> 920  
 <211> 46  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28..-1

<400> 920  
 Met Thr Pro Ala Leu Arg Cys Ala Phe Ala Leu Ala Ile Ala Gly Leu  
 -25 -20 -15  
 Val Ser Leu Leu Met Gln Pro Glu Gly Ala Leu Gly Glu Glu Ala Ala  
 -10 -5 1  
 Ser Ala Ala Ala Gln Gly Arg Gln Leu Ala Glu Leu Arg Leu  
 5 10 15

<210> 921  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -38..-1

<400> 921  
 Met Ser Gly Leu Phe Pro Val Pro Val Arg Val Asn Val Asp Ile Ala  
 -35 -30 -25  
 Gln Asn Ile Thr Cys Ser Ser Phe Ser Leu Leu Leu Ile Phe Leu Ser  
 -20 -15 -10  
 Phe Pro Tyr Thr Leu Cys Ile Leu Tyr Arg Val Lys Ser Tyr Thr Pro  
 -5 1 5 10  
 Thr Glu Ser Ile Thr Ala Phe Asn Leu Thr Ile Gly Xaa Phe Pro Tyr  
 15 20 25  
 Leu Xaa Xaa Ser Thr Pro  
 30

<210> 922  
 <211> 39  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -33...-1

&lt;400&gt; 922

Met Cys Arg Ala Ala Cys Ile Ile Arg Met Ala Val Arg Ile Ser Phe  
                   -30                  -25                  -20  
 Phe Leu Ser Tyr His Ala Leu Ser Leu Cys Leu Cys Thr Cys Ala Phe  
                   -15                  -10                  -5  
 Ala Phe Leu Ser Leu Leu Gly  
       1                              5

&lt;210&gt; 923

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 923

Met Lys Phe Leu Leu Leu Xaa Ala Leu Gly Phe Leu Xaa Gln Val Asn  
                   -15                  -10                  -5  
 Pro Xaa Pro Ile Xaa Gly Gly Ser Lys Met Cys Glu Xaa His Pro Arg  
       1                              5                  10                  15  
 Ile Leu Gln Asp Met Leu Pro Leu Gly Gly Asp Ser Ile Val His Val  
                               20                  25                  30  
 Gln Arg Xaa Gln Lys Met Leu His Gln Leu Leu  
                   35                              40

&lt;210&gt; 924

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -42...-1

&lt;400&gt; 924

Met Val Pro Trp Val Arg Thr Met Gly Gln Lys Leu Lys Gln Arg Leu  
                   -40                  -35                  -30  
 Arg Leu Asp Val Gly Arg Glu Ile Cys Arg Gln Tyr Pro Leu Phe Cys  
                   -25                  -20                  -15  
 Phe Leu Leu Leu Cys Leu Ser Ala Ala Ser Leu Leu Leu Asn Arg Tyr  
                   -10                  -5                  1                  5  
 Ile His Ile Leu Met Ile Phe Trp Ser Phe Val Ala Gly Val Val Thr  
                   10                  15                  20  
 Phe Tyr Cys Ser Leu Gly Pro Asp Ser Leu Leu Pro Asn Ile Phe Phe  
                   25                  30                  35  
 Thr Ile Lys Tyr Lys Pro Lys Gln Leu Gly Leu Gln Glu Leu Phe Pro  
                   40                  45                  50  
 Gln Gly His Ser Cys Ala Val Cys Gly  
 55                              60

&lt;210&gt; 925

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -34...-1

&lt;400&gt; 925

Met Ala Trp Gly Ser Pro Gly Lys Ile Phe Leu Met Gly Phe Leu Gly  
                                   -30                                  -25                                  -20  
 Gly Glu Leu Val Phe Leu Leu Cys Leu Phe Xaa Leu Phe Phe Phe Ser  
                                   -15                                  -10                                  -5  
 Phe Leu Lys Arg Ser Phe Ala Leu Glu Cys Asn  
                   1                                  5

&lt;210&gt; 926

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 926

Met Phe Phe Ser Ile Leu Leu Leu Leu Ala Pro Pro Leu Pro Ser Ala  
                   -15                                  -10                                  -5  
 Val Ser Leu Leu Pro Phe Phe Phe Tyr Cys Val Gln  
   1                                  5                                  10

&lt;210&gt; 927

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -22...-1

&lt;400&gt; 927

Met Val Asp Phe Ile Leu Arg Ser Leu Leu Leu Val Cys Ser Trp Leu  
                   -20                                  -15                                  -10  
 Ser Ile Ser Leu His Ala His Thr Thr Ala Phe Cys Thr Tyr Ser Lys  
                   -5                                  1                                  5                                  10  
 Lys Ile His Thr Val Met Ser Phe Phe Cys  
                                   15                                  20

&lt;210&gt; 928

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 928

Met Arg Ser Leu Leu Tyr Phe Leu Cys Val Ser Ser Tyr Val Thr Ser  
                   -15                                  -10                                  -5  
 Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe  
   1                                  5                                  10

&lt;210&gt; 929

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> SIGNAL  
<222> -15...-1

<400> 929

```

Met Pro Phe Ile Ser Phe Leu Cys Leu Ile Ala Leu Ala Gly Thr Ser
-15          -10          -5          1
Ser Thr Met Leu Arg Ser Ala Leu Ala Gly Thr Ser Ser Thr Met Xaa
          5          10          15
Xaa Arg Ser Gly Xaa Ser Gly Xaa Pro Xaa Leu Val Xaa Val Leu Arg
          20          25          30
Gly Asn Ala Phe Ser Phe Phe Pro Phe Ser Leu Met Xaa Ala Met Gly
          35          40          45
Cys His Arg Trp
50

```

<210> 930

<211> 22

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 930

```

Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser Ser Ser
-15          -10          -5
Arg Ile Leu Leu Val Lys
1          5

```

<210> 931

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 931

```

Met Cys Leu Cys Pro Cys Trp Asp Val Phe Thr Val Phe Val Cys Val
-40          -35          -30
Ser Val Cys Val Ser Val Ser Val Pro Val Gly Met Tyr Leu Val Cys
-25          -20          -15
Val Cys Val Cys Val Cys Val Cys Xaa Cys Xaa Arg
-10          -5          1

```

<210> 932

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34...-1

<400> 932

```

Met Leu Ile Ala Lys Gln Ala Gln Pro Gln Gly Leu Thr Ala Ile Cys
          -30          -25          -20
Phe Pro Leu Thr Pro Leu Phe Ser Leu Leu Met Leu Thr Gln Ser Pro
          -15          -10          -5
Leu Ala Gly Gln Glu Gly Arg Glu Gly Gly Lys Glu Arg Tyr Leu Leu
          1          5          10

```

Val Ile  
15

<210> 933  
<211> 62  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -26...-1

<400> 933  
Met Leu Arg Thr Trp Ser Ser Leu Pro Trp Thr Arg Phe Arg Val Cys  
-25 -20 -15  
Leu Leu Ser Leu Ser Leu Phe Leu Trp Ala Asn Arg Leu Glu Asp Ser  
-10 -5 1 5  
Arg Ser Cys Gln Pro Asn Pro Met Ser Leu Thr Thr Leu Pro Gly His  
10 15 20  
Arg Leu Lys Glu Ala Val Trp Leu Pro Ala Pro Ser Leu Gly  
25 30 35

<210> 934  
<211> 72  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -29...-1

<400> 934  
Met Ala Pro Phe Leu Arg Gln Val Asp Xaa Trp Gly Ala Gln Ala Gly  
-25 -20 -15  
Leu Val Val Xaa Trp Leu Leu Pro Xaa Gln Cys Ser Cys Glu Arg Ser  
-10 -5 1  
Glu Gln Tyr Leu Ser Thr Cys Leu Pro Gln His Ser Ser Ile Lys Gln  
5 10 15  
Ser Cys Ile Lys His Pro Ala Gly Pro Ile Pro Ala Gly His Leu Gln  
20 25 30 35  
Gly Lys Ala Thr Ala Ala Pro Leu  
40

<210> 935  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -19...-1

<400> 935  
Met Glu Phe Gly Leu Lys Trp Leu Phe Leu Val Ala Ile Leu Lys Gly  
-15 -10 -5  
Val Arg Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
1 5 10  
Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Gly Ser Gly Phe Val Phe  
15 20 25  
Asp Lys Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
30 35 40 45  
Gln Trp Val Ala Gly Ile Gly Gly Gly  
50

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<210> 936
<211> 128
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> -16..-1
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<400> 936															
Met	Ala	Leu	Ala	Met	Leu	Val	Leu	Val	Val	Ser	Pro	Trp	Ser	Ala	Ala
	-15					-10					-5				
Arg	Gly	Val	Leu	Arg	Asn	Tyr	Trp	Glu	Arg	Leu	Leu	Arg	Lys	Leu	Pro
1			5						10					15	
Gln	Ser	Arg	Pro	Gly	Phe	Pro	Ser	Pro	Pro	Trp	Gly	Pro	Ala	Leu	Ala
			20					25					30		
Val	Gln	Gly	Pro	Ala	Met	Phe	Thr	Glu	Pro	Ala	Asn	Asp	Thr	Ser	Gly
	35						40					45			
Ser	Lys	Glu	Asn	Ser	Ser	Leu	Leu	Asp	Ser	Ile	Phe	Trp	Met	Ala	Ala
	50					55					60				
Pro	Lys	Asn	Arg	Arg	Thr	Ile	Glu	Val	Asn	Arg	Cys	Arg	Arg	Arg	Asn
65					70					75					80
Pro	Gln	Lys	Leu	Ile	Lys	Val	Lys	Asn	Asn	Ile	Asp	Val	Cys	Pro	Glu
				85					90					95	
Cys	Gly	His	Leu	Lys	Gln	Lys	Xaa	Val	Leu	Cys	Ala	Thr	Ala	Met	Lys
			100					105					110		

```
<210> 937
<211> 30
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -20...-1
```

```

<400> 937
Met Phe Phe Tyr Ser His Phe Leu Leu Leu Phe Pro Leu Ser Leu Leu
-20              -15              -10              -5
Phe Thr Leu Gly Phe Leu Phe Val Phe Phe Phe Phe Phe
      1              5              10

```

```
<210> 938
<211> 101
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -46..-1
```

```

<400> 938
Met Lys Gln Ser Lys Arg Xaa Met Val Lys Arg Arg Arg Ser Pro Ala
  -45                      -40                      -35
Leu Gly Glu Glu Arg Phe Ser Pro Ser Ser Ile Leu His Pro Arg Leu
-30                      -25                      -20                      -15
Pro Leu Val Leu Leu Gly Thr Arg Val Pro Leu Ser Gly Gly Gly Pro
                      -10                      -5                      1
Gly Glu Pro Asp Gln Gly Arg Ser Ala Pro Ser Trp Lys Ser Leu Ala
  5                      10                      15
Ser Thr His Xaa His Ser Arg Pro Ala Ala Gly Ala Thr Pro Ala Arg
  20                      25                      30

```

Pro Ala Thr Gln Ser Gln Leu Gly Pro Phe Ala Pro Pro Leu Pro Gly  
 35 40 45 50  
 Val Arg Pro Ala Pro  
 55

<210> 939  
 <211> 32  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 939  
 Met Leu Leu Glu Ser Leu Cys Val Leu Ser Leu Leu Val Ser Phe Lys  
 -15 -10 -5  
 Ser Ala Cys Leu Thr Arg Glu Pro Ala Phe Asp Ser Gln Ala Arg Pro  
 1 5 10

<210> 940  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -46...-1

<400> 940  
 Met Val Phe Gly Tyr Trp Lys Gln Pro Leu Ile Thr Leu Ala Lys Lys  
 -45 -40 -35  
 Ser Val Lys Cys Ala Arg Glu Cys Leu Arg Cys Ser Leu Arg Pro Leu  
 -30 -25 -20 -15  
 Val Leu Leu Tyr Leu Ser Phe Ala Ala Leu Gly Val Val Ala Leu Arg  
 -10 -5 1  
 Ser Val Glu Ser Pro Leu Ala Glu Thr His Ser Cys Trp Leu Ser Leu  
 5 10 15  
 Gly Met Cys Val Leu Gln Cys Glu Gln Gln Trp Val Pro Thr Pro Val  
 20 25 30  
 Ser Phe Leu Cys Gly Leu Ser Gly Ser Ser Thr Ile Ile Val  
 35 40 45

<210> 941  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<400> 941  
 Met Cys Val Val Cys Ser Val His Gly Val Cys Cys Val Tyr Val Val  
 -20 -15 -10  
 Cys Leu Val Ser Cys Val Leu Cys Val Val Cys Pro Val Cys Trp Val  
 -5 1 5  
 Met Cys Cys Val Trp Cys Ile Cys Val Cys Val Trp Cys Val Cys Cys  
 10 15 20  
 Met Cys Cys Val Leu Ser Cys Val Val Ser His Gly Leu Cys Gly Val  
 25 30 35 40  
 Ser Trp

```
<210> 942
<211> 59
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -19..-1
```

<400> 942

Met	Glu	Leu	Gly	Leu	Ser	Trp	Val	Phe	Leu	Val	Ala	Val	Leu	Glu	Val
				-15					-10					-5	
Val	Gln	Cys	Glu	Ile	Gln	Leu	Ile	Asp	Ala	Gly	Gly	Gly	His	Val	Gln
			1				5					10			
Ala	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Asp	Phe	Leu	Phe
	15					20					25				
Arg	Ser	Tyr	Trp	Met	Thr	Trp	Val	Arg	His	Pro					
30					35				40						

```
<210> 943
<211> 41
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -39..-1
```

```

<400> 943
Met Ser Ile Leu Leu Arg Val Leu Gly Ile Lys Gly Cys Trp Ile Leu
          -35                      -30                      -25
Ser Asn Pro Phe Ser Ala Cys Ile Glu Met Ile Leu Leu Phe Leu Phe
          -20                      -15                      -10
Leu Ile Leu Phe Ile Trp His Ile Arg
      -5                      1

```

```
<210> 944
<211> 27
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -25..-1
```

```

<400> 944
Met Ala Glu Lys Ala Gly Ser Thr Phe Ser His Leu Leu Val Pro Ile
-25                               -20             -15             -10
Leu Leu Leu Ile Gly Trp Ile Val Gly Cys Thr
          -5              1

```

```
<210> 945
<211> 34
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -19..-1
```

<400> 945  
Met Ala Glu Ser Arg Gly Arg Leu Tyr Leu Trp Met Cys Leu Ala Ala  
                  -15                  -10                  -5

Ala Leu Ala Ser Phe Leu Met Gly Phe Met Val Gly Trp Phe Ile Lys  
                   1                  5                  10  
 Pro Leu  
           15

<210> 946  
 <211> 40  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 946  
 Met Leu Thr Ser Leu Pro Phe Leu Leu Pro Thr Ile Ser Phe Leu Leu  
       -25                  -20                  -15  
 Leu Leu Tyr Phe Phe Xaa Ile Ala Val Thr His Pro Ser Val Leu Ile  
       -10                  -5                  1                  5  
 Asn Phe Ser Phe Ser Phe Pro Arg  
                   10

<210> 947  
 <211> 36  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 947  
 Met Arg Lys Asp Val Arg Phe Leu Leu Phe Phe Thr Cys Gly Leu Pro  
       -20                  -15                  -10                  -5  
 Ala Leu His Gly Asp Ser Arg Val Glu Cys Ser Lys Ala His Pro Pro  
                   1                  5                  10  
 Ala Met Tyr Tyr  
           15

<210> 948  
 <211> 48  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 948  
 Met Leu Phe Trp Leu Pro Ser Pro Ser Glu Thr Thr Ser Ala Trp Thr  
       -25                  -20                  -15  
 Leu Leu Ser Ile Ser Leu Ser Val Phe Trp Ser Glu Pro Phe Asn Lys  
       -10                  -5                  1                  5  
 Ser Leu Gly Ser Ser Lys Leu Pro Cys His Phe Phe Ser Ile Lys Arg  
                   10                  15                  20

<210> 949  
 <211> 65  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

&lt;222&gt; -47...-1

&lt;400&gt; 949

Met Pro Val Cys Phe Tyr Ser Leu Ile Cys Phe Phe Ile Tyr Phe Cys  
                   -45                  -40                  -35  
 Leu Leu Ser Pro Arg Glu Thr Ile Glu Glu Val Ala Leu Phe Gln Phe  
                   -30                  -25                  -20  
 Ser Leu Leu Xaa Leu Gly Glu Gly Leu Thr Phe Leu Cys Leu Cys Gln  
                   -15                  -10                  -5                  1  
 Val Met Thr Asn Xaa Met Gln Leu Leu Phe Leu Ser Gly Val Val Cys  
                   5                  10                  15  
 Gly

&lt;210&gt; 950

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -13...-1

&lt;400&gt; 950

Met Ala Pro Leu Leu Leu Ser Leu Ser Cys Ser Phe Ser Cys His Val  
                   -10                  -5                  1  
 Thr Leu Leu Pro Arg  
                   5

&lt;210&gt; 951

&lt;211&gt; 47

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 951

Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn Leu  
                   -20                  -15                  -10                  -5  
 Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu  
                   1                  5                  10  
 Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr Arg Arg  
                   15                  20                  25

&lt;210&gt; 952

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 952

Met Val Phe Trp Glu Ile Ser Val Gln Ile Ile Leu Ile Ser Glu Leu  
                   -20                  -15                  -10  
 Leu Leu Leu Arg Ser Val Thr Ser His Asn Thr Met Met Arg Ala Leu  
                   -5                  1                  5  
 Ser Ser Gln Met Leu Ser Gln Ser Phe Pro Arg Pro Ser Phe Gly Phe  
                   10                  15                  20  
 Ile Ser Lys Ile His Pro Ser His Pro Pro  
                   25                  30

<210> 953  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -51...-1

<400> 953  
 Met Phe Phe Leu Asn Ile Ala Met Phe Ile Val Val Met Val Gln Ile  
           -50                          -45                          -40  
 Cys Gly Arg Asn Gly Lys Arg Ser Asn Arg Thr Leu Arg Glu Glu Val  
           -35                          -30                          -25                          -20  
 Leu Arg Asn Leu Arg Ser Val Val Ser Leu Thr Phe Leu Leu Gly Met  
                                   -15                                  -10                                  -5  
 Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Leu Asn Ile Pro Phe  
                           1                                  5                                  10  
 Met Tyr Leu Phe Ser Ile Phe Asn Ser Leu  
           15                                  20

<210> 954  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17...-1

<400> 954  
 Met Asn Lys His Phe Leu Phe Leu Phe Leu Leu Xaa Xaa Leu Ile Val  
           -15                          -10                          -5  
 Ala Val Thr Ser Leu Gln Cys Ile Thr Cys His Leu Arg Thr Arg Thr  
           1                                  5                                  10                                  15  
 Asp Arg Cys Arg Arg Gly Phe Gly Xaa Cys Thr Ala Gln Lys Gly Glu  
                                   20                                  25                                  30  
 Ala Cys Met Leu Leu Arg Ile His Gln Arg  
                           35                                  40

<210> 955  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -35...-1

<400> 955  
 Met Tyr Ile Lys Met Glu Ser Val Thr Leu Ser Pro Ala Pro Val Phe  
           -35                          -30                          -25                          -20  
 Pro Val Pro Ala Gln Leu Leu Leu Leu Thr Ser His Phe Leu Gly Glu  
                                   -15                                  -10                                  -5  
 Ser Leu Gly Gly Gly Thr Leu Leu Val Pro Leu Leu Pro Pro Gly  
                           1                                  5                                  10

<210> 956  
 <211> 40  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -27...-1

&lt;400&gt; 956

Met Xaa Xaa Ala Leu Leu Arg Ser Arg Met Ile Gln Gly Arg Ile Leu  
           -25                  -20                  -15  
 Leu Leu Thr Ile Cys Ala Ala Gly Ile Xaa Gly Thr Arg Gln Phe Gly  
       -10                  -5                          1                  5  
 Tyr Asn Leu Ser Ile Ile Asn Asp  
                           10

&lt;210&gt; 957

&lt;211&gt; 54

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -47...-1

&lt;400&gt; 957

Met Met Gly Xaa Leu Cys Pro Arg Ser Leu Pro Ile Pro Pro Met Ile  
           -45                  -40                  -35  
 Leu Ser Trp Trp Lys Met Gln Trp Lys Pro Leu Ala Leu Glu Asn Phe  
       -30                  -25                  -20  
 Ser Gly Ser Cys Leu Phe Ser Xaa Ala Trp Leu Xaa Cys Xaa Cys His  
       -15                  -10                  -5                  1  
 Gly Asp Asp Asp Leu Ser  
                           5

&lt;210&gt; 958

&lt;211&gt; 48

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 958

Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Gly Asn Ser Val  
       -15                  -10                  -5                  1  
 Glu Thr Val Arg Gly Gly Gly Arg Thr Trp Ala Trp Gly Arg Lys Thr  
           5                  10                  15  
 Gln Lys Leu Leu Ala His Leu Arg Gly Ile Leu Gly Ala Trp Xaa Arg  
       20                  25                  30

&lt;210&gt; 959

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 959

Met Leu Val Leu Val His Ser Ser Leu Ser Lys Thr Leu Ser Gln Lys  
           -10                  -5                  1  
 Lys Lys Lys Phe Thr Xaa Pro Thr Arg  
       5                  10

<210> 960  
 <211> 48  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 960  
 Met Ser Phe Ser Ser Ala Leu Ile Leu Val Ile Ser Cys Leu Leu Leu  
                           -15                          -10                          -5  
 Ala Phe Glu Cys Val Cys Ser Cys Phe Ser Gly Ser Phe Asn Cys Asp  
                           1                          5                          10  
 Val Arg Val Ser Ile Ser Asp Leu Ser Cys Phe Leu Leu Trp Gly Lys  
           15                          20                          25

<210> 961  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 961  
 Met Gly Phe Trp Cys Gly Cys Pro Phe Cys Leu Xaa Val Phe Leu Leu  
           -20                          -15                          -10  
 Thr Asp Arg Thr Leu Ser Cys Arg Ser Val Gly Val  
           -5                          1                          5

<210> 962  
 <211> 27  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 962  
 Met Val Leu Leu Ser Leu Ser Leu Trp Gly Ile Ser Thr Leu Ser Ser  
           -15                          -10                          -5                          1  
 Thr Thr Ile Glu Leu Ile Tyr Thr Pro Ile Gly  
                           5                          10

<210> 963  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 963  
 Met Ala Ser Leu Leu Ser Gly Phe Thr Ser Phe Cys Leu Leu His Val  
           -25                          -20                          -15                          -10  
 His Ser Phe Leu Pro Pro Val Phe Ser Thr Gln Asn  
                           -5                          1

<210> 964

<211> 42  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -30...-1

<400> 964  
 Met Glu Thr Ala Leu Xaa Xaa Thr Pro Gln Lys Arg Gln Val Met Phe  
 -30 -25 -20 -15  
 Leu Ala Ile Leu Leu Xaa Xaa Trp Glu Ala Gly Ser Glu Ala Val Arg  
 -10 -5 1  
 Tyr Ser Ile Pro Glu Glu Thr Glu Ser Gly  
 5 10

<210> 965  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -35...-1

<400> 965  
 Met Met Leu Asp Phe Ala Leu Ser Pro Arg Leu Glu Arg Ser Gly Leu  
 -35 -30 -25 -20  
 Ile Met Ala Cys Cys Thr Leu Asp Leu Leu Gly Ser Ser Ser Pro Pro  
 -15 -10 -5  
 Thr Ser Ala Ser Gln Val Ala Gly Thr Gly His Val Pro Pro His Pro  
 1 5 10  
 Ala Ser Phe Phe Tyr Phe Xaa Val Xaa Gln Val Tyr Tyr Val Ser Gln  
 15 20 25  
 Leu Ile  
 30

<210> 966  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 966  
 Met Arg Thr Pro Gln Leu Ala Leu Leu Gln Val Phe Phe Leu Val Phe  
 -20 -15 -10  
 Pro Asp Gly Val Arg Pro Gln Pro Ser Ser Ser Pro Ser Gly Ala Val  
 -5 1 5 10  
 Pro Thr Ser Leu Glu Leu Gln Arg Gly Thr Asp Gly Gly Thr Leu Gln  
 15 20 25  
 Ser Pro Ser Glu Ala Thr Ala Thr Arg Pro Ala Val Pro Gly Leu Arg  
 30 35 40

<210> 967  
 <211> 46  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

<222> -21...-1

<400> 967

Met Pro Arg Pro Arg Ala Cys Ala Ser Trp Pro Leu Leu Ala Ala Val  
 -20 -15 -10  
 Ser Gly Leu Arg Gly Leu Glu Trp Pro Pro Ser Trp Arg Arg Val Val  
 -5 1 5 10  
 Ala Ala Val Gly Val Cys Arg Val Arg Asp Trp Gly Pro Arg  
 15 20 25

<210> 968

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 968

Met Asn Gly Ile Phe Leu Leu Leu Ile Ser Val Leu Thr Val Ile Trp  
 -15 -10 -5  
 Phe Trp Lys Thr His Pro Gly  
 1 5

<210> 969

<211> 27

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18...-1

<400> 969

Met Val Phe Leu Val Xaa Leu Leu Cys Ile Ile Xaa Leu Tyr Leu Ile  
 -15 -10 -5  
 Arg Gly Ser Glu Trp Xaa Leu Pro Pro Asn Trp  
 1 5

<210> 970

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18...-1

<400> 970

Met Met Thr Leu Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser  
 -15 -10 -5  
 Trp Ala Leu Phe Trp Ile His Met Asn Phe Arg Arg Ala Phe Phe His  
 1 5 10  
 Leu Arg Trp Phe Asp Ile Asn Ser Thr Glu Ser Val Asn Cys Phe Gly  
 15 20 25 30  
 Gln Tyr Gly Leu Ala  
 35

<210> 971

<211> 37

<212> PRT

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 971

Met Ser Ile Arg Ser Asn Trp Ser Ser Val Glu Ser Lys Ser Arg Ile  
                           -25                          -20                          -15  
 Ser Leu Leu Val Phe Cys Leu Asn Asp Leu Ser Asn Ala Val Xaa Xaa  
                           -10                          -5                          1  
 Gly Ile Glu Xaa Pro  
                           5

&lt;210&gt; 972

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 972

Met Ala Trp Ile Pro Leu Phe Leu Gly Val Leu Ala Tyr Cys Thr Gly  
                           -15                          -10                          -5  
 Ser Val Ala Ser Tyr Glu Leu Thr His Pro Pro Ser Val Ser Val Ser  
 1                          5                          10                          15  
 Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp  
                           20                          25                          30  
 Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu  
                           35                          40                          45  
 Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe  
                           50                          55                          60  
 Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr  
 65                          70                          75                          80  
 Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser  
                           85                          90                          95  
 Thr Val Val Phe Gly Gly Thr  
                           100

&lt;210&gt; 973

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 973

Met Val Cys Val Ile Phe Lys Glu Leu Met Glu Phe Glu Phe Pro Gly  
                           -25                          -20                          -15  
 Phe Cys Phe Xaa Leu Cys Phe Gly Arg Ser Ser Leu Cys Cys Arg Xaa  
                           -10                          -5                          1

&lt;210&gt; 974

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -30...-1

&lt;400&gt; 974

```

Met Glu Ser Ser Gly Thr Pro Ser Val Thr Leu Ile Val Gly Ser Gly
-30          -25          -20          -15
Leu Ser Cys Leu Ala Leu Xaa Thr Leu Ala Val Val Tyr Ala Ala Leu
          -10          -5          1
Trp Arg Tyr Ile Arg Ser Glu Arg Ser Ile Ile Leu Ile Asn Phe Cys
          5          10          15
Leu Ser Ile Ile Ser Ser Asn Ile Leu Ile Leu Val Gly Gln Thr Gln
          20          25          30
Thr His Asn Lys Glu Tyr Leu His Asn His His Cys Ile Phe
35          40          45

```

&lt;210&gt; 975

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -31...-1

&lt;400&gt; 975

```

Met Gly Val Cys Cys Ala Gln Asn Cys Ser Val Ser Gly Xaa Xaa Arg
-30          -25          -20
Asn Ala Leu Xaa Phe Leu Ala Ser Ser Phe Cys Phe Gly Glu Ala Asp
-15          -10          -5          1
Ser Gly Ser Arg Cys Cys Leu Lys Ile Ile Leu Gly Phe Tyr Leu Ile
          5          10          15
Arg Tyr Ser Leu Ile Thr Tyr Gln Val Arg
          20          25

```

&lt;210&gt; 976

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 976

```

Met Lys Ile Leu Tyr Leu Phe Phe Phe Leu Lys Trp Ser His Pro Gly
          -15          -10          -5
Trp Ser Ala Thr Xaa Trp Ser Trp His Thr Ala Thr Ser Ala Ser Leu
          1          5          10
Ile Gln Val Ile Leu Pro Pro Trp
15          20

```

&lt;210&gt; 977

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 977

```

Met Thr Pro Cys Phe Leu Gln Met Asp Asn Leu Thr Pro Leu Phe Leu
-25          -20          -15
Ser Gly Cys Phe Leu Phe Leu Ser Xaa Cys Xaa Ile Tyr Leu Ala Arg
-10          -5          1          5

```

Ile Leu

&lt;210&gt; 978

&lt;211&gt; 48

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -40...-1

&lt;400&gt; 978

Met	Gly	Ser	Ala	Gly	Arg	Leu	His	Tyr	Leu	Xaa	Met	Thr	Ala	Glu	Asn
-40					-35					-30					-25
Pro	Thr	Pro	Gly	Asp	Leu	Ala	Pro	Xaa	Pro	Leu	Ile	Thr	Cys	Lys	Leu
				-20					-15					-10	
Cys	Leu	Cys	Glu	Gln	Ser	Xaa	Gly	Gln	Asp	Asp	His	Thr	Pro	Gly	Met
			-5					1				5			

&lt;210&gt; 979

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -49...-1

&lt;400&gt; 979

Met	Asn	His	Leu	Pro	Pro	Asn	His	Tyr	Arg	Xaa	His	Val	Phe	Thr	Cys
				-45					-40					-35	
His	Val	Asp	Gln	Tyr	Leu	Thr	Val	Glu	Thr	Ala	Gly	Gly	Met	Glu	Lys
			-30					-25					-20		
Glu	Ala	Val	Ser	Val	Thr	Val	Leu	Leu	Ser	Ala	Ala	Pro	Cys	Leu	Leu
			-15				-10					-5			
Ser	Cys	Phe	Leu	Gly	Ser	Ser	Val	Ser	Gly	Leu	Ala	Phe	Trp	Val	Ser
	1				5					10				15	
Gln	Gln	Lys	Thr	Lys	Gly	Pro	Glu	Arg	Cys	Lys	Asn	Thr	His	His	Xaa
				20					25					30	
Ala	Xaa	Asn	Asn	Phe	Pro	Ala	Arg								
				35											

&lt;210&gt; 980

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -40...-1

&lt;400&gt; 980

Met	Asn	Lys	Ile	Lys	Glu	Asn	Thr	His	Thr	His	Thr	His	Thr	His	Thr
-40					-35					-30					-25
His	Lys	Asn	Asn	Thr	Lys	Leu	Val	Ser	Asn	Leu	Phe	Leu	Phe	Met	Leu
				-20					-15					-10	
Pro	Leu	Trp	Cys	Ser	Ile	Gly	Thr	Cys	Thr						
			-5					1							

&lt;210&gt; 981

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -42...-1

&lt;400&gt; 981

Met His Asp Ser Ser Gly Lys Asn Asn Phe Arg Lys Ile Pro Val Val  
                   -40                  -35                  -30  
 Asn Leu Ile Tyr Leu Tyr Val Asp Ile His Ile His Lys Leu Phe Leu  
                   -25                  -20                  -15  
 Tyr Ser Leu Phe Thr Glu Asn Val Leu Ala His Pro Cys Ile Val Leu  
                   -10                  -5                  1                  5  
 Arg Arg Leu

&lt;210&gt; 982

&lt;211&gt; 37

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -33...-1

&lt;400&gt; 982

Met Gly Arg Leu His Arg Pro Arg Ser Ser Thr Ser Tyr Arg Asn Leu  
                   -30                  -25                  -20  
 Pro His Leu Phe Leu Phe Phe Leu Phe Val Gly Pro Phe Ser Cys Leu  
                   -15                  -10                  -5  
 Gly Ser Tyr Ser Arg  
                   1

&lt;210&gt; 983

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -27...-1

&lt;400&gt; 983

Met Gln Ser Gln Ala Ala Arg Glu His Lys Pro Gly Xaa Ser Arg Leu  
                   -25                  -20                  -15  
 Leu Leu Leu Leu Leu Leu Xaa Leu Pro Leu Pro Pro Xaa Leu Arg  
                   -10                  -5                  1                  5  
 Thr Arg Xaa Phe Ser Xaa Thr Thr Leu Thr Ala Gly  
                   10                  15

&lt;210&gt; 984

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 984

Met Arg Leu Trp Ser Leu Ala Cys Leu Ser Pro Pro Ala Val Gln Leu  
                   -15                  -10                  -5                  1  
 Gly Ser Gln Gln Ala Thr Asp Trp Trp  
                   5                  10

<210> 985  
 <211> 32  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 985  
 Met Ser Pro Leu Phe Ile Leu Ile Val Leu Ile Trp Ile Phe Ser Phe  
 -25 -20 -15 -10  
 Phe Phe Phe Ile Thr Leu Val Arg Gly Ser Ile Asn Leu Phe Phe Phe  
 -5 1 5

<210> 986  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 986  
 Met Asn Leu Gly Gly His Ser Asp His Ser Thr Phe Leu Phe Phe Leu  
 -20 -15 -10  
 Phe Phe Ser Val Phe Cys Phe Phe Phe  
 -5 1

<210> 987  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 987  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val  
 -20 -15 -10  
 Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile  
 -5 1 5 10  
 Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile  
 15 20 25  
 Val Asn Ser Gly Ser Leu His Glu Xaa Leu Val Asn Leu His Glu Arg  
 30 35 40  
 Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser  
 45 50 55  
 Leu Gly Thr Val Asp Val Leu Lys Gln His Arg  
 60 65 70

<210> 988  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 988

490

Met Ala His Cys Ser Leu Glu Leu Leu Gly Ser Ser Ser Pro Pro Ile  
                   -15                  -10                  -5  
 Ser Ala Ser Gln Ser Thr Gly Ile Thr Ser Val Ser  
           1                  5                  10

&lt;210&gt; 989

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17..-1

&lt;400&gt; 989

Met Pro Ser Gln Leu Leu Leu Leu Ser Leu Ser Leu Phe Leu Phe Phe  
                   -15                  -10                  -5  
 Trp Arg Gln Ser Leu Val Leu Trp Pro Arg Leu Glu Cys Ser Cys Val  
           1                  5                  10                  15  
 Ile Ala Ala His Cys Ser Leu Thr Ser Gln Ala Arg  
                   20                  25

&lt;210&gt; 990

&lt;211&gt; 83

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -46..-1

&lt;400&gt; 990

Met Tyr Thr Asn Lys Tyr Thr Leu Ile Tyr Asn Ile Leu Ile Tyr Asn  
           -45                  -40                  -35  
 Ile Cys Xaa Xaa Tyr Met Trp Leu Ile Leu Ile Tyr Met Tyr Leu His  
           -30                  -25                  -20                  -15  
 Ile Cys Leu Phe Cys Cys Xaa Phe Ile Ser Ser Cys Asn Ser Val Phe  
                   -10                  -5                  1  
 Pro Cys Val Ile Xaa Phe Leu Leu Pro Glu Glu Leu Leu Xaa Val Xaa  
           5                  10                  15  
 Leu Xaa Xaa Xaa Phe Xaa Val Arg Trp Ser Leu Xaa Xaa Ser Ser Arg  
           20                  25                  30  
 Leu Glu Cys  
 35

&lt;210&gt; 991

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -31..-1

&lt;400&gt; 991

Met Leu Leu Thr His Asn Glu Asp Tyr Met Pro Gly Asn Xaa Xaa Xaa  
           -30                  -25                  -20  
 Xaa Xaa Leu Trp Ser Leu Ile Gln Ala Val His Ile Cys Leu Gly Arg  
           -15                  -10                  -5                  1  
 Lys Lys Lys

&lt;210&gt; 992

&lt;211&gt; 89

<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -19...-1

<400> 992  
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly  
                  -15                  -10                  -5  
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys  
                  1                  5                  10  
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
          15                  20                  25  
Ser Asp Tyr Xaa Xaa Thr Xaa Ile Arg Xaa Ala Xaa Gly Lys Gly Leu  
30                  35                  40                  45  
Xaa Trp Ile Xaa Xaa Ile Thr Thr Ser Gly Asn Thr Ala Xaa Tyr Ala  
                  50                  55                  60  
Xaa Ser Val Lys Xaa Arg Phe Thr Ile  
                  65                  70

<210> 993  
<211> 55  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -17...-1

<400> 993  
Met Lys Arg Phe Phe Leu Phe Val Cys Leu Xaa Phe Asp Glu Ser Cys  
                  -15                  -10                  -5  
Ser Val Thr Arg Leu Gly Cys Cys Gly Ala Ile Ser Ala His Cys Xaa  
          1                  5                  10                  15  
Leu Arg Leu Pro Gly Ser Ser Xaa Xaa Pro Ala Ser Thr Ser Arg Val  
                  20                  25                  30  
Xaa Gly Ile Thr Gly Met Arg  
                  35

<210> 994  
<211> 40  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -38...-1

<400> 994  
Met Ser Cys His Ser Leu Leu Ala Cys Lys Val Phe Thr Glu Lys Ser  
                  -35                  -30                  -25  
Pro Thr Lys His Ile Arg Glu His His Cys Met Leu Phe Val Ser Phe  
                  -20                  -15                  -10  
Leu Leu Leu Leu Leu Gly Ser Arg  
          -5                  1

<210> 995  
<211> 50  
<212> PRT  
<213> Homo sapiens

<220>

<221> SIGNAL  
<222> -26...-1

<400> 995

Met Thr Ser Ser Val His Leu Leu Val Phe Lys Asp His Leu Leu Ser  
-25 -20 -15  
Met Leu Ser Cys Cys Gln Gly Ala Cys Cys Pro Ser Thr Pro His Glu  
-10 -5 1 5  
Gly Thr Arg Ser Thr Val Ser Trp Ile Pro Pro Thr Tyr Lys Ala Ala  
10 15 20  
Thr Gln

<210> 996

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 996

Met Val Arg Ala Ser Ile Leu Leu Ser Met Phe Cys Val Ser His Thr  
-15 -10 -5  
Val Gln Thr Ala Thr Tyr Thr  
1

<210> 997

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 997

Met Glu Lys Thr Ala Leu Ser Ser Phe Thr Trp Trp Ala Pro Ala Cys  
-15 -10 -5  
Cys Ala Pro Arg Thr Tyr Val Val Ser Ala Thr Thr Leu Ser Ala Val  
1 5 10 15  
Gln Gly His Cys Pro Leu Gln Ser Arg Thr Ser Thr Lys Gly Lys Leu  
20 25 30  
Trp Pro Phe Gly  
35

<210> 998

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 998

Met Ile Phe Thr Phe Gln Gln Ile Gly Gly Lys Leu Leu Leu Ser Gly  
-20 -15 -10  
Leu Thr Gln Glu Cys Leu Gly Ala Leu Pro Glu Ala Asn Val Phe Cys  
-5 1 5  
Arg Gly Gly Cys Thr Ala Thr Val Leu Lys His Gly Lys Ala Ser Pro  
10 15 20 25  
Glu Ser

<210> 999  
 <211> 46  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 999  
 Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr  
           -30                  -25                  -20  
 Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu  
           -15                  -10                  -5                  1  
 Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met  
                   5                  10                  15

<210> 1000  
 <211> 44  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -40...-1

<400> 1000  
 Met Ile Trp Leu Ser Phe Cys Leu Leu Leu Val Tyr Arg Asn Ala Cys  
           -40                  -35                  -30                  -25  
 Asp Phe Cys Thr Leu Thr Leu Tyr Pro Gly Thr Leu Leu Lys Leu Leu  
                   -20                  -15                  -10  
 Ile Ser Leu Arg Ser Phe Trp Ala Glu Thr Thr Gly  
                   -5                  1

<210> 1001  
 <211> 43  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 1001  
 Met Phe Ser Ser Pro Gly Leu Arg Thr Leu Phe Val Leu Val Gly Ser  
           -25                  -20                  -15                  -10  
 Leu His Leu Phe Leu Ser Val Leu Ala Ser Lys Ser Arg Asn Ser Lys  
                   -5                  1                  5  
 Lys Gln Arg Leu Phe Leu Leu Val Pro Leu Tyr  
           10                  15

<210> 1002  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 1002  
 Met Leu Thr Asp Gly Ile Leu Met Arg Val Asn Val Cys Ser Leu Pro

[illegible]

```
<210> 1003
<211> 49
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -33...-1
```

```

<400> 1003
Met Phe Asn Trp Asn Pro Trp Leu Thr Thr Leu Ile Thr Gly Xaa Ala
      -30                      -25                      -20
Gly Pro Leu Leu Ile Leu Leu Leu Ser Leu Ile Phe Gly Pro Cys Ile
      -15                      -10                      -5
Leu Asn Ser Phe Leu Asn Xaa Ile Lys Gln Arg Ile Ala Ser Gly Lys
      1                      5                      10                      15
Arg

```

```
<210> 1004
<211> 102
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -29..-1
```

```

<400> 1004
Met Ala Gly Ser Arg Gln Arg Gly Leu Arg Ala Arg Val Arg Pro Leu
-25 -20 -15
Phe Cys Ala Leu Leu Ser Leu Xaa Xaa Xaa Pro Xaa Xaa Arg
-10 -5 1
Arg Xaa Arg Arg Pro Arg Gly Arg Val Ala Thr Ser Pro Phe Arg Val
5 10 15
Xaa Ile Gln Leu Gln Gly Ala Ala Pro Gly Ala Glu Arg Arg Asp Arg
20 25 30 35
Ala Leu Leu Gly Pro Arg Gly Glu Cys Tyr Ser Lys Phe Arg Ser Asn
40 45 50
Ser Ser Ser Thr Ile Phe Lys Lys Xaa Lys Arg Leu Ser Val Xaa Xaa
55 60 65
Asp Xaa Ser Gly Pro Gly
70

```

```
<210> 1005
<211> 96
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -19..-1
```

```
<400> 1005
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly
      -15                      -10                      -5
Val His Cys Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
```

```

      1           5           10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Leu
  15           20           25
Ser Asn Asp Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
  30           35           40           45
Val Trp Val Ser His Ile Asp Ser Ser Xaa Thr Ile Thr Asn Tyr Ala
      50           55           60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Trp
      65           70           75

```

<210> 1006  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

```

<400> 1006
Met Gly Leu Phe Leu Gly Phe Leu Ala Cys Ser Val Ala Tyr Gln Cys
-15           -10           -5           1
His Ser Ala Phe Val Thr Val Ala Ser Gln Tyr Thr Leu Lys Ser Glu
      5           10           15
Thr Leu Met Pro Ala Ala
      20

```

<210> 1007  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -49...-1

```

<400> 1007
Met Trp Glu Asp Ser Arg Asn Lys Arg Gly Gly Arg Trp Leu Val Ser
      -45           -40           -35
Leu Ala Lys Gln Gln Arg His Ile Glu Leu Asp Arg Leu Trp Leu Glu
      -30           -25           -20
Thr Phe Ser Val Phe Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala Thr
      -15           -10           -5
Gly Ile Leu Ala Phe Val Phe Lys Asp Trp Ile Arg Asp Gln Leu Asn
      1           5           10           15
Leu Phe Ile Asn Asn Asn Val Lys Ala Tyr Arg Asp Asp Ile Asp Leu
      20           25           30
Gln Xaa Leu Ile Asp Phe Ala Gln Glu Tyr Trp Ser Cys Cys Gly Xaa
      35           40           45
Glu Ala Pro Ile Xaa Gly Thr Gly
      50           55

```

<210> 1008  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

```

<400> 1008
Met Phe Leu Ser Leu Ser Thr Ala Phe Trp Val Val Tyr Ala Met Ile

```

496

Ile Tyr Ser Ala Leu Ser Ala Gly Phe Ile Ile Phe Phe Leu Val Val  
                   -10                  -5                  1  
                   5                  10                  15  
 Phe Asn  
       20

<210> 1009  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400> 1009  
 Met Tyr Ile Val Met Asp Leu Pro Leu Trp Leu Ser His Glu Val Gln  
                   -30                  -25                  -20  
 Ser Tyr Ile Pro Ser Phe Phe Leu Phe Phe Cys Phe Glu Thr Gly Ser  
                   -15                  -10                  -5  
 His Ser Val Thr His Gly  
           1

<210> 1010  
 <211> 54  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 1010  
 Met Val Ala His Asp Tyr Gln Asn Ile Ile Ser Leu Phe Phe Leu Ala  
                   -25                  -20                  -15  
 Phe Ser Phe Ser Phe Phe Pro Ser Ser Phe Ser Ser Phe Phe Leu Xaa  
                   -10                  -5                  1                  5  
 Phe Leu Ser Phe Phe Ser Ser Phe Phe Leu Ser Leu Leu Ser Phe Pro  
                   10                  15                  20  
 Ser Phe Leu Pro Pro Gly  
                   25

<210> 1011  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 1011  
 Met Ala Ala Leu Arg Ala Leu Cys Gly Phe Arg Gly Val Ala Ala Gln  
                   -15                  -10                  -5                  1  
 Val Leu Arg Xaa Gly Ala Gly Val Arg Leu Pro Ile Gln Pro Ser Arg  
                   5                  10                  15  
 Gly Val Arg Gln Trp Gln Pro Asp Val Glu Trp Ala Gln Gln Phe Gly  
                   20                  25                  30  
 Gly Ala Val Met Tyr Pro Ser Lys Glu Thr Ala His Trp Lys Pro Pro  
                   35                  40                  45  
 Pro Trp Asn Asp Val Asp Pro Pro Lys Asp Thr Ile Val Lys Asn Ile  
                   50                  55                  60                  65  
 Thr Leu Asn Phe Gly Pro Gln His Pro Ala Ala His Gly Val Leu Arg

497

70 75 80  
 Leu Val Met Glu Leu Ser Gly Glu Met Val Arg Lys Cys Asp Pro His  
 85 90 95  
 Ile Gly Leu Leu His Arg Gly Thr Glu Lys Leu Ile Glu Tyr Lys Xaa  
 100 105 110  
 Tyr Leu Gln Ala Leu Pro Tyr Phe  
 115 120

<210> 1012  
 <211> 50  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 1012  
 Met Leu Ile Trp Ser Ser Ser Ser Phe Pro Ala Pro Pro Leu Phe Leu  
 -25 -20 -15  
 Val Phe Leu His Leu Phe Leu Xaa Val Tyr Leu Gly Leu Val Met Pro  
 -10 -5 1  
 Thr Gln Gln Tyr Leu Leu Leu Gln Ser Pro Leu Met Phe Thr Asp Lys  
 5 10 15 20  
 Ala Gln

<210> 1013  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -46...-1

<400> 1013  
 Met Cys Arg Met Cys Arg Phe Val Thr Trp Ile Asn Val Cys His Gly  
 -45 -40 -35  
 Asp Leu Leu His Arg Ser Ser Arg Arg Leu Gly Val Lys Pro Ser Thr  
 -30 -25 -20 -15  
 His Trp Leu Phe Phe Leu Met Leu Ser Leu Cys Thr Pro Pro Asp Arg  
 -10 -5 1  
 Pro Trp Cys Val Leu Phe Pro Pro Leu  
 5 10

<210> 1014  
 <211> 40  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 1014  
 Met Xaa Thr Gln Glu Ala Gly Leu Ile Phe Phe Ser Pro Pro Phe Ser  
 -30 -25 -20  
 Leu Ser Leu Ser Leu Ser Leu Pro Leu Ser Leu Xaa Leu Leu Xaa Xaa  
 -15 -10 -5 1  
 Pro His Ser Arg Thr Pro Gln Arg  
 5

<210> 1015

<211> 43  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -13...-1

<400> 1015  
 Met Glu Phe Leu Leu Trp Ser Leu Xaa Ser Asn Gly Lys Arg Gly  
                   -10                  -5                  1  
 Gln Ala Trp Arg Leu Met Pro Val Val Pro Ala Val Trp Glu Pro Glu  
       5                  10                  15  
 Ala Gly Gly Leu Leu Gln Leu Gly Gly Ser Arg  
 20                  25                  30

<210> 1016  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -37...-1

<400> 1016  
 Met Met Val Thr Tyr Arg Trp Gly Phe Gly Val Asp Val Xaa Phe Val  
           -35                  -30                  -25  
 Ala Val Asp Ala Ile Pro Phe Cys Leu Leu Val Phe Phe Leu Ile Val  
       -20                  -15                  -10  
 Arg Thr Leu Ser Cys Arg Ser Val Gly Val Cys Trp Arg Ser Thr Pro  
       -5                  1                  5                  10  
 Asp Pro Val Cys Leu Gly Ile Thr Ser Arg Gly Cys Arg Thr Glu Ile  
           15                  20                  25  
 Leu Gln Asn Ser Lys Cys Cys Ser Leu Ile Leu Pro Leu Glu Ala Ser  
           30                  35                  40  
 Ser Gln Arg Gly Thr Glu Cys Met  
       45                  50

<210> 1017  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 1017  
 Met Leu Tyr Pro Leu Pro Glu Ile Phe Leu Pro Phe Ser Leu Ser Pro  
                   -15                  -10                  -5  
 Ala Asn Ala Gln Ser Lys Phe Ser Leu Tyr Phe Phe Pro Leu Val Lys  
           1                  5                  10  
 Pro Gly  
 15

<210> 1018  
 <211> 48  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

&lt;222&gt; -27...-1

&lt;400&gt; 1018

Met Ser Leu Glu Pro Ala Ser Xaa Leu Leu Gly Val Arg Arg Arg Leu  
           -25                  -20                  -15  
 Leu Cys Leu Xaa Phe Xaa Arg Leu Leu Leu Gly Thr Ser Leu Leu Lys  
           -10                  -5                  1                  5  
 Phe Val Xaa Ser Xaa Ser Pro Pro Xaa Pro Xaa Thr Leu Thr Ser Ser  
                           10                          15                          20

&lt;210&gt; 1019

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 1019

Met Leu Ile Leu Tyr Leu Ala Thr Leu Leu Asn Leu Ser Val Leu Ile  
                           -20                          -15                          -10  
 Leu Cys Val Cys Val Cys Val Cys Val Tyr Asp Leu Tyr Ile Xaa Arg  
                           -5                          1                          5  
 Gly

&lt;210&gt; 1020

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 1020

Met Ala Pro Leu Gly Thr Thr Val Leu Leu Trp Ser Leu Leu Arg Ser  
           -15                  -10                  -5  
 Ser Pro Gly Val Glu Arg Val Cys Phe Arg Ala Arg Ile Gln Pro Trp  
 1                          5                          10                          15  
 His Gly Gly Leu Leu Gln Pro Leu Pro Cys Ser Phe Glu Met Gly Leu  
                           20                          25                          30  
 Pro Arg Arg Arg Phe Ser Ser Glu Ala Ala Glu Ser Gly Ser Pro Glu  
           35                          40                          45  
 Thr Lys Lys Pro Thr Phe Met Asp Glu Glu Val Gln Ser Ile Leu Thr  
           50                          55                          60  
 Lys Met Thr Gly Leu Asn Leu Gln Lys Thr Phe Lys Pro Ala Ile Gln  
 65                          70                          75                          80  
 Glu Leu Lys Pro Pro Thr Tyr Lys Leu Met Xaa Gln Ala Gln Leu Glu  
                           85                          90                          95  
 Glu Ala Thr Arg Gln  
                           100

&lt;210&gt; 1021

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -34...-1

&lt;400&gt; 1021

500

Met Leu Leu Thr Phe Ser Ser Ser Ser Arg His Arg Arg Leu Tyr Arg  
                   -30                  -25                  -20  
 Arg Arg Arg His His Leu Leu Phe Val Val Leu Leu Pro Pro Pro Pro  
                   -15                  -10                  -5  
 Gly Ser Val Xaa Leu Cys Ser Xaa Xaa Xaa Xaa Val Leu Xaa Xaa  
           1                  5                  10  
 Xaa Lys Phe Arg Xaa Gly Leu His Gly Ala Met Leu Pro Gly Leu Phe  
 15                  20                  25                  30  
 Arg Gly Arg Pro Arg Ala Ala Leu Arg Leu Arg Val Ser Pro Xaa Cys  
                   35                  40                  45  
 Pro Gly Trp Lys Val Ala Arg Ser Arg Leu Thr Ala Thr Ser Ala Ser  
           50                  55                  60  
 Arg Xaa Arg  
           65

&lt;210&gt; 1022

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -13...-1

&lt;400&gt; 1022

Met Leu Leu Leu Leu Gln Leu Asn Leu Lys Thr Leu Ser Ser Ser Thr  
                   -10                  -5                  1  
 Ile Ala Leu Lys Lys Ile Ser Gly Glu Leu Leu Arg Lys Arg Lys Arg  
   5                  10                  15

&lt;210&gt; 1023

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1023

Met Ser Leu Phe Val Leu Leu Ile Ile Thr Gln Leu Leu Tyr Gly Gly  
 -15                  -10                  -5                  1  
 Ile Leu

&lt;210&gt; 1024

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -28...-1

&lt;400&gt; 1024

Met Asn Cys Phe Cys Asn Phe Val Lys Thr Ser Glu Ala Tyr Met Ile  
                   -25                  -20                  -15  
 Leu Phe Leu Gly Val Leu Leu Ser Ala Ser Asp Leu Cys Val Tyr Pro  
                   -10                  -5                  1  
 Ile Gly  
 5

&lt;210&gt; 1025

&lt;211&gt; 33

<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -14...-1

<400> 1025  
Met Ser Val Ile Leu Ala Leu Trp Glu Ala Glu Ala Gly Gly Ser Pro  
                    -10                    -5                    1  
Glu Ile Gly Ser Ser Gly Pro Ala Ala Pro Thr Trp Arg Ser Pro Val  
          5                          10                          15  
Gln

<210> 1026  
<211> 61  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -29...-1

<400> 1026  
Met Tyr Gly Glu Ser Thr Leu Phe Ile His Ser Ser Val His Gly His  
                    -25                    -20                    -15  
Leu Gly Cys Leu Leu Ala Val Arg Ser Ser Ala Thr Val Asn Ile  
                    -10                    -5                    1  
Thr Tyr Xaa Xaa Val Cys Val Asp Ile Xaa Xaa His Phe His Met Leu  
          5                          10                          15  
Met Ser Gly Ile Thr Gly Ser Tyr Gly Asn Ser Leu Ser  
20                          25                          30

<210> 1027  
<211> 74  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -51...-1

<400> 1027  
Met Ala Ala Ser Val Leu Asn Thr Val Leu Arg Arg Leu Pro Met Leu  
          -50                    -45                    -40  
Ser Leu Phe Arg Gly Ser His Arg Val Gln Val Thr Leu Arg Lys Thr  
-35                    -30                    -25                    -20  
Phe Cys Thr Thr Ser Ser Trp Leu Tyr Leu Leu Glu Val Val Ala Pro  
                    -15                    -10                    -5  
Leu Ser Gly Ile His Glu Trp Arg Pro Ser His Val Cys Leu Ser Cys  
          1                          5                          10  
Leu Gly Ser Thr Ser Cys Asn Pro Pro Glu  
15                          20

<210> 1028  
<211> 84  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -65...-1

&lt;400&gt; 1028

Met Leu Arg Ser Ala Cys Val Ser Gln His Ala Gly Gly Ile Trp Val  
 -65 -60 -55 -50  
 Asp Arg Gly Gly Pro Gln Cys Gln Arg Val Phe Thr Phe Cys Arg Gly  
 -45 -40 -35  
 Leu Ser Pro Asn Phe Gly Arg Ser Glu Thr Gln Arg Glu Arg Trp Ile  
 -30 -25 -20  
 Arg Pro Gly Gln Leu Met Val Val Ala Glu Thr Ser Gln Gly Ser Trp  
 -15 -10 -5  
 Ser Ala Pro Thr Ser Pro Xaa Thr Ser Cys Pro Pro Pro Asn Thr Xaa  
 1 5 10 15  
 Thr Thr Pro Xaa

&lt;210&gt; 1029

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -45..-1

&lt;400&gt; 1029

Met Val Ser Arg Ser Leu Arg Gly Arg Arg Thr Trp Val Arg Cys Met  
 -45 -40 -35 -30  
 Arg Arg Leu Pro Pro Ile Pro Ala Trp Ser Gln Gly Lys Gly Met Pro  
 -25 -20 -15  
 Gly Phe Val Ser Leu Leu Val Val His Ala Ala Asp Ala Trp Val Ala  
 -10 -5 1  
 Gln Arg Leu Ser Thr Pro Tyr Phe Ser Leu Phe Leu Ser Ile Pro Arg  
 5 10 15  
 Cys Ser Phe Pro Arg Arg Ser Ile Asp Arg Thr Cys Ser Ser Xaa Leu  
 20 25 30 35  
 Asp Ser Glu Gly Ser Ser Ser Ile Xaa Pro Ser Thr Pro Phe  
 40 45

&lt;210&gt; 1030

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -21..-1

&lt;400&gt; 1030

Met Val Gly Ala Leu Pro Pro Ala Ser Leu Leu Pro Cys Ser Leu Ile  
 -20 -15 -10  
 Ser Asp Cys Cys Ala Ser Asn Glu Arg Gly Ser Met Gly Val Gly Pro  
 -5 1 5 10  
 Ser Glu Pro Arg Arg Gly  
 15

&lt;210&gt; 1031

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20..-1

&lt;400&gt; 1031

Met Arg Met Thr Lys Asp Pro Leu Gly Ser Leu Ile Ala Ser Leu Ala  
 -20 -15 -10 -5  
 Pro Ser Thr Gly Leu Gly  
 1

<210> 1032  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 1032  
 Met Lys Leu Gln Phe Ala Phe Cys Tyr Phe Leu Tyr Leu Asp Thr Phe  
 -25 -20 -15  
 Phe Leu Phe Leu Phe Phe Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Gly  
 -10 -5 1  
 Arg Ser Ala Val Ala Xaa Pro Gln Leu Xaa Ala Ala Ser Thr Phe Xaa  
 5 10 15 20  
 Phe Gln Ala Ile Phe Leu Pro Gln Xaa  
 25

<210> 1033  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -69...-1

<400> 1033  
 Met Ala Ala Gly Glu Leu Glu Gly Gly Lys Pro Leu Ser Gly Leu Leu  
 -65 -60 -55  
 Asn Ala Leu Ala Gln Asp Thr Phe His Gly Tyr Pro Gly Ile Thr Glu  
 -50 -45 -40  
 Glu Leu Leu Arg Ser Gln Leu Tyr Pro Glu Val Pro Pro Glu Glu Phe  
 -35 -30 -25  
 His Pro Phe Leu Ala Lys Met Arg Gly Ile Leu Lys Val Leu Leu Phe  
 -20 -15 -10  
 Ser Val Val Ser Gly Leu Glu Gln Asn Pro Leu Ala Ala Gly Phe Arg  
 -5 1 5 10  
 Leu Ser His Pro  
 15

<210> 1034  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 1034  
 Met Met Met Ser Asn Val Met Leu Met Leu Gln Leu Gln Pro Leu Leu  
 -30 -25 -20  
 Ala Xaa Ser Leu Ile Leu Ser Pro Ser Pro Arg Pro Val Leu Gly Phe  
 -15 -10 -5 1  
 Phe Arg Gln Val His Leu Leu Thr Arg Ser His Phe Ser Arg Trp  
 5 10 15

<210> 1035  
 <211> 37  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 1035  
 Met Ile Ile Leu Ile Asn Gln Leu Leu Phe Ile Cys Pro Pro Pro Pro  
 -20 -15 -10 -5  
 Pro Ile Ser Ala Ser Ser Asn Tyr His Phe Thr Leu Tyr Leu His Asp  
 1 5 10  
 Ile Asn Phe Phe Ser  
 15

<210> 1036  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 1036  
 Met Thr Asp Val Leu Leu Gln Leu Leu Leu Arg Val Cys Ser Pro Arg  
 -15 -10 -5 1  
 Thr Arg

<210> 1037  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -13...-1

<400> 1037  
 Met Gly Leu Phe Leu Cys Cys Ser Leu Leu Ile Phe Cys Leu Val Val  
 -10 -5 1  
 Leu Ile Ile Thr Glu Leu Gly Tyr Gly  
 5 10

<210> 1038  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1038  
 Met Gly Ser Trp Ala Leu Thr Trp Leu His Pro Ala Glu Ala Gly Thr  
 -10 -5 1  
 Arg Val Pro Phe Cys Ser Trp Glu Lys Ser Asp Gly Arg Ser  
 5 10 15

<210> 1039

<211> 65  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -42...-1

<400> 1039  
 Met Met Leu Xaa Xaa Xaa Arg Gly Tyr Pro His Arg Thr Glu Arg Tyr  
                   -40                  -35                  -30  
 Asp Gly Phe Leu Lys Tyr Ser Asp Pro Asn Asp Ile Ala Leu Ser Val  
                   -25                  -20                  -15  
 Leu Ser Leu Val Ile Asn Phe Ser Trp Ser Arg Lys Cys Phe Val Pro  
                   -10                  -5                  1                  5  
 Tyr Tyr Ile Pro Phe Lys Pro Tyr Arg Xaa Pro Tyr Pro Thr Ala Ala  
                   10                  15                  20  
 Arg

<210> 1040  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -39...-1

<400> 1040  
 Met Tyr Val Cys Ile Tyr Ile Xaa Leu Xaa Asp Leu Tyr Asp Phe Phe  
                   -35                  -30                  -25  
 Leu Leu Gly Thr Tyr Phe Phe Glu Arg Lys Cys Phe Val Cys Xaa Leu  
                   -20                  -15                  -10  
 Phe Val Phe Leu Leu Ser Gly Leu Asn Tyr Phe Ser Ile Leu Ser Phe  
                   -5                  1                  5  
 Tyr Pro Arg  
 10

<210> 1041  
 <211> 50  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -40...-1

<400> 1041  
 Met Cys Ile Phe Cys Leu Phe His Leu Leu Tyr His Lys Leu Leu Ser  
                   -40                  -35                  -30                  -25  
 Arg Ser Leu Phe Phe Cys Cys Ile Phe Ser Gly Phe Ile Thr Phe Ile  
                   -20                  -15                  -10  
 Phe Ser Phe Ser Phe Cys Glu Cys Ile Val Gly Met Tyr Ile Tyr Gly  
                   -5                  1                  5  
 Ala Arg  
 10

<210> 1042  
 <211> 40  
 <212> PRT  
 <213> Homo sapiens

<220>

&lt;221&gt; SIGNAL

&lt;222&gt; -27...-1

&lt;400&gt; 1042

Met Xaa Ile Cys Tyr Asn Ile Phe Gln Asn Ile Leu Gly Leu Leu Leu  
 -25 -20 -15  
 Ile Phe Leu Tyr Leu Ser Leu Asn Leu Phe Cys Ile Phe Phe Ser Val  
 -10 -5 1 5  
 Pro Ala Leu Gln Pro Arg Arg Leu  
 10

&lt;210&gt; 1043

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 1043

Met Ala Ser Ser Met Leu Xaa Ser Phe Gln Thr Phe Met Met Leu Thr  
 -25 -20 -15  
 Leu Leu Gly Phe Pro Ser Lys Ala Leu Thr Phe Ile Ser  
 -10 -5 1

&lt;210&gt; 1044

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 1044

Met Gly Arg Ser Lys Arg Gln Leu Leu Ser Leu Pro Gly Ser Phe Ile  
 -20 -15 -10 -5  
 Pro Gly Asn Cys Arg Pro Arg Ile Leu Ser Asn Gly Glu Xaa Arg Arg  
 1 5 10  
 Lys

&lt;210&gt; 1045

&lt;211&gt; 48

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -25...-1

&lt;400&gt; 1045

Met Arg Ser Asp Gly Phe Ile Arg Gly Phe Cys Phe Cys Phe Phe Leu  
 -25 -20 -15 -10  
 Ile Phe Leu Leu Pro Leu Pro Ala Met Ile Leu Arg Pro Leu Gln  
 -5 1 5  
 Pro Cys Gly Ile Ile Ser Pro Ile Lys Pro Leu Phe Pro Phe Phe Phe  
 10 15 20

&lt;210&gt; 1046

&lt;211&gt; 39

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 1046

Met	Asn	Thr	Leu	Trp	Thr	Ala	Ser	Ser	Leu	Pro	Leu	Ser	Thr	His	Ser
	-15					-10					-5				
Gln	Arg	Thr	Met	Ile	His	Trp	Asn	Val	Phe	Leu	Trp	Asn	Ser	Phe	Tyr
1				5					10					15	
Ser	Cys	Ile	Lys	Ile	Phe	Pro									
			20												

&lt;210&gt; 1047

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -31...-1

&lt;400&gt; 1047

Met	Thr	Trp	Thr	Lys	Cys	Pro	Leu	Pro	Leu	Gly	Pro	Ala	Phe	Phe	Thr
	-30					-25				-20					
Gln	Cys	Cys	Leu	Ile	Gly	Leu	Leu	Val	Pro	Leu	Leu	Gly	Trp	Gly	Asn
-15					-10					-5					1
Gln	Asn	Thr	Gln	Trp	Tyr	Pro	Thr	Ser	Lys	Met	Pro	Asp	Gly		
			5					10					15		

&lt;210&gt; 1048

&lt;211&gt; 37

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -32...-1

&lt;400&gt; 1048

Met	Gly	Arg	Ser	Asn	Asp	Phe	Arg	Phe	Ala	Phe	Leu	Thr	Cys	Phe	Leu
	-30					-25					-20				
Gly	Trp	Glu	Ile	Val	Tyr	Phe	Leu	Val	Leu	Leu	Arg	Val	Leu	Tyr	Thr
-15						-10					-5				
Leu	Gln	Trp	Gly	Gly											
1				5											

&lt;210&gt; 1049

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1049

Met	Lys	Thr	Asp	Asn	Leu	Thr	Ser	Phe	Leu	Thr	Tyr	Met	Pro	Leu	Ile
			-15					-10				-5			
Ser	Ser	Ser	Cys	Ser	Ile	Ala	Pro								
		1				5									

&lt;210&gt; 1050

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<220>
<221> SIGNAL
<222> -79..-1
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```
<210> 1051
<211> 79
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> -14..-1
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```
<210> 1052
<211> 30
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -27..-1
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<400> 1052
Met Glu Ser Ser Thr Phe Ala Leu Val Pro Val Phe Ala His Leu Ser
      -25      -20      -15
Ile Leu Gln Ser Leu Val Pro Ala Ala Gly Ala Xaa Ser Pro
      -10      -5      1

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<210> 1053  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -78...-1

<400> 1053  
 Met Gly Cys Leu Leu Ala Ser Glu Tyr Pro Leu Ser Glu Pro Trp Ala  
                   -75                  -70                  -65  
 Pro Gly Pro Phe Thr Gln Tyr Leu Val Asp His His His Thr Leu Leu  
                   -60                  -55                  -50  
 Cys Asn Gly Tyr Trp Leu Ala Trp Leu Ile His Val Gly Glu Ser Leu  
                   -45                  -40                  -35  
 Tyr Ala Ile Val Leu Cys Lys His Lys Gly Ile Thr Ser Gly Arg Ala  
                   -30                  -25                  -20                  -15  
 Gln Leu Leu Trp Phe Leu Gln Thr Phe Phe Phe Gly Ile Ala Ser Leu  
                   -10                  -5                  1  
 Xaa Ile Leu Ile  
                   5

<210> 1054  
 <211> 32  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1054  
 Met Cys Cys Trp Ile Trp Val Ala Ser Ile Leu Leu Arg Ile Phe Ala  
                   -15                  -10                  -5  
 Ser Val Leu Ile Arg Asp Ile Tyr Leu Trp Phe Ser Phe Phe Phe Phe  
                   1                  5                  10                  15

<210> 1055  
 <211> 37  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 1055  
 Met Ile Ser Ser His Leu Tyr Asn Phe Ser Leu Leu Phe Phe Xaa Leu  
                   -20                  -15                  -10  
 Trp Leu Arg Tyr Lys Glu Ser Gly Arg Glu Gly Asn Cys Glu Glu Gly  
                   -5                  1                  5  
 Ala Phe Ser Arg Trp  
 10

<210> 1056  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 1056

```

Met Gly Trp Gln Arg Leu Leu Leu Leu Pro Arg Pro Pro Ala Ser Thr
      -15          -10          -5
Gly Ala Ser Asn Ala Thr Arg Xaa Pro Lys Xaa Leu Tyr Arg Xaa Tyr
  1          5          10          15
Asn His Gly Val Leu Lys Ile Thr Ile Cys Lys Ser Cys Gln Lys Pro
      20          25          30
Val Asp Lys Tyr Ile Glu Tyr Asp Pro Val Ile Ile Leu Xaa Asn Ala
      35          40          45
Ile Leu Cys Lys Ala Xaa Ala Tyr Arg His Ile Leu Phe Asn Thr Gln
      50          55          60
Ile Asn Asn Lys Leu Pro Ile Leu Leu Ala Phe Leu Pro Ser Cys Gly
      65          70          75
Xaa Thr Ala His Asp Gly Lys Lys Lys Pro Asn Phe Ile Leu Leu Leu
  80          85          90          95
Lys Xaa Tyr Tyr Tyr Leu Ala Thr Glu Asn
      100          105

```

&lt;210&gt; 1057

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 1057

```

Met Ala Ala Gly Val Ser Leu Leu Ala Leu Val Val Arg Val Ile Leu
      -15          -10          -5
Ser Thr Ala Ile Leu Cys Pro Ser Gly Ala Ser Arg Arg Gln Arg Ser
      1          5          10
Ser Glu Val Glu Trp Gly Thr Asp Ser
  15          20

```

&lt;210&gt; 1058

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1058

```

Met Asn Pro Leu Phe Trp Leu Ile Leu Cys Ser Gly Leu Leu Cys Asn
-15          -10          -5          1
Lys Ser Phe

```

&lt;210&gt; 1059

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1059

```

Met Arg Gly Ala Trp Ile Ser Ile Phe Leu Ser Ser Leu Ser Leu Ser
      -15          -10          -5

```

Leu Ser Leu Phe  
1

<210> 1060  
<211> 32  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -24...-1

<400> 1060  
Met Ser Gln Lys Arg Leu Asp Phe Ile Tyr Gln Leu Phe Val Leu Leu  
-20 -15 -10  
Pro His Phe Phe Leu Ser Phe Leu Ser Pro Phe Tyr Leu His Pro Trp  
-5 1 5

<210> 1061  
<211> 52  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -33...-1

<400> 1061  
Met Tyr Leu Tyr Leu Leu Ser Ile Cys Met Ser Ser Leu Lys Lys Cys  
-30 -25 -20  
Leu Phe Lys Phe Leu Ala His Phe Leu Ile Gly Leu Thr Val Cys Phe  
-15 -10 -5  
Gly Glu Gly Xaa Leu Met Ser Tyr Arg Ser Ser Tyr Leu Leu Leu Lys  
1 5 10 15  
Gly Pro Pro Gly

<210> 1062  
<211> 27  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -22...-1

<400> 1062  
Met Gly Phe Trp Cys Glu Cys Pro Phe Cys Leu Leu Val Phe Leu Leu  
-20 -15 -10  
Thr Glu Trp Thr Ser Ser Lys Leu Gln Lys Thr  
-5 1 5

<210> 1063  
<211> 24  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -22...-1

<400> 1063  
Met Trp Trp Gly Arg Cys Phe Ile Arg Val Leu His Leu Phe Pro Leu  
-20 -15 -10

Thr Pro Ala Ser Thr Gly His Trp  
-5 1

<210> 1064  
<211> 58  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -29...-1

<400> 1064  
Met Arg Asp Pro Leu Ala Asp Met Val His Ser Tyr Leu Ser Ser Ser  
-25 -20 -15  
Leu Phe Met Ala Leu Pro Pro Val Leu Ser Ser His Gly Ser Arg Asn  
-10 -5 1  
Leu Arg Ile Trp Gly Ser Pro Phe Gly Gly Ala Leu Thr Lys Gly Lys  
5 10 15  
Ala Pro Pro Thr Pro Ala Gln Pro Ala Leu  
20 25

<210> 1065  
<211> 28  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -17...-1

<400> 1065  
Met Ser Ser Ala Trp Leu Cys Leu Pro Cys Ser Leu Cys Val Ser Gln  
-15 -10 -5  
Leu Leu Pro Ser Tyr Ser Leu Leu Ile Pro Ala Pro  
1 5 10

<210> 1066  
<211> 27  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -21...-1

<400> 1066  
Met Ser Pro Met Trp Ala Gly Leu Leu Ser Leu Leu Gly Pro Leu Xaa  
-20 -15 -10  
Pro Pro Met Arg Ala Cys Ser Val Cys Val Leu  
-5 1 5

<210> 1067  
<211> 39  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -18...-1

<400> 1067  
Met Ser Leu Asn Glu Leu Ser Ile Ala Asp Leu Leu Pro Ser Ser Ser

Phe Ala Asn Pro Lys Leu Ser Gly Pro Ile Ser Ile Ser Val Thr Ser  
          1               5                  10  
Ala Gly Ser Pro Pro Gly Ala  
15                    20

```
<210> 1068
<211> 26
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -15..-1
```

```

<400> 1068
Met Lys Asp Leu Leu Gly Thr Ala Phe Leu Glu Gly Ser Leu Ala Ala
-15          -10          -5          1
Tyr Leu Thr Met Ala Asn Ile Thr His Val
      5          10

```

```
<210> 1069
<211> 29
<212> PRT
<213> Homo sapiens
```

```

<220>
<221> SIGNAL
<222> -19..-1

```

```

<400> 1069
Met Ala Asn Asp Ile Lys His Leu Phe Met Cys Leu Leu Thr Ile Cys
      -15      -10      -5
Ile Ser Ser Leu Glu Lys Leu Pro Phe Phe Phe Phe
      1          5          10

```

```
<210> 1070
<211> 98
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -24..-1
```

[illegible]

```
<210> 1071
<211> 19
<212> PRT
```

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 1071

Met Met Pro Pro Ala Leu Phe Phe Leu Leu Arg Ile Ala Trp Leu Leu  
-15 -10 -5  
Gly Leu Phe  
1

<210> 1072

<211> 38

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<400> 1072

Met Asn Cys Val Thr Leu Ile Gln Ala Leu Ser Leu Trp Ala Ser Val  
-20 -15 -10  
Ser Pro Ser Trp Met Cys Arg Pro Pro Ala Ser Phe Ile Ile Thr Thr  
-5 1 5 10  
Thr Thr Thr Thr Cys Gly  
15

<210> 1073

<211> 19

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1073

Met Leu Ser Leu Leu Ser Leu Met Ala Arg Thr Asp Leu Val Phe Cys  
-15 -10 -5  
Ser Pro Arg  
1

<210> 1074

<211> 255

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34..-1

<400> 1074

Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala Val Ala  
-30 -25 -20  
Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val  
-15 -10 -5  
Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu  
1 5 10  
Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro  
15 20 25 30  
Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys

515

```

          35          40          45
Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile
          50          55          60
Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly
          65          70          75
Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg
          80          85          90
Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe
          95          100          105          110
Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa
          115          120          125
Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg
          130          135          140
Val Thr Trp Ile Val Glu Phe Phe Ala Xaa Trp Ser Asn Asp Cys Gln
          145          150          155
Ser Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr
          160          165          170
Gly Leu Asn Phe Gly Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser
          175          180          185          190
Thr Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr
          195          200          205
Leu Ile Leu Phe Gln Gly Gly Lys Glu Ala Met Arg Arg Pro Gln
          210          215          220

```

&lt;210&gt; 1075

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 1075

```

Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
          -15          -10          -5
Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
          1          5          10          15
Thr Gly Leu Thr Thr Ala Lys Met Pro Ser Val Pro Leu Ser Ser Asp
          20          25          30
Pro Leu Pro Thr His Thr Thr Ala Phe Ser Pro Ala Ser Thr Phe Glu
          35          40          45
Arg Glu Asn Asp Phe Ser Glu Thr Thr Thr Ser Leu Ser Pro Asp Asn
          50          55          60
Thr Ser Thr Gln Val Ser Pro Asp Ser Leu Asp Asn Ala Ser Ala Phe
          65          70          75
Xaa Thr Thr Gly Val Ser Ser Val Gln Thr Pro Xaa Leu Pro Thr His
          80          85          90          95
Ala Asp Ser Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser
          100          105          110
Gly Ser Ala Xaa Met Gln Asn Ser Thr Leu Pro Gln Ala Ala Met Leu
          115          120          125
Ser Gln Met Ser Gln Glu Arg Gly Val
          130          135

```

&lt;210&gt; 1076

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 1076

```

Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
    -15          -10          -5
Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
    1          5          10          15
Thr Gly Val Ser Ser Val Gln Thr Pro Gln
          20          25

```

&lt;210&gt; 1077

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 1077

```

Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
    -15          -10          -5
Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
    1          5          10          15
Thr Gly Val Ser Ser Val Gln Thr Pro His Leu Pro Thr His Ala Asp
          20          25          30
Ser Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser Gly Ser
          35          40          45
Ala Xaa Met Gln Asn Ser Thr Leu Pro Gln Ala Ala Met Leu Ser Gln
          50          55          60
Met Ser Gln Glu Arg Gly Val
    65          70

```

&lt;210&gt; 1078

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -36...-1

&lt;400&gt; 1078

```

Met Arg Gly Ala Thr Trp Pro Trp Pro Cys Leu Pro Ala Arg Thr Ser
    -35          -30          -25
Thr Ala Ala Ser Ile Ala Arg Leu Phe Leu Leu Ser Gly Thr Ile Trp
    -20          -15          -10          -5
Ile Ala Ile Cys Lys Pro Thr Thr Asn Gly
          1          5

```

&lt;210&gt; 1079

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -64...-1

&lt;400&gt; 1079

```

Met Gly Val Leu Pro Asp Leu Val Val Glu Ile Phe Gly Val Asn Lys
          -60          -55          -50
Cys Arg Leu Ser Trp Gly Leu Val Leu Glu Ser Leu Gln Gln Pro Leu
          -45          -40          -35

```

Ile Asn Arg His Leu Ile Tyr Cys Leu Gly Asp Ile Ile Leu Xaa Xaa  
                   -30                  -25                  -20  
 Leu Asp Leu Ser Ala Leu Leu Arg Ser Leu Leu Leu Pro Xaa Leu Xaa  
                   -15                  -10                  -5  
 Gln Ile Pro Gln Ala Thr Leu Arg  
 1                                  5

&lt;210&gt; 1080

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1080

Met Thr Ala Leu Gly Phe Val Leu Leu Ala Pro Arg Gly Trp Gly Ser  
                   -15                  -10                  -5                  1  
 Leu Thr Val Met Val Glu Gly Lys Glu Glu Gln Val Thr Ser Tyr Thr  
                                   5                  10                  15  
 Asp Gly Ser Arg Gln Arg Asp Ser Asn Phe  
                   20                  25

&lt;210&gt; 1081

&lt;211&gt; 64

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -39...-1

&lt;400&gt; 1081

Met Lys Arg Ile Arg Arg Lys Arg Arg Asn Glu Val Thr Ile Gln Pro  
                                   -35                  -30                  -25  
 Phe Pro Ile Arg Leu Pro Leu Leu Pro Pro Leu Ile Ser Phe Leu His  
                   -20                  -15                  -10  
 Thr Leu Gln Val Val Cys Ser Val Ile Met Lys Ser Ile Arg Lys Ala  
                   -5                  1                  5  
 Phe Val Leu Cys Gly Phe Leu Tyr Phe Glu Phe Phe Asp Gln Lys Leu  
 10                                  15                  20                  25

&lt;210&gt; 1082

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -22...-1

&lt;400&gt; 1082

Met Leu Pro Leu Leu His Cys Phe Phe Xaa Val Xaa Leu Phe Xaa Xaa  
                   -20                  -15                  -10  
 Val Xaa Val Xaa Xaa Ala Ala Leu Leu Arg Tyr Asn Xaa Ser Ile Gln  
                   -5                  1                  5                  10  
 Xaa Gly Arg Ala Gln Xaa Leu Xaa Pro Xaa Ile Pro Xaa Leu Trp Glu  
                                   15                  20                  25  
 Thr Lys Xaa Gly Arg Leu Leu Glu Pro Arg Asn  
                   30                  35

&lt;210&gt; 1083

<211> 30  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 1083  
 Met Val Ser Val Phe Arg Ser Glu Glu Met Cys Leu Ser Gln Leu Phe  
           -20                  -15                  -10  
 Leu Gln Val Glu Ala Ala Tyr Cys Cys Val Ala Glu Leu Gly  
           -5                          1                          5

<210> 1084  
 <211> 41  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 1084  
 Met Ala Ala Leu Arg Ser Thr Leu Thr Trp Thr Glu Val Val Gly Trp  
                   -25                  -20                  -15  
 Trp Ser Val Ala Ser Leu Leu Ser Asp Val Ala Ala Trp Trp Pro Pro  
                   -10                  -5                          1  
 His Ser Thr Ser Thr Arg Gly Gly Val  
           5                          10

<210> 1085  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -44...-1

<400> 1085  
 Met Asn Ala Leu Val Asp Gly Lys Arg Leu Xaa Xaa Cys Ile Arg Tyr  
                   -40                  -35                  -30  
 Phe Asp Ser Ile Ser Leu Tyr Ser Lys Ala Ser Leu Ser Cys Cys Leu  
                   -25                  -20                  -15  
 Val Cys Val Phe Thr Cys Ser Leu Leu Ala Phe Phe Ser Pro Cys  
                   -10                  -5                          1

<210> 1086  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 1086  
 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly  
                   -15                  -10                  -5  
 Val Gln Cys Glu Leu Gln Val Val Glu Ser Gly Gly Gly Leu Val Gln  
                   1                          5                          10  
 Pro Gly Arg Ser Leu Arg Leu Ser Cys Arg Thr Ser Gly Phe Ala Phe

519

15                      20                      25  
 Asp Asp Tyr Asn Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 30                      35                      40                      45  
 Glu Trp Val Gly Phe Ile Arg Ser Lys Pro Tyr Gly Glu Thr Thr Thr  
                     50                      55                      60  
 Tyr Ala Ala Trp  
                     65

<210> 1087  
 <211> 19  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1087  
 Met Ser Leu Phe Xaa Leu Xaa Xaa Leu Arg Gln Ser Phe Thr Xaa Xaa  
                     -10                      -5                      1  
 Ala Gln Ala  
                     5

<210> 1088  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 1088  
 Met Ile Ser Ala His Cys Ser Phe Tyr Phe Leu Ala Ser Ser Ser Leu  
                     -15                      -10                      -5  
 Ser Thr Ser Ala Ser Xaa Arg Thr Gly Ile Thr Asp Val Ser  
                     1                      5                      10

<210> 1089  
 <211> 43  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<400> 1089  
 Met Asn Ala Glu Asn Asn Phe Phe Gly Phe Val Cys Leu Phe Val Phe  
                     -20                      -15                      -10  
 Leu Tyr Thr Thr Pro Cys Asn Cys Phe Gly Leu Glu His Leu Trp Ile  
                     -5                      1                      5  
 Leu Ser Phe Met Val Val Leu Gly Xaa Thr Arg  
                     10                      15

<210> 1090  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

&lt;400&gt; 1090

Met Thr Met Ala Val Gly Ala Ala Xaa Xaa Leu Pro Cys Cys Cys His  
                   -20                  -15                  -10  
 Leu Leu Thr Cys Val Ser Ser Leu Arg Xaa Asp Ile Tyr Pro His  
                   -5                  1                  5

&lt;210&gt; 1091

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -25...-1

&lt;400&gt; 1091

Met Arg Arg Lys Arg Arg Glu Arg Lys Glu Arg Lys Ser Ile Leu Leu  
                   -25                  -20                  -15                  -10  
 Ala Ala Leu Ser Arg Asn Ile Ser Pro Gly Gln Thr Tyr Arg Thr Ser  
                                   -5                  1                  5  
 Pro Ala

&lt;210&gt; 1092

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -23...-1

&lt;400&gt; 1092

Met Gly Ser Pro Tyr Val Ala His Val Gly Leu Glu Leu Leu Thr Ser  
                   -20                  -15                  -10  
 Ser Asp Pro Pro Ser Leu Ala Ser Gln Val Leu Gly Ile His  
                   -5                  1                  5

&lt;210&gt; 1093

&lt;211&gt; 45

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 1093

Met His Leu Tyr Thr His Val Cys Trp Leu Thr Leu Thr Leu Ala His  
                                   -15                  -10                  -5  
 Ser His Ser Leu Thr His Thr His Thr Leu Thr Pro Ser His Thr Arg  
                   1                  5                  10  
 Thr His Ser His Thr Cys Ala Cys Leu His Ala His Lys  
           15                  20                  25

&lt;210&gt; 1094

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1094

```

Met Arg Leu Ser Leu Thr Phe Tyr His Phe Pro Leu Cys Trp Gly His
-15          -10          -5          1
Gln Ala Val Pro Thr Trp Trp Xaa Xaa Ile Ile Gln Pro Cys His Cys
          5          10          15
Ala Leu Cys Thr Ser Ala Glu Gly Val Gln Ser His Ile Ile Ser Xaa
          20          25          30
Ile Tyr Arg
          35

```

&lt;210&gt; 1095

&lt;211&gt; 80

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 1095

```

Met Asn Val Leu Ile Ile Val Phe Val Ala Phe Ala Phe Gly Phe Leu
          -10          -5          1
Val Met Lys Ser Leu Leu Lys Pro Met Ser Arg Arg Val Phe Leu Met
          5          10          15
Leu Ser Ser Arg Ile Phe Met Val Ser Gly Leu Arg Phe Lys Ser Leu
          20          25          30
Ile His Leu Glu Leu Ile Phe Val Tyr Lys Leu Arg Asp Glu Asp Pro
35          40          45          50
Val Ser Phe Phe Tyr Met Trp Leu Ala Asn Tyr Pro Ser Thr Ile Cys
          55          60          65

```

&lt;210&gt; 1096

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 1096

```

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu Leu
-20          -15          -10          -5
Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys Ser Pro
          1          5          10
Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu Cys Ala Gln
          15          20          25
His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser His Thr Ala Gly
          30          35          40
Ser Ser Cys Asn Thr Xaa Ala Ser Cys Gln Gln Gln Ala Arg Asn Val
45          50          55          60
Gln His Tyr His Met Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn
          65          70          75
Xaa Leu Asp Trp Arg Arg Arg Ala Arg Ile Xaa Gly Pro Trp Xaa Glu
          80          85          90
Leu His Gly Xaa
          95

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&lt;210&gt; 1097

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 1097

Met Val Phe Leu Phe Leu Met Ile Ser Val Phe Ala Gly Cys Gln Ile  
                    -10                    -5                    1  
Pro Ser Gly  
                    5

&lt;210&gt; 1098

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -21...-1

&lt;400&gt; 1098

Met Gly Ser Arg Pro Val Ser Xaa Ala Gly Leu Glu Leu Leu Ala Ser  
                    -20                    -15                    -10  
Ser Asn Ser Ser Ala Leu Pro Phe Gln Cys Ser Gly Ile Thr Gly Met  
                    -5                    1                    5                    10  
Ser Xaa His Thr Leu Ala  
                    15

&lt;210&gt; 1099

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -13...-1

&lt;400&gt; 1099

Met Leu Cys His Leu Ser Leu Val Phe Leu Gly Xaa Gly Gln Phe Trp  
                    -10                    -5                    1  
Ser Gln Asn  
                    5

&lt;210&gt; 1100

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 1100

Met Thr Asn Leu Phe Met Cys Leu Phe Ala Ile Cys Ile Ser Ser Asn  
                    -15                    -10                    -5  
Ala Lys Cys Leu Phe Ser Leu Phe Pro Phe Phe Ile Glu Gly  
                    1                    5                    10

&lt;210&gt; 1101

&lt;211&gt; 48

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -27...-1

&lt;400&gt; 1101

Met	Leu	Gly	Tyr	Ile	Trp	Xaa	Gln	Asp	Lys	Val	Phe	Ala	Asn	Cys	Val
		-25					-20					-15			
Leu	Phe	Thr	Leu	Leu	Val	Ser	Thr	Arg	Ser	Gly	Arg	Ser	Arg	Ala	Gly
	-10					-5				1				5	
Cys	Ala	Trp	Arg	Trp	Arg	Gly	Arg	Trp	Ser	Val	Gly	Gln	Lys	Gly	Xaa
			10					15						20	

&lt;210&gt; 1102

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1102

Met	Xaa	Leu	Ile	Leu	Ser	Leu	Gln	Val	Cys	Arg	Pro	Ala	Thr	Leu	Asp
-15					-10				-5					1	
Gln	Ala	Thr	Arg	Ala	Thr	Thr	Pro	Cys	Arg	Leu	Arg				
		5					10								

&lt;210&gt; 1103

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -37...-1

&lt;400&gt; 1103

Met	Cys	His	Arg	Arg	Trp	Leu	His	Leu	Ser	Thr	Arg	His	Leu	Gly	Phe
	-35					-30						-25			
Lys	Pro	Arg	Ile	His	Tyr	Val	Phe	Val	Leu	Met	Leu	Ser	Leu	Pro	Leu
-20					-15						-10				
Pro	Pro	Thr	Pro	Gln	Gln	Ala	Leu	Gly							
-5				1											

&lt;210&gt; 1104

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 1104

Met	Asp	His	Val	Val	Ile	Phe	Val	Ile	Phe	Pro	Ala	Ala	Leu	Leu	Leu
			-15					-10					-5		
Cys	Trp	Gly	Gly	Leu	Ile	Pro	Leu	Cys	Ile	Ile	Tyr	Pro	Pro	Ile	Ala
		1				5						10			
Asp	Thr	Val	Gly												
15															

&lt;210&gt; 1105

&lt;211&gt; 30

<212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 1105  
 Met Leu Thr Asn Leu Phe Phe Gln Val Ala His Pro Leu Ile Ile Ile  
 -25 -20 -15 -10  
 Leu Xaa Phe Asp Ile Tyr Ser Leu Ala Phe Ile His Asp Val  
 -5 1 5

<210> 1106  
 <211> 27  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1106  
 Met Leu Phe Gly Leu Arg Gly Met Leu Pro Leu Thr Gln Gln Ala Pro  
 -10 -5 1  
 Ile Pro His Leu Arg Cys Lys Leu Ser Val Thr  
 5 10

<210> 1107  
 <211> 79  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 1107  
 Met Arg Val Cys Met Arg Leu Cys Ala Cys Val Tyr Ala Cys Val Cys  
 -20 -15 -10  
 Ala Ser Val Ser Ala Cys Val Tyr Xaa Cys Val Cys Met Xaa Val Arg  
 -5 1 5 10  
 Ala His Leu Cys Val Cys Met Cys Val Cys Met Cys Val His Leu Cys  
 15 20 25  
 Val Cys Met Cys Val Cys Val Cys Ala Ser Val Cys Val Cys Met Cys  
 30 35 40  
 Ala Cys Val Cys Met Cys Val Cys Val Arg Ala Ser Val Cys Val  
 45 50 55

<210> 1108  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 1108  
 Met Val Ile Thr Ser Asn Ser Tyr Leu Ile Ala Asn Leu Val Leu Phe  
 -20 -15 -10  
 Ile Ser Ile Ala Ala Leu Arg  
 -5 1

<210> 1109  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -51...-1

<400> 1109  
 Met Glu Glu Leu Asp Arg Lys Trp Arg Glu Lys Val Leu Pro Ala Ala  
           -50                          -45                          -40  
 Lys Leu Ile Lys Arg Arg Asn Leu Phe Ser Thr Cys Thr Pro Gln Tyr  
           -35                          -30                          -25                          -20  
 Gly Thr His Ala Ala Phe Leu Ser Leu His Ala Ser Leu Val Thr Lys  
                                   -15                                  -10                                  -5  
 Ala Phe Ser Ile Asn Ser Trp Glu Trp  
                           1                                  5

<210> 1110  
 <211> 27  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 1110  
 Met Val Ser Gly Ala Gln Ala Pro Ser Ser Gln Arg Pro Leu Leu Leu  
           -25                          -20                          -15                          -10  
 Cys Pro Leu Ser Ser Gly Ser Pro Cys Pro Arg  
                                   -5                                  1

<210> 1111  
 <211> 32  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 1111  
 Met Ser Cys Leu Leu Arg Ala Tyr Ile Ile Trp Ile Phe Pro Ser Phe  
           -25                          -20                          -15  
 Leu Pro Ser Leu Leu Ser Ser Phe Leu Leu Ser Leu Pro Pro Ser Gly  
           -10                          -5                                  1                                  5

<210> 1112  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -36...-1

<400> 1112  
 Met Phe Gln Leu Leu Ile Leu Cys Gln Met Asn Ser Leu Lys Ile Phe  
           -35                          -30                          -25  
 Ser Pro Ile Leu Gly Trp Ser Leu His Phe Val Tyr Cys Phe Leu Cys

<210> 1116

<211> 51  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -42..-1

<400> 1116  
 Met Ile Ser Ser Ser Leu Ser Gly Arg Val Pro Val Ile Leu Gly Asn  
           -40                  -35                  -30  
 Leu Met Gly Val Gly Ala Ala Val Arg Arg Met Gly Phe Ser Leu Ile  
           -25                  -20                  -15  
 Leu Pro Thr Ser Pro Ser Pro Ala His Ser Gly Ser Ala Pro Ser Ala  
           -10                  -5                  1                  5  
 Gly Pro Arg

<210> 1117  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -46..-1

<400> 1117  
 Met Gly Ile Ile Gln Xaa Ile Leu Ala Thr Ser Arg Asp Cys Tyr Ser  
           -45                  -40                  -35  
 Phe Lys Lys Lys Pro Ile Pro Lys Lys Pro Thr Met Leu Ala Leu Ala  
           -30                  -25                  -20                  -15  
 Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr Ser Leu Leu Ser Gly Ser  
                   -10                  -5                  1  
 His Gly Lys Xaa Asn Gln Asp Val  
           5                  10

<210> 1118  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23..-1

<400> 1118  
 Met Met Leu Ser Thr Phe Ser Tyr Ala Cys Leu Pro Phe Val Cys Leu  
           -20                  -15                  -10  
 Leu Leu Arg Asn Val Tyr Ser Asp Leu Leu Pro Asn Arg  
           -5                  1                  5

<210> 1119  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24..-1

<400> 1119  
 Met Leu Ala Ile Leu Thr Gly Gly Arg Trp Tyr Leu Ile Val Val Leu  
                   -20                  -15                  -10

Val Cys Ile Ser Leu Val Ile Ile Asp Asp Asp Glu His Gly  
                   -5                                  1                                  5

<210> 1120

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 1120

Met Leu Leu Pro Leu Gly Leu Lys Val Leu Gly Leu Gln Ala Arg Gly  
                                   -10                                  -5                                  1

Thr Thr

<210> 1121

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 1121

Met Arg Pro Thr Met Glu Phe His Ser Val Leu Cys Gly Val Thr Pro  
                                   -25                                  -20                                  -15

Thr Leu Leu Val Met Trp Leu Ser Pro Gln Met Ala Ser Ser Pro Ser  
                                   -10                                  -5                                  1

Gln Ala Pro Gly Met Glu Pro Cys Ala Ser Gly Ile Ser Gln Arg Ala  
   5                                  10                                  15                                  20

<210> 1122

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -33...-1

<400> 1122

Met Gly Lys Lys Lys Ile Trp Thr Pro Ser Ser Tyr Pro Met Pro Ser  
                                   -30                                  -25                                  -20

His Lys His Val Ser Leu Cys Leu Leu Thr Val Ala Val Leu Val Leu  
                                   -15                                  -10                                  -5

Thr Phe Lys Ser Leu Ile His Phe Glu Xaa Ile Phe Ala Tyr Glu Ile  
   1                                  5                                  10                                  15

Gly Val Gln Gly

<210> 1123

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 1123

Met Ser Pro Val Leu Cys Phe His Arg Cys Ser Cys Pro Ser Leu Leu

529

Ser Pro Ile Ser Pro Ser Gln Ala Cys Pro Glu Pro Leu Leu Gly  
 -20 -15 -10  
 -5 1 5

<210> 1124  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<400> 1124  
 Met Leu Gln Leu Ser Phe Ser Val Phe Ile Leu Ile Met Phe Val Cys  
 -20 -15 -10  
 Met Cys Val Cys Val Cys Val Cys Val Tyr Arg Leu Phe Ser Ser Ser  
 -5 1 5  
 Ser Pro  
 10

<210> 1125  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -91...-1

<400> 1125  
 Met Lys Ser Thr Val Ser Ser Arg Glu Val Ala Thr Val Asp Lys Met  
 -90 -85 -80  
 Lys Arg Arg His Ala Glu Tyr Cys Ala Gln Gly Leu Gln Arg Phe Lys  
 -75 -70 -65 -60  
 Ala Gln Leu Ser Gln Asp Thr Leu Pro Xaa His Pro His Leu Glu Xaa  
 -55 -50 -45  
 Glu Lys Gly Leu Glu Gly Leu Glu Glu Asn Val Pro Leu Lys Gly Glu  
 -40 -35 -30  
 Lys Pro Gly Glu Gly Gly Pro Glu Ser Pro Lys Lys Arg Arg Arg Val  
 -25 -20 -15  
 Leu Leu Gly Ala Gly Ile Pro Pro Val Ser Ser Ala Pro Arg Arg Gln  
 -10 -5 1 5  
 Ser Gln Gln Ala Thr  
 10

<210> 1126  
 <211> 36  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 1126  
 Met His Asn Ser Cys Arg Pro Val His Leu Phe Phe Phe Phe Xaa  
 -20 -15 -10 -5  
 Glu Thr Gly Ser Arg Ser Asn Xaa Trp Leu Glu Xaa Ser Gly Ala Ile  
 1 5 10  
 Ile Ala Asn Ser  
 15

<210> 1127  
 <211> 44  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -42...-1

<400> 1127  
 Met Glu Ala Tyr Leu Asn Asp Ser Leu Leu Thr Pro Ser Asp Ser Pro  
                   -40                  -35                  -30  
 Asp Phe Glu Ser Val Gln Ala Gly Pro Xaa Ala Arg Pro Thr Phe Arg  
                   -25                  -20                  -15  
 Leu Tyr Leu Ser Leu Pro Val Ser Gln Ala Gly Pro  
 -10                                  -5                                  1

<210> 1128  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1128  
 Met Pro Ala Leu Gly Pro Ala Leu Leu Gln Gly Ser Leu Xaa Arg Val  
                                   -10                                  -5                                  1  
 Gly Pro His Pro Pro Ala Pro Ser Thr Asn Cys Ile His Ser Gln Trp  
                   5                                  10                                  15  
 His Val Ser Ala Ala Xaa Gly Lys Gly Pro His Leu Arg His Pro Leu  
                   20                                  25                                  30  
 Xaa Gly Xaa Tyr Gln Leu Pro Val Pro Ala Glu Pro Trp Ala Ala Ala  
 35                                  40                                  45                                  50  
 Gly Gly His Ser Val His  
                                   55

<210> 1129  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 1129  
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu  
                                   -15                                  -10                                  -5  
 Cys Cys Ser Ser Tyr  
                                   1

<210> 1130  
 <211> 22  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1130

Met Ala His Ser Ile Leu Leu Leu Ala Ser Gln Ala Gly Cys Leu Arg  
                   -10                  -5                  1  
 Ser Phe Leu Gly Asn Trp  
                   5

<210> 1131  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20..-1

<400> 1131  
 Met Thr Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Phe Lys  
       -20                  -15                  -10                  -5  
 Gly Val His Cys Glu Gly Xaa Ile Gly Gly Val Gly Gly Ala  
                   1                  5                  10

<210> 1132  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14..-1

<400> 1132  
 Met Asn Thr Val Phe Leu Leu Leu Phe Phe Gly Cys Phe Phe Phe Glu  
                   -10                  -5                  1

<210> 1133  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24..-1

<400> 1133  
 Met Trp Ala Ser Ser Pro Trp Pro Ser Ala Trp Ser Cys Cys Cys Leu  
                   -20                  -15                  -10  
 Ser Ser Ser Ser Phe Ile Ala Gly Arg Arg Arg Gly Trp Thr Gln Met  
                   -5                  1                  5  
 Trp Leu Thr Arg Pro Phe Ser Pro Gln Ala Ser Ser Pro Ser Ala  
       10                  15                  20

<210> 1134  
 <211> 49  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -33..-1

<400> 1134  
 Met Thr Met Pro Ile Ser Ser Tyr Ser Gln Asn Val Leu Ser Asn Phe  
                   -30                  -25                  -20  
 His Asp Gly Tyr Phe Met Leu Ile Ile Leu Ser Ala Ile Leu Leu Asn

-15                      -10                      -5  
 Ser Phe Ile Gly Cys Val Ser Phe Tyr His Cys Phe Ser Trp Gly Ser  
     1                      5                      10                      15  
 Gly

<210> 1135  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 1135  
 Met Leu Thr His Gly Ala Ser Leu Ser Leu Val Ile Phe Leu Leu Thr  
     -20                      -15                      -10                      -5  
 Val Lys His Cys Phe Arg Tyr Arg Val Tyr Lys Thr  
                                  1                      5

<210> 1136  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 1136  
 Met Ser Ser Val Glu Thr Asp Trp Gly Phe Trp Thr Ser Ile Pro Ile  
     -20                      -15                      -10  
 Leu Pro Leu Ser Ser Gly Arg Gln Leu Pro Leu Pro Thr Arg Glu Trp  
     -5                      1                      5                      10  
 Gly Met Trp

<210> 1137  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -33...-1

<400> 1137  
 Met Phe Ala Ser Pro Arg Arg Trp Ser Ser Xaa Lys Ala Phe Ser Gly  
                          -30                      -25                      -20  
 Gln Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe  
                          -15                      -10                      -5  
 Ser Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys  
     1                      5                      10                      15  
 Val Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp  
                          20                      25                      30  
 Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val  
                          35                      40                      45  
 Val Xaa

<210> 1138  
 <211> 63  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 1138

Met Pro Ile His Ser Val Phe Leu Cys Ala Pro Ala Leu Val Phe Pro  
 -15 -10 -5  
 Arg Pro Val Ala Trp Lys Ala Glu Arg Pro Ser Leu Cys Phe Gly Ala  
 1 5 10 15  
 Ser Leu Pro Pro Leu Gly Arg Ser Leu Leu Gly Gln Gly Ser Ser Phe  
 20 25 30  
 Ile Ser Trp Gly Thr Gln Ala Ala Ile Val Glu Leu Xaa Pro His  
 35 40 45

&lt;210&gt; 1139

&lt;211&gt; 80

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -62...-1

&lt;400&gt; 1139

Met Val Tyr Asp Glu Lys Ser Leu Ser Cys Ser His Thr Pro Ala Thr  
 -60 -55 -50  
 Gln Phe Leu Ser Trp Asp Ala Ser Ser Val Tyr Ser Phe Leu Tyr Ile  
 -45 -40 -35  
 Leu Ser Ala Arg Val Asn Val Asp Val Xaa Xaa Tyr Ile Arg Val Tyr  
 -30 -25 -20 -15  
 Ile Leu Ala Cys Val Phe Phe Leu Ser His Pro Leu Phe Xaa Xaa Pro  
 -10 -5 1  
 Asn Gly Ser Val Tyr Cys Xaa Arg His Ser Pro Pro Tyr Leu Phe Cys  
 5 10 15

&lt;210&gt; 1140

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -36...-1

&lt;400&gt; 1140

Met Leu Pro Leu Ser Pro Thr Lys Phe Leu Asn Val Phe Leu Gly Leu  
 -35 -30 -25  
 Phe Leu Tyr Tyr Leu Gln Leu Val Cys Leu Leu Ile Ile Ser Leu Val  
 -20 -15 -10 -5  
 Leu Ile Ser Gly Leu Gly  
 1

&lt;210&gt; 1141

&lt;211&gt; 48

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 1141

Met Asp Lys Val Glu Leu Pro Pro Pro Asp Leu Gly Pro Ser Ser Ala

534

				-25					-20					-15	
Leu	Asn	Gln	Thr	Leu	Met	Leu	Leu	Arg	Glu	Val	Leu	Ala	Ser	His	Asp
			-10					-5					1		
Ser	Ser	Val	Val	Pro	Leu	Asp	Ala	Arg	Gln	Ala	Asp	Phe	Val	Gln	Gly
	5					10					15				

&lt;210&gt; 1142

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -32...-1

&lt;400&gt; 1142

Met	Gly	Gly	Thr	Ala	Gly	Trp	Ser	Ser	Gln	Asn	Thr	His	Asn	Ile	Xaa
		-30				-25					-20				
Val	His	His	Leu	Val	Trp	Leu	Trp	Phe	Val	Val	Pro	Gln	Thr	Ile	Thr
	-15				-10					-5					
Met	Ile	Thr	Pro	Lys	Ile	Thr	Glu	His	Arg	Pro	Xaa	Ile	Thr	Asp	Xaa
1			5				10						15		
Xaa	Ile	Met	Xaa	Thr	Phe	Glu	Xaa	Leu	Gly	Glu	Leu	Pro			
			20				25								

&lt;210&gt; 1143

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1143

Met	Cys	Leu	Ser	Val	Ala	Leu	Tyr	Leu	Cys	Val	Cys	Val	Cys	Val	Cys
		-15				-10				-5					
Leu	Ile	Ala	Arg	Val	Tyr	Phe	Cys	Ile	Tyr	Val	Cys	Val	Trp		
	1				5					10					

&lt;210&gt; 1144

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 1144

Met	Leu	His	Leu	Leu	Phe	Gly	Leu	Phe	Pro	Val	Leu	Trp	Met	Phe	Leu
			-10			-5							1		
Val	Tyr	Phe	Phe	Leu	Ser	Ser	Phe	Phe	Phe	Phe	Phe	Phe			
	5					10						15			

&lt;210&gt; 1145

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1145

Met Tyr Val Cys Xaa Cys Val Tyr Leu Phe Cys Ala Cys Met Cys Val  
 -15 -10 -5  
 Cys Ala Phe Phe Phe  
 1

&lt;210&gt; 1146

&lt;211&gt; 55

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -36..-1

&lt;400&gt; 1146

Met Lys Xaa Asn Asn Leu Arg Arg Gln Ser Pro Ala Leu Arg His Cys  
 -35 -30 -25  
 Trp Arg Xaa Glu Thr Asp Phe Phe Leu Phe Thr Leu Ile Gly Ala Ser  
 -20 -15 -10 -5  
 Leu Leu Gln Ser Ala Ser Gly Pro Cys Arg Ile Ser Xaa Xaa Leu Lys  
 1 5 10  
 Trp His Ser Lys Gly Thr Leu  
 15

&lt;210&gt; 1147

&lt;211&gt; 54

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20..-1

&lt;400&gt; 1147

Met Trp Pro Lys Xaa Gly Leu Leu Gly Leu Gly Leu Pro Leu Leu Pro  
 -20 -15 -10 -5  
 Pro Asn His Pro Ser Val Ala Gln Gly Thr Leu Val Ser Ser His Ser  
 1 5 10  
 Gly Ser Gly Ser Glu Gly Arg Val Ala Leu Arg Ser Asp Val His Ser  
 15 20 25  
 Pro Lys Thr Thr Xaa Gln  
 30

&lt;210&gt; 1148

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -42..-1

&lt;400&gt; 1148

Met Tyr Leu Ile Arg Glu Ser His Ala Ser Gly Ser Ser Ser Val Thr  
 -40 -35 -30  
 Ser Ser Cys Ser Leu Xaa Ser Xaa Ser Pro Asn Pro Gln Ala Met Ala  
 -25 -20 -15  
 Xaa Leu Phe Leu Ser Ala Pro Pro Gln Ala Glu Val Thr Phe Glu Asp  
 -10 -5 1 5  
 Val Ala Val Tyr Leu Ser Arg Glu Glu Trp Gly Arg Leu Gly Pro Ala  
 10 15 20

536

Gln Arg Gly Xaa Tyr Arg Asp Val Met Leu Glu Thr Tyr Xaa Asn Xaa  
           25                          30                          35  
 Val Ser Leu Gly Val Gly Pro Ala Gly Pro Lys Xaa Gly Val Ile Ser  
           40                          45                          50  
 Gln Leu Glu Arg Gly Asp Glu Pro Trp Val Leu Asp Val Gln Gly Thr  
 55                          60                          65                          70  
 Ser Gly Lys Glu His Leu Lys Lys Ser Thr Ala Gln Leu Leu Gly Pro  
                           75                          80                          85  
 Glu Leu Lys Tyr Lys Glu Leu  
                           90

<210> 1149  
 <211> 55  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -37...-1

<400> 1149  
 Met Ile Pro Arg Arg Thr Ser Ala Ser Arg Ala Pro Ser Val Pro Gln  
           -35                          -30                          -25  
 Asn Ala Gly Leu Ser Pro Leu Pro Ala Leu Ser Ser Leu Cys Val Ser  
           -20                          -15                          -10  
 Trp Gly Thr Ser Ser Thr Val Thr Arg Leu Arg Pro Trp Ile Ser Pro  
 -5                          1                          5                          10  
 Thr Trp Thr Ser Arg Ala Arg  
                           15

<210> 1150  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1150  
 Met Val Cys Ile Phe Cys Phe Leu Thr Ser Lys Ala Phe Pro Asn Pro  
                           -10                          -5                          1  
 Arg Ser Gln Asp Phe Leu Leu Asp Phe Ser Arg His Xaa Ile Gly Leu  
           5                          10                          15  
 Gly Phe Thr Phe Arg Ser Ala Met His Phe Glu Asn Phe Arg Leu Xaa  
           20                          25                          30  
 Gly Leu Gly Gln Asp Ser Leu Cys  
 35                          40

<210> 1151  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 1151  
 Met Xaa Xaa Tyr Xaa Xaa Xaa Gly Phe Cys Ser Val Thr Ser Ser Pro  
           -20                          -15                          -10                          -5  
 Leu Ala Ser Ala Gly Arg Thr Thr Arg  
                           1                          5

<210> 1152  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 1152  
 Met Ser Leu Xaa Xaa Leu Cys Asp Pro Asp Leu Val Pro Cys Pro Leu  
                   -20                  -15                  -10  
 Leu Ile Ser Val Ala Leu Ser Val Lys Phe His Ile Xaa Gln Gln Val  
                   -5                          1                          5  
 Asn Leu Pro Cys Ser Ser  
 10                          15

<210> 1153  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -39...-1

<400> 1153  
 Met Met Ile Leu Ile Leu Ile Leu Glu His Ile Val Thr Xaa Lys Arg  
                   -35                  -30                  -25  
 Asn Pro Lys Pro Val Thr Val Pro Ala Phe Leu Xaa Pro Cys Leu Thr  
                   -20                  -15                  -10  
 Ser Phe Ser Cys Xaa Gly Ala Ser Phe Ser Leu Xaa Gly Xaa Arg Arg  
                   -5                          1                          5  
 Gly Trp Gln His Gly Ser Cys Cys Ser Thr Ile Pro Leu Phe Xaa Thr  
 10                          15                          20                          25  
 Leu Asn Ser Leu Gly Gln Gly Leu Ile Gly Pro Ala Tyr Ile Gly Ala  
                           30                          35                          40

<210> 1154  
 <211> 19  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1154  
 Met Ser Thr His Ala Ile Ser Ile Leu Leu Cys Ile Gly Ala Ser Ser  
                   -15                  -10                  -5  
 Gln Gly Arg  
 1

<210> 1155  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

&lt;400&gt; 1155

```

Met Glu Glu Gln Glu Thr Glu Glu Val Gly Gly Arg Ser Ser Arg Lys
  -30              -25              -20
Asn Ala Ala Thr Val Asn Ala Ala Ser Leu Pro Pro Cys Phe Gly Val
  -15              -10              -5              1
Lys Ser Cys Arg Cys Arg Arg Cys Ser Cys Arg Arg Cys Leu Leu Tyr
              5              10              15
Phe Ser Trp Pro Arg Gly Arg Ile Ser Pro Pro Val Gly Gln Cys Ala
              20              25              30
Gly Arg Gly
  35

```

&lt;210&gt; 1156

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -33...-1

&lt;400&gt; 1156

```

Met Arg Gly Ile Gln Ala Lys Gly Ser Pro Gly Gln Ser Ser Ala Xaa
              -30              -25              -20
Val Leu Xaa Pro Cys Cys Cys His Ala Gly Ala Ser Ser Gly Ala Thr
              -15              -10              -5
Ala Trp Glu Glu Thr Pro Arg Ser Arg Cys His Ile Ala Val Xaa Ser
  1              5              10              15
Thr Asn Thr Ala Ser Arg Gly Arg Thr Trp Cys Arg Ala Thr Gly Pro
              20              25              30
Cys Pro Ser Gly Pro Thr Arg Gly Val Ser Arg Ser Arg Gly Leu Gly
              35              40              45
Ala Gly Phe Leu Ser Pro Phe Cys Cys Leu Phe Ala Phe His Pro Arg
              50              55              60
Leu Pro Trp Cys Ala Glu Val Pro Val Pro Ala Ala Ala His His Met
              65              70              75
Arg Cys Gly Gly Asp Leu Leu Ala Ala Pro Pro Pro Gly Pro Ser Trp
  80              85              90              95
Phe Ala Arg Phe Pro Pro Leu Val Pro Glu Ser Phe Pro His His Ser
              100              105              110
Val

```

&lt;210&gt; 1157

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 1157

```

Met Phe Ser Ser Arg Ser Phe Met Val Ser Gly Leu Ile Trp Val Phe
              -20              -15              -10
Gly Leu Val Ser Val Leu Ser Xaa Phe Leu Cys Met Val Tyr Asp Gln
              -5              1              5
Gly Gln
  10

```

&lt;210&gt; 1158

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -13...-1

&lt;400&gt; 1158

Met	Leu	Leu	Ala	Val	Ser	Leu	Ser	Leu	Val	Ser	Asn	Cys	Asn	Phe	Val
			-10					-5					1		
Leu	Thr	Asp	Gln	Leu	Phe	Pro	Ala	Pro	Ala	Ser	Leu	Ile	Pro	Glu	
5						10					15				

&lt;210&gt; 1159

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 1159

Met	Asn	Gln	Asp	Phe	Asn	Pro	Glu	Ile	Glu	Ala	Ser	Pro	Gln	Val	Lys
			-25						-20				-15		
Thr	Gly	Val	Phe	Leu	Phe	Ser	Ile	Ile	Gly	Ser	Phe	Gly	Phe	Pro	Gly
			-10				-5					1			
Met	Cys	Asn	Cys	Lys	Asn	Pro	Ala	Arg							
5						10									

&lt;210&gt; 1160

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 1160

Met	Pro	Cys	Ser	Trp	Ser	His	Ile	Val	Ser	Ser	Leu	Phe	Ser	Trp	Leu
-20				-15						-10				-5	
Leu	Ser	Leu	Thr	Ser	Val	Pro	Gly								
			1												

&lt;210&gt; 1161

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -28...-1

&lt;400&gt; 1161

Met	Phe	Phe	Phe	Gly	Tyr	Ser	Glu	Asp	Ile	Tyr	Cys	Val	Ser	Gly	Pro
			-25				-20				-15				
Val	Leu	Ser	Cys	Cys	Cys	Leu	Thr	Ala	Gly	Arg	Ala	Arg	Leu	Trp	
	-10						-5					1			

&lt;210&gt; 1162

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 1162

Met Pro Tyr Ala Ala Leu Ile Cys Pro Trp Ser Ser Gln Val Pro Ser  
 -15 -10 -5  
 Ser Pro Pro Ala Ser Leu Glu Ala Ser Ser Asn Val Tyr Leu Gln Glu  
 1 5 10 15  
 Ser Arg Ala Ala Tyr Ala Ser Val Pro Ala Gly Pro Glu Val Ala Thr  
 20 25 30  
 Gln His Thr Ser Ser Pro Val Thr Pro Met  
 35 40

&lt;210&gt; 1163

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1163

Met Gln Leu Leu Tyr Leu Thr Tyr Ser Leu Ala Phe Leu Leu Phe Ile  
 -15 -10 -5  
 Lys Ala Gly Thr  
 1

&lt;210&gt; 1164

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 1164

Met Ala Pro Ser Arg Pro Arg Ala Ala Ala Val Thr Ser Ser Ala Ala  
 -20 -15 -10 -5  
 Pro Ser Arg Ala Arg Gln Gly Ala  
 1

&lt;210&gt; 1165

&lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -42...-1

&lt;400&gt; 1165

Met Leu Ala Ser Ala Pro Arg Leu Asn Ser Ala Asp Arg Pro Met Lys  
 -40 -35 -30  
 Thr Ser Val Leu Arg Gln Arg Lys Gly Ser Val Arg Lys Gln His Leu  
 -25 -20 -15  
 Leu Ser Trp Ala Xaa Gln Xaa Gly Arg Xaa Gln Val Val Glu Ile Leu  
 -10 -5 1 5  
 Gln Ser Glu Lys Gln Thr Xaa Xaa Asp  
 10 15

<210> 1166  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -38...-1

<400> 1166  
 Met Tyr Pro Leu Gly Arg Gly Glu Gln Gly Pro Ala Ala Pro Lys Ser  
                   -35                  -30                  -25  
 Trp Leu Leu Leu Pro Thr Thr Leu Ala Leu His Gly Ser Leu Asp Ala  
                   -20                  -15                  -10  
 Val Ser Gln Ala Gln Gly Arg Pro Gly His Pro Asp Ala Pro Pro  
           -5                          1                          5

<210> 1167  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1167  
 Met Arg Val Phe Ile Ala Ala Leu Phe Thr Ile Ala Glu Thr Trp Asn  
           -15                  -10                  -5  
 Gln Pro Lys Cys Pro  
   1                          5

<210> 1168  
 <211> 55  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -30...-1

<400> 1168  
 Met Ala Lys Gly Leu Arg Val Asn Leu Gly Glu Leu Val Glu Ser Met  
   -30                  -25                  -20                  -15  
 Arg Leu Cys Phe Leu Ser Val His Phe Arg Leu Arg Trp Gly Asp Ser  
                   -10                  -5                  1  
 Cys Pro Ser Ser Pro His Arg Glu Thr Phe Pro Ala Gly Pro Val Asn  
           5                  10                  15  
 Gly Pro Leu Tyr His Pro Arg  
   20                  25

<210> 1169  
 <211> 87  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17...-1

<400> 1169  
 Met Pro Ser Pro Gln Leu Leu Val Leu Phe Gly Ser Gln Thr Gly Thr  
           -15                  -10                  -5

Ala Gln Asp Val Ser Glu Arg Leu Gly Arg Glu Ala Arg Gly Arg Arg  
 1 5 10 15  
 Leu Gly Cys Arg Val Gln Ala Leu Asp Ser Tyr Pro Val Val Asn Leu  
 20 25 30  
 Ile Asn Glu Pro Leu Val Ile Phe Val Cys Ala Thr Xaa Gly Gln Gly  
 35 40 45  
 Asp Pro Pro Asp Asn Met Lys Asn Phe Trp Arg Phe Ile Phe Arg Lys  
 50 55 60  
 Asn Leu Pro Ser Thr Ala Arg  
 65 70

<210> 1170  
 <211> 48  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -41...-1

<400> 1170  
 Met Ser Ser Ile Leu Gly Val Ser Ser Ser Trp Trp Tyr Leu Tyr Tyr  
 -40 -35 -30  
 Gly Tyr Cys Ile Phe Val Lys Lys Cys Ser Phe Cys Ser Phe Leu Phe  
 -25 -20 -15 -10  
 Leu Ala Cys Ile Phe Gln Gly Xaa Ser Xaa Xaa Xaa Asn Thr Gln Ser  
 -5 1 5

<210> 1171  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 1171  
 Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys  
 -25 -20 -15  
 Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly  
 -10 -5 1  
 Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val  
 5 10 15 20  
 Gly Val Trp

<210> 1172  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -46...-1

<400> 1172  
 Met Ser Xaa Xaa Xaa Arg Leu Xaa Arg Gln Leu Leu Ser Gln Xaa Arg  
 -45 -40 -35  
 Xaa Met Thr Cys Glu Asn Glu Ala Gly Ala Gln Cys Gln Lys Ser Ser  
 -30 -25 -20 -15  
 Phe Ile Gly Ser Cys Ser Val Met Ser Ser Gly Ala Leu Cys Val Pro  
 -10 -5 1  
 Leu Tyr Tyr Leu Ala Lys Gly Asn Met Cys Ser Ile Cys Gly Met Leu

5 10 15  
 Lys Glu Met Asn Gly Leu Trp Ser Glu Cys Asp Ser Leu Lys Asn Thr  
 20 25 30  
 Phe Ile Val Trp Xaa Cys Ile Phe Ser Cys Leu Gly Met Gln Leu Xaa  
 35 40 45 50  
 Ser Ser Xaa Val Ser Asn Val Arg Leu Leu Leu Ser His  
 55 60

<210> 1173  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 1173  
 Met Pro His Pro Leu Ala Thr Ser Ala Phe Leu Arg Ser Ala Phe Pro  
 -25 -20 -15  
 Phe Val Cys Leu Thr Phe Cys Val Gly Gly Gly Pro Gly Ile Ser Gly  
 -10 -5 1 5  
 Val Tyr Arg Leu Leu Met Ala Asn Ala Thr Arg Arg Glu Ser Glu Val  
 10 15 20  
 Ser Leu Arg Gly Leu Gly Arg Asp Gly Glu Gly Ala Arg Ala Thr Pro  
 25 30 35

<210> 1174  
 <211> 27  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 1174  
 Met Thr Val Gly Leu His Ile Leu Arg Asp Ser Leu Met Val Phe Leu  
 -20 -15 -10  
 Asn Leu Phe Phe Leu Asn Cys Asp Pro His Arg  
 -5 1

<210> 1175  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 1175  
 Met Val Arg Trp Gly His Pro Pro Met Phe Cys Val Ser Leu Leu Leu  
 -20 -15 -10  
 His His Ala Tyr Pro Leu Pro Ser Thr Met Ile Val Ser Phe Pro Arg  
 -5 1 5 10  
 Pro Pro Leu

<210> 1176  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 1176

Met Ala Gly Ala Ala Arg Trp Val Gly Gln Xaa Ser Ser Ala Met Val  
 -25 -20 -15  
 Cys Phe Gly Cys Pro Gly Gly Ala Ser Ser Arg Cys Arg Ser Pro Arg  
 -10 -5 1 5  
 Gly Arg Gln Ala Ser Arg Val Pro Arg Leu Glu Asn Gly Ala Gln Arg  
 10 15 20  
 Val Val Arg Thr Met Val His Leu Val Leu Gln Pro Lys Arg Val Thr  
 25 30 35  
 Leu Val His Pro Pro Arg Gly Leu Glu Pro Val Cys Thr Pro Ile Ala  
 40 45 50  
 Xaa Met Xaa Pro Lys Ser His Gly Leu Arg Ser Ser Leu  
 55 60 65

&lt;210&gt; 1177

&lt;211&gt; 47

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -34...-1

&lt;400&gt; 1177

Met Gly Val Val Ser Gly Gly Val Gly Asp Leu Thr Thr Lys Thr Gln  
 -30 -25 -20  
 Glu Asn Gly Leu Leu Pro Xaa Leu Leu Ser Xaa Leu His Gly Leu Leu  
 -15 -10 -5  
 Tyr Gly Ser Pro Asp Ala Glu Leu Thr Gly Pro Asp Pro Trp Asp  
 1 5 10

&lt;210&gt; 1178

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1178

Met Gly Phe Leu Ser Xaa Thr Cys Val Leu Ser Cys Xaa Arg Ser Leu  
 -15 -10 -5 1  
 Ser

&lt;210&gt; 1179

&lt;211&gt; 48

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -39...-1

&lt;400&gt; 1179

Met Glu Tyr Gly Ser Ala Lys Leu Ser Ser Gly Arg Val Phe Tyr Leu  
 -35 -30 -25  
 Pro Arg Asp Phe Gly Ile Glu Arg Arg Val Leu Val Cys Phe Phe Asn  
 -20 -15 -10

545

Ser Val Ser Phe Leu Phe Gly Val Ser Xaa Lys Lys Ser Xaa Gln Trp  
           -5                          1                          5

&lt;210&gt; 1180

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -13..-1

&lt;400&gt; 1180

Met Leu Ser Gly Leu Val Leu Asn Ser Trp Ala Leu Ala Tyr Gln Leu  
                           -10                          -5                          1

Ala

&lt;210&gt; 1181

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16..-1

&lt;400&gt; 1181

Met Arg Leu Val Phe Phe Xaa Gly Xaa Ser Ile Ile Leu Val Leu Gly  
           -15                          -10                          -5

Ser Thr Phe Xaa Ala Tyr Leu

1

5

&lt;210&gt; 1182

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16..-1

&lt;400&gt; 1182

Met Leu Ser Ser Asp Phe Phe Leu Leu Phe Val Ser Leu Ser Leu Ser  
           -15                          -10                          -5

Pro Phe Pro Phe Phe Leu Phe Pro Pro Leu Phe Ser Cys Phe Leu Leu  
   1                          5                          10                          15

Pro Thr Arg

&lt;210&gt; 1183

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14..-1

&lt;400&gt; 1183

Met Phe Ile Ala Ala Leu Phe Thr Val Ala Lys Ile Trp Asn Gln Pro  
                           -10                          -5                          1

Lys Cys Pro Ser Thr Asp Glu Trp Ile Asn Lys Met Trp Tyr Ile Tyr  
   5                          10                          15

Thr Met Glu Tyr Tyr Pro Asp Ile Lys Lys Asn Gly Ile Leu Thr Phe

20 25 30  
 Lys Ala Thr Arg Met Asn Arg Lys Thr Leu  
 35 40

<210> 1184  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 1184  
 Met Cys Val Cys Gly Cys Leu Cys Val Trp Met Cys Val Cys Gly Xaa  
 -15 -10 -5 1  
 Val Cys Ile Tyr Ile Xaa Val Tyr Val Cys Thr Cys Val Arg Gly  
 5 10 15

<210> 1185  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 1185  
 Met Gly Val Arg Thr Val Cys His Phe Ile Gln Val Phe Leu Ser Leu  
 -25 -20 -15  
 Phe Val Phe Phe Trp Leu Val Gly Phe Ser Phe Phe Phe Leu Xaa  
 -10 -5 1 5  
 Phe Ser Thr Lys Gln Val Arg Val Glu Gln His Cys Asp Phe Lys Ser  
 10 15 20  
 Thr Pro Xaa Val Glu Ser Ser Ser Thr Val Gly His Ala  
 25 30 35

<210> 1186  
 <211> 63  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 1186  
 Met Tyr His Ile Leu Phe Ile His Ser Phe Ile Asp Arg Tyr Leu Ser  
 -25 -20 -15  
 Cys Phe Tyr Leu Leu Ala Ile Val Ser Asn Ala Val Met Asn Met Gly  
 -10 -5 1 5  
 Val Gln Met Ser Val Leu Ser Pro Cys Phe Ala Phe Val His Ser Ile  
 10 15 20  
 Lys Asn Val Lys Val Leu Cys Phe Leu Leu Phe Phe Leu Phe Gly  
 25 30 35

<210> 1187  
 <211> 37  
 <212> PRT  
 <213> Homo sapiens

<220>

<221> SIGNAL  
<222> -22...-1

<400> 1187  
Met Gln Phe Thr Val Leu Met Cys Pro Val Gln Trp Leu Leu Val Tyr  
-20 -15 -10  
Ser Pro Ser Cys Ala Ala Thr Ile Thr Val Asn Phe Lys Thr Phe Ser  
-5 1 5 10  
Ser Pro Gln Thr Gly  
15

<210> 1188  
<211> 40  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -37...-1

<400> 1188  
Met Arg Arg Ala Trp Thr Gln Glu Arg Glu Pro Arg Pro Cys Glu Pro  
-35 -30 -25  
Ala Glu Arg Ala Asp Pro Ala Pro Val Ser Cys Leu Ser Ala Gly Leu  
-20 -15 -10  
Arg Val Cys Cys Ser Gln Arg Ser  
-5 1

<210> 1189  
<211> 37  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -25...-1

<400> 1189  
Met Leu His Leu Ile Cys Ile Ser Leu Ile Val Asn Asp Phe Phe Ile  
-25 -20 -15 -10  
Cys Leu Leu Ala Ile Cys Val Ser Ser Phe Glu Asn Cys Leu Phe Met  
-5 1 5  
Ser Leu Ala His Ser  
10

<210> 1190  
<211> 96  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -63...-1

<400> 1190  
Met Arg Ser Glu Arg Pro Met Val Trp Cys Cys Leu Phe Val Arg Ser  
-60 -55 -50  
Gln Arg Lys Arg Lys Gln Ser Thr Gln Asp Glu Asp Ala Val Ser Leu  
-45 -40 -35  
Cys Ser Leu Asp Ile Ser Glu Pro Ser Asn Lys Arg Val Lys Pro Leu  
-30 -25 -20  
Ser Arg Val Thr Ser Leu Ala Asn Leu Ile Pro Pro Val Lys Ala Xaa  
-15 -10 -5 1

Pro Leu Lys Arg Phe Ser Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg  
                   5                  10                  15  
 Ser Glu Ser Arg Pro Asp Ile Leu Ala Pro Arg Pro Trp Ser Arg Asn  
           20                  25                  30

<210> 1191  
 <211> 48  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20..-1

<400> 1191  
 Met Val Phe Trp Thr Lys Phe Cys Ile Leu Ile Ser Thr Ala Phe Pro  
 -20                  -15                  -10                  -5  
 Ser Leu Leu Thr Gln Ile Ile Phe Pro Lys Ser Ile Thr Phe Ala Phe  
                   1                  5                  10  
 Gln Phe Phe Trp Asn Arg Glu Lys Gln Lys Thr Lys Thr Pro Thr Gly  
           15                  20                  25

<210> 1192  
 <211> 65  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -37..-1

<400> 1192  
 Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile  
           -35                  -30                  -25  
 Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe  
           -20                  -15                  -10  
 Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu  
           -5                  1                  5                  10  
 Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu His  
           15                  20                  25  
 Gly

<210> 1193  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16..-1

<400> 1193  
 Met Ser Val Ser Ala Leu Leu Leu Glu Xaa Leu Gln Xaa Ala Ile Pro  
           -15                  -10                  -5  
 Arg Xaa Thr Ser Gly Xaa Gln Asp Leu Pro Asn Trp  
   1                  5                  10

<210> 1194  
 <211> 50  
 <212> PRT  
 <213> Homo sapiens

<220>

&lt;221&gt; SIGNAL

&lt;222&gt; -39...-1

&lt;400&gt; 1194

Met Gln Ala Cys Tyr Met Gly Met Trp Tyr Thr Ala Glu Ala Trp Gly  
                                   -35                                  -30                                  -25  
 Thr Ile Glu Ser Leu Thr Gln Val Val Ser Val Ile Ala Ile Val Ser  
                                   -20                                  -15                                  -10  
 Phe Thr Thr Leu Cys Ser Ser Leu Tyr Ser Pro Gln Val Val Pro Ser  
                                   -5                                  1                                  5  
 Val Gly  
 10

&lt;210&gt; 1195

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -62...-1

&lt;400&gt; 1195

Met Met Leu Arg Gly Gly Gly Thr Phe Lys Xaa Cys Leu Ser His Glu  
                                   -60                                  -55                                  -50  
 Gly Ser Ser Phe Thr Lys Gly Leu Ala Gln Glu Cys Val Ser Xaa Ser  
                                   -45                                  -40                                  -35  
 Cys Gly Thr Arg Leu Ile Thr Ala Val Ala Ser Xaa Tyr Lys Ala Arg  
                                   -30                                  -25                                  -20                                  -15  
 Leu Pro Leu Ala Ala Cys Pro Leu Leu Leu Pro Ile Phe Ser His Ala  
                                   -10                                  -5                                  1  
 Arg Ser Ser  
                                   5

&lt;210&gt; 1196

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -40...-1

&lt;400&gt; 1196

Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu Asn  
                                   -40                                  -35                                  -30                                  -25  
 Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys  
                                   -20                                  -15                                  -10  
 Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp  
                                   -5                                  1                                  5  
 Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr Asp Met  
                                   10                                  15                                  20  
 Glu His Thr Thr  
 25

&lt;210&gt; 1197

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -41...-1

&lt;400&gt; 1197

```

Met Ser Pro Ala Pro Asp Ala Ala Pro Ala Pro Ala Ser Ile Ser Leu
-40 -35 -30
Phe Asp Leu Ser Ala Asp Ala Pro Val Phe Gln Gly Leu Ser Leu Val
-25 -20 -15 -10
Ser His Ala Pro Gly Glu Ala Leu Ala Arg Ala Pro Arg Thr Ser Cys
-5 1 5
Ser Gly Ser Gly Glu Arg Glu Ser Pro Glu Arg Lys Leu Leu Gln Gly
10 15 20
Pro Met Asp Ile Ser Glu Lys Leu Phe Cys Ser Thr Cys Asp Gln Thr
25 30 35
Phe Gln
40

```

&lt;210&gt; 1198

&lt;211&gt; 56

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -35...-1

&lt;400&gt; 1198

```

Met Leu Leu His Tyr Leu Lys Leu Lys Gly Asp Gln Trp Lys Leu Ser
-35 -30 -25 -20
Ser Val Ser Thr Leu Ile Leu Phe Ile Phe Ile Gly Ser Leu Gln Pro
-15 -10 -5
Val Pro Thr Arg Phe Lys Arg Phe Ser Cys Leu Xaa His Leu Ser Ser
1 5 10
Arg Asp His Arg Gln Ala Leu Arg
15 20

```

&lt;210&gt; 1199

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -153...-1

&lt;400&gt; 1199

```

Met Ala Glu Gly Asp Asn Arg Ser Thr Asn Leu Leu Ala Ala Glu Thr
-150 -145 -140
Ala Ser Leu Glu Glu Gln Leu Gln Gly Trp Gly Glu Val Met Leu Met
-135 -130 -125
Ala Asp Lys Val Leu Arg Trp Glu Arg Ala Trp Phe Pro Pro Ala Ile
-120 -115 -110
Met Gly Val Val Ser Leu Val Phe Leu Ile Ile Tyr Tyr Leu Asp Pro
-105 -100 -95 -90
Ser Val Leu Ser Gly Val Ser Cys Phe Val Met Phe Leu Cys Leu Ala
-85 -80 -75
Asp Tyr Leu Val Pro Ile Leu Ala Pro Arg Ile Phe Gly Ser Asn Lys
-70 -65 -60
Trp Thr Thr Glu Gln Gln Gln Arg Phe His Glu Ile Cys Ser Asn Leu
-55 -50 -45
Val Lys Thr Arg Arg Arg Ala Val Gly Trp Trp Lys Arg Leu Phe Thr
-40 -35 -30
Leu Lys Glu Glu Lys Pro Lys Met Tyr Phe Met Thr Met Ile Val Ser
-25 -20 -15 -10
Leu Ala Ala Val Ala Trp Val Gly Gln Gln Val His Asn Leu Leu Leu

```

551

Thr Tyr Leu Ile Val Thr Ser Leu Leu Leu Leu Pro Gly Leu Asn Gln  
           10                  15                  20  
 His Gly Ile Ile Leu Lys Tyr Ile  
       25                  30

&lt;210&gt; 1200

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 1200

Met Ala Ala Leu Lys Ala Leu Val Ser Gly Cys Gly Arg Leu Leu Arg  
       -25                  -20                  -15  
 Gly Leu Leu Ala Gly Pro Ala Ala Thr Ser Trp Ser Arg Leu Pro Ala  
       -10                  -5                  1                  5  
 Arg Gly Phe Arg Glu Val Val Glu Thr Gln Glu Gly Lys Thr Thr Ile  
                   10                  15                  20  
 Ile Glu Gly Arg Ile Thr Ala Thr Pro Lys Glu Ser Pro Asn Pro Pro  
           25                  30                  35  
 Asn Pro Ser Gly Gln Cys Pro Ile Cys Arg Trp Asn Leu Lys His Lys  
       40                  45                  50  
 Tyr Asn Tyr Asp Asp Val Leu Leu Leu Ser Gln Phe Ile Arg Pro His  
       55                  60                  65                  70  
 Gly Gly Met Leu Pro  
                           75

&lt;210&gt; 1201

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -23...-1

&lt;400&gt; 1201

Met Gly Ser Leu Leu Phe Ile Arg Gln Thr Leu Val Gly Phe Lys Gln  
                   -20                  -15                  -10  
 Val Val Ala Trp Thr Phe Ala Ser Asp Ser His Cys Xaa Xaa Val Xaa  
           -5                  1                  5  
 Met Val Xaa Xaa Ser Gln Leu Xaa Asn Pro Pro Leu  
       10                  15                  20

&lt;210&gt; 1202

&lt;211&gt; 48

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 1202

Met Leu Ala Arg Ala Ala Glu Xaa Thr Gly Ala Leu Leu Leu Arg Gly  
                   -20                  -15                  -10  
 Ser Leu Leu Ala Ser Xaa Arg Ala Xaa Xaa Xaa Pro Pro Leu Gly Leu  
           -5                  1                  5  
 Xaa Arg Asn Thr Xaa Gly Thr Val Arg Ala Ala Ala Gly Gly Leu Gly

10 15 20

<210> 1203  
<211> 28  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -17...-1

<400> 1203  
Met Asn Ala Ser Leu Leu Ser Phe Cys Leu Cys Ser Asp Phe Ile Ser  
-15 -10 -5  
Gln Asp Ala Leu Leu Leu Thr Val Ile Phe Pro Pro  
1 5 10

<210> 1204  
<211> 79  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -60...-1

<400> 1204  
Met Leu Asn Met Glu Pro Tyr Thr Val Ser Gly Met Ala Arg Gln Asp  
-60 -55 -50 -45  
Ser Ser Ser Glu Val Gly Glu Asn Gly Arg Ser Val Asp Gln Gly Gly  
-40 -35 -30  
Gly Gly Ser Pro Arg Lys Lys Val Ala Leu Thr Glu Asn Tyr Glu Leu  
-25 -20 -15  
Val Gly Val Ile Val His Ser Gly Gln Ala His Ala Gly His Tyr Tyr  
-10 -5 1  
Ser Phe Ile Lys Asp Arg Arg Gly Cys Gly Lys Gly Lys Trp Leu  
5 10 15

<210> 1205  
<211> 23  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -20...-1

<400> 1205  
Met Xaa Xaa Ala His Phe Ser Leu His Leu Xaa Ser Ser Arg Xaa Pro  
-20 -15 -10 -5  
Pro Ile Leu Ala Ser Pro Val  
1

<210> 1206  
<211> 33  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -17...-1

<400> 1206

Met Ile Arg Pro Val Cys Glu Leu Ser Ile Phe Phe Thr Tyr Val Leu  
 -15 -10 -5  
 Ala Ile Tyr Ile Ser Pro Ser Val Asn Cys Leu Phe Ile Ser Phe Pro  
 1 5 10 15

```
<210> 1207
<211> 84
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -29..-1
```

```
<400> 1207
Met Arg Gly Cys Gln Leu Leu Gly Leu Arg Ser Ser Trp Pro Gly Asp
             -25               -20              -15
Leu Leu Ser Ala Arg Leu Leu Ser Gln Glu Lys Arg Ala Ala Glu Thr
             -10               -5                1
His Phe Gly Phe Glu Thr Val Ser Glu Glu Glu Lys Arg Gly Asp Leu
      5                   10                  15
Thr Ser Val Val Ser Leu Glu Tyr Pro Glu Val Gln Leu Gln Gly Gln
20                      25                 30                 35
Arg Val Tyr Ala Phe Leu Ser Pro Ile Cys Thr Tyr Gly Ser Glu Gly
          40                     45                    50
Cys Ser Leu Lys
           55
```

```
<210> 1208
<211> 55
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -35..-1
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```

<400> 1208
Met Glu Asn Leu Pro Phe Pro Leu Lys Leu Leu Ser Ala Ser Ser Leu
-35          -30          -25          -20
Asn Thr Pro Ser Ser Thr Pro Trp Val Leu Asp Ile Phe Leu Thr Leu
          -15          -10          -5
Val Phe Ala Leu Gly Phe Phe Phe Leu Leu Leu Pro Tyr Phe Ser Tyr
          1          5          10
Leu Arg Cys Asp Asn Pro Pro
          15          20

```

```
<210> 1209
<211> 20
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -13..-1
```

```
<400> 1209
Met Cys Val Cys Val Phe Ala Ile Phe Gly Val Arg Cys Cys Val Cys
          -10                -5                1
Val Arg Cys Ile
      5
```

<210> 1210  
 <211> 46  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -44...-1

<400> 1210  
 Met Ile Cys Ile Phe Tyr Ser Lys Ile Ser Ile Ser Val Gly Cys Gly  
                   -40                  -35                  -30  
 Arg Thr Ala Ala Glu Gln Val Gly Cys Lys Gln Arg Ser Phe His Xaa  
                   -25                  -20                  -15  
 Pro Cys Pro Leu Leu Phe Pro Gly Ala Cys Phe Pro Cys Pro  
                   -10                  -5                  1

<210> 1211  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1211  
 Met Asn Leu Ile Cys Val Ser Leu Met Ala Ser Asp Gly Ala Ser Ser  
                   -15                  -10                  -5  
 Pro Val Leu Gly Gly Ser Ser His Ser Ser Ser Xaa Xaa  
 1                  5                  10

<210> 1212  
 <211> 59  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -47...-1

<400> 1212  
 Met Gly Ser Val Thr Gly Ala Val Leu Lys Thr Leu Leu Leu Ser  
                   -45                  -40                  -35  
 Thr Gln Asn Trp Asn Arg Val Glu Ala Gly Asn Ser Tyr Asp Cys Asp  
                   -30                  -25                  -20  
 Asp Pro Leu Val Ser Ala Leu Pro Gln Ala Ser Phe Ser Ser Ser Ser  
                   -15                  -10                  -5                  1  
 Glu Leu Ser Ser Ser His Ser Pro Gly Phe Ala  
                   5                  10

<210> 1213  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 1213  
 Met Met Ser Glu Xaa Ser Gln Asp Leu Val Val Lys Cys Ala Pro Pro  
                   -30                  -25                  -20

555

Xaa Pro Phe Phe Leu Leu Phe Leu Phe Ser Ser Cys Asp Val Pro Val  
 -15 -10 -5 1  
 Pro Leu His Leu Leu Gln Trp Leu Gln Ser Phe Leu Arg Pro Arg  
 5 10 15

&lt;210&gt; 1214

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -27..-1

&lt;400&gt; 1214

Met Phe Arg Cys Val Arg Phe Leu Pro Ser Gly Gly Phe Val Val Leu  
 -25 -20 -15  
 Leu Thr Ser Gly Val Lys Pro Gln Thr Phe Ala Val Ser Val Thr Ala  
 -10 -5 1 5  
 Leu Lys Gly Gly Met Pro Gly Val Val His Ser Ser Gly Gly Phe Val  
 10 15 20  
 Val Leu Leu Thr Ser Gly Ala Xaa Cys Arg Pro  
 25 30

&lt;210&gt; 1215

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -30..-1

&lt;400&gt; 1215

Met Arg Val Gly Arg Arg Glu Gly His Pro Leu Phe Pro Asn Val Pro  
 -30 -25 -20 -15  
 Arg Cys Leu Phe Leu Asn Ala Arg Leu Ala Gly Thr Leu Cys Gln Leu  
 -10 -5 1  
 Lys Leu Leu Gln Phe Gly Arg Leu Gly Asn Thr Glu Ser His Leu His  
 5 10 15  
 Gly Leu Ala Gly  
 20

&lt;210&gt; 1216

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -31..-1

&lt;400&gt; 1216

Met Tyr Phe Asp Ile Gln Ile Val Ser Asp Val Val Ser Gly Ile Pro  
 -30 -25 -20  
 Phe Lys Leu Leu Cys Pro Leu Thr Cys Pro His His Ser Leu Ser Thr  
 -15 -10 -5 1  
 Val

&lt;210&gt; 1217

&lt;211&gt; 47

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -31...-1

&lt;400&gt; 1217

Met	Leu	Phe	Ile	Phe	Ser	Asp	Ile	Asp	Trp	Lys	Met	Asp	Leu	Cys	Phe
	-30					-25					-20				
Phe	Ser	Phe	Ser	Pro	Phe	Leu	Pro	Ser	Leu	Pro	Leu	Leu	Glu	Ala	Glu
-15				-10					-5						1
Arg	Met	Arg	Val	Ser	Asp	Gln	Leu	Gln	Tyr	Thr	Thr	Gly	Xaa	Gly	
			5					10					15		

&lt;210&gt; 1218

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -36...-1

&lt;400&gt; 1218

Met	Glu	Leu	Glu	Ala	Met	Ser	Arg	Tyr	Thr	Ser	Pro	Val	Asn	Pro	Ala
	-35					-30					-25				
Val	Phe	Pro	His	Leu	Thr	Val	Val	Leu	Leu	Ala	Ile	Gly	Met	Phe	Phe
-20				-15						-10					-5
Thr	Ala	Trp	Phe	Phe	Val	Tyr	Glu	Val	Thr	Ser	Thr	Lys	Tyr	Thr	Arg
			1				5						10		
Asp	Ile	Tyr	Lys	Glu	Leu	Leu	Ile	Ser	Leu	Val	Ala	Arg			
	15						20					25			

&lt;210&gt; 1219

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 1219

Met	Lys	Gly	Ala	Leu	Lys	Leu	Ile	Ser	Thr	Asn	Phe	Ser	Leu	Cys	Gln
	-15					-10					-5				
Ser	Val	Gln	Cys	Pro	Ser	Glu	Glu	Thr	Ile	Thr	Asp	Leu	Val	Ser	Val
1				5					10						15
Pro	Cys	Gln	Xaa	Gly	Leu										
				20											

&lt;210&gt; 1220

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -69...-1

&lt;400&gt; 1220

Met	Thr	Ser	Gln	Pro	Val	Pro	Asn	Glu	Thr	Ile	Ile	Val	Leu	Pro	Ser
			-65					-60					-55		
Asn	Val	Ile	Asn	Phe	Ser	Gln	Ala	Glu	Lys	Pro	Glu	Pro	Thr	Asn	Gln
			-50					-45					-40		

Gly	Gln	Asp	Ser	Leu	Lys	Lys	His	Leu	His	Ala	Glu	Ile	Lys	Val	Ile
		-35					-30					-25			
Gly	Thr	Ile	Gln	Ile	Leu	Cys	Gly	Met	Met	Val	Leu	Ser	Leu	Gly	Ile
		-20				-15					-10				
Ile	Leu	Ala	Ser	Ala	Ser	Phe	Ser	Pro	Asn	Phe	Thr	Gln	Val	Thr	Ser
-5					1				5					10	
Thr	Leu	Leu	Asn	Ser	Ala	Tyr	Pro	Phe	Ile	Gly	Pro	Gly			
			15					20							

```
<210> 1221
<211> 55
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -40..-1
```

```

<400> 1221
Met Val Asp Glu Cys Leu Thr Glu Pro Val Trp Gly Ser Lys Arg Gln
-40                      -35                      -30                      -25
Gly Cys Ser Ser Gln Ala Glu Ala Ser Cys Asp Ile Val Ser Ala Ala
-20                      -15                      -10
Cys Lys Cys Gly Ser Ser Gln Ala Ala Ile Asp Cys Glu Thr Ser Ser
-5                      1                      5
Cys Ser Glu Asp Phe Pro Val
10                      15

```

```
<210> 1222
<211> 31
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -14...-1
```

```

<400> 1222
Met Ala Trp Trp Phe Ser Gly Thr Phe Pro Leu Thr His Pro Cys Ser
          -10          -5          1
Gly Tyr Gly Ser Leu Met Ala Pro Ser Ser Pro Thr Pro Ser Gly
      5              10              15

```

```
<210> 1223
<211> 78
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -57..-1
```

<400> 1223															
Met	Val	Ala	Lys	Asp	Tyr	Pro	Phe	Tyr	Leu	Thr	Val	Lys	Arg	Ala	Asn
		-55					-50					-45			
Cys	Ser	Leu	Glu	Leu	Pro	Pro	Ala	Ser	Gly	Pro	Ala	Lys	Asp	Ala	Glu
		-40					-35					-30			
Glu	Pro	Ser	Asn	Lys	Arg	Val	Lys	Pro	Leu	Ser	Arg	Val	Thr	Ser	Leu
		-25			-20					-15					-10
Ala	Asn	Leu	Ile	Pro	Pro	Val	Lys	Ala	Thr	Pro	Leu	Lys	Arg	Phe	Ser
			-5						1				5		
Gln	Thr	Leu	Gln	Arg	Ser	Ile	Ser	Phe	Arg	Ser	Glu	Ser	Ala		
		10					15					20			

<210> 1224  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 1224  
 Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly  
                   -25                  -20                  -15  
 Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val  
                   -10                  -5                  1  
 Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu  
 5                  10                  15                  20  
 His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro  
                   25                  30                  35  
 Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu  
                   40                  45                  50  
 Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly  
                   55                  60                  65

<210> 1225  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400> 1225  
 Met Leu Gly Gly Ala Val Ile Ala Gly Arg Pro Leu Gly Arg Trp Glu  
                   -30                  -25                  -20  
 Ser Thr Ala Gln Xaa Ile Leu Ala Phe Leu Gln Ser Pro Arg Ala Ile  
                   -15                  -10                  -5  
 Leu Pro Gly Asn Phe Phe Glu Lys Asn Ala Gln Ile Gln Gly Gly Pro  
                   1                  5                  10  
 Trp Gly Gly Gly Ser Gly Lys Thr Cys Ala Pro Gly Arg Xaa Asp Pro  
 15                  20                  25                  30  
 Gly Trp Glu Cys Gly Ala Gly Gly Gly Xaa Gly Glu Ala Ala Gly Ser  
                   35                  40                  45  
 Arg Xaa Arg Xaa Ser  
                   50

<210> 1226  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1226  
 Met Ser Met Ala Cys Phe Phe His Leu Phe Val Ser Ser Leu Ile Ser  
                   -15                  -10                  -5  
 Phe Glu Gln Cys Phe Xaa Met Leu Arg Lys Leu Leu Lys Ile Ile  
 1                  5                  10                  15

<210> 1227

<211> 79  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -45...-1

<400> 1227  
 Met Gly Ser Arg Gly Asp Pro Leu Ile Cys Gly Leu Gln Arg Ser Val  
 -45 -40 -35 -30  
 Gly Glu Val Trp Phe Pro Gly Trp Gly His Thr Ile Thr His Cys Phe  
 -25 -20 -15  
 Pro Trp Leu Glu Val Gly Leu Phe Phe Trp Leu His Ala Ala Pro Gly  
 -10 -5 1  
 Arg Ala Ile Ala Leu Pro His Phe Ser Ser Phe Ser Val Gly Gln Xaa  
 5 10 15  
 Val His Leu Val Ser Pro Leu Xaa Xaa Leu Asp Ile Ser Val Glu  
 20 25 30

<210> 1228  
 <211> 55  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 1228  
 Met His Leu Leu Gln Glu Glu Leu Leu Leu Leu Pro Arg Gly Leu  
 -15 -10 -5  
 Cys Gln Val Cys Pro Arg Leu Cys Leu Gln Arg Xaa Val Gly Glu Leu  
 1 5 10  
 Gln Xaa Xaa Xaa Pro Asp Val Gly Thr Ala Leu Leu Pro Asp Val Asn  
 15 20 25  
 Arg Thr Ser Cys Thr Thr Trp  
 30 35

<210> 1229  
 <211> 39  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 1229  
 Met Cys Leu Ser Cys Ile Gln Gly Ser Phe Phe Val Glu Ile Leu Gln  
 -25 -20 -15  
 Leu Val Thr Arg Leu Leu Leu Ser Pro Ser Gln Ser Thr Gln Thr His  
 -10 -5 1  
 Thr His Thr His Thr His Thr  
 5 10

<210> 1230  
 <211> 39  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

&lt;222&gt; -32...-1

&lt;400&gt; 1230

Met Thr Ile Leu Arg Glu Met Xaa Xaa Ser Leu Tyr Val Leu Glu Ala  
                   -30                  -25                  -20  
 Lys Asp Thr Ala Ile Leu Leu Leu Val Xaa Val Ser Asp Lys Asn Glu  
                   -15                  -10                  -5  
 Gln Gln Leu Gly Arg Gly Val  
   1                                  5

&lt;210&gt; 1231

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 1231

Met Arg Leu Ser Ser Ser Cys Gly Leu Pro Val Lys Thr Leu Pro Phe  
                                   -25                                  -20                                  -15  
 Ile Cys Cys Asn Leu Tyr Phe Leu Leu Phe Cys Arg Ser Ser Phe Leu  
                                   -10                                  -5                                  1  
 Tyr Phe Gly Tyr Asp Pro Ile Asn Thr Tyr Met Tyr Tyr Asn Val Phe  
                   5                                  10                                  15  
 Ser His Ser  
 20

&lt;210&gt; 1232

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -68...-1

&lt;400&gt; 1232

Met Leu Leu Thr Arg Pro Ala Val Ser Ala Gly Gly Ala Xaa Arg Phe  
                                   -65                                  -60                                  -55  
 Ser Pro Gly Ser Arg Gly Arg Gly Ser Asp Leu Glu Arg Gly Leu Cys  
                                   -50                                  -45                                  -40  
 Pro Ala His Pro Gly Ala Pro Pro Leu Pro Arg Pro Pro Asp Arg Leu  
                                   -35                                  -30                                  -25  
 Pro His Ser Phe Ser Pro Thr Gly Cys Leu Leu Xaa Pro Leu Leu Val  
                   -20                                  -15                                  -10                                  -5  
 Ser Cys Leu Gly Ser Leu Leu Pro Val Thr Gln Thr Leu Gly Ser Phe  
                                   1                                  5                                  10  
 Ser Ala Gly Pro Cys Phe Arg Thr Leu  
                   15                                  20

&lt;210&gt; 1233

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -25...-1

&lt;400&gt; 1233

Met His Ser Leu Cys Pro Leu Ser Gln Phe Leu Pro Ile Leu Xaa Ser

561

-25                      -20                      -15                      -10  
 Leu Ser Ser Ser Val Pro Ser Arg Ala Gly Ser Ala Phe Pro Ser Ala  
                                  -5                      1                      5  
 Leu Gly Pro Leu Tyr Gln Pro Leu Leu Gly Pro Pro Ala Trp  
                                  10                      15                      20

<210> 1234  
 <211> 59  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -44...-1

<400> 1234  
 Met Arg Thr Gln Val Tyr Glu Gly Leu Cys Lys Asn Tyr Phe Ser Leu  
                                  -40                      -35                      -30  
 Ala Val Leu Gln Arg Asp Arg Ile Lys Leu Leu Phe Phe Asp Ile Leu  
                                  -25                      -20                      -15  
 Val Phe Leu Ser Val Xaa Leu Leu Phe Leu Leu Phe Leu Val Asp Ile  
                                  -10                      -5                      1  
 Met Ala Asn Xaa Thr Thr Ser Leu Gly Arg Pro  
                                  5                      10                      15

<210> 1235  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -45...-1

<400> 1235  
 Met Gly Gln Phe Thr Ala Ala Met Val Gly Arg Ile Ser Cys Leu Gly  
                                  -45                      -40                      -35                      -30  
 Val Trp Lys Leu Pro Arg Val Glu Ser Cys Ser Gln Pro Ala Arg Pro  
                                  -25                      -20                      -15  
 Leu Leu Ser Leu Ala Gln Thr Thr Thr Lys Thr Thr Ala Thr Thr  
                                  -10                      -5                      1  
 Thr Thr Thr Lys His Ala Thr Cys Ala Leu Ala Tyr Thr Asn Thr Pro  
                                  5                      10                      15  
 Thr Glu Pro Xaa Gln Ala Asp Lys Ala Ser Arg Arg Ala Ser Gly Xaa  
                                  20                      25                      30                      35  
 Leu Xaa Xaa Ala Ala Arg His Ile Pro Trp His Gly Ala Thr Ala Ala  
                                  40                      45                      50  
 Gln Leu Pro Ala Pro Pro Pro Ser Val Ile Ser Ala Leu  
                                  55                      60

<210> 1236  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 1236  
 Met Leu Ile Phe Ile Ile Ala Ile Leu Phe Pro Asn Ser Gly Ser Cys  
                                  -15                      -10                      -5  
 Phe Ala Phe Ser Cys His Val Ser Phe Phe Phe Phe

1

5

10

<210> 1237  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 1237  
 Met Val Arg Cys Ala Cys Phe Pro Phe Phe Pro Phe Ala Phe Cys His  
 -15 -10 -5 1  
 Asp Cys Lys Phe Leu Gly Ala Ser Gln Ser Cys Phe Leu Leu Ser Arg  
 5 10 15  
 Gln Asn Cys Val Ser Thr Gly Xaa Pro Ser Ser Lys Ser Asp Ile Asn  
 20 25 30  
 Ser Arg Ser Gly Ser Cys Ser Leu Ala Arg  
 35 40

<210> 1238  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 1238  
 Met Val Ser Leu Arg Val Gly Ala Ser Pro Phe Arg Phe Pro Leu Ala  
 -25 -20 -15  
 Pro Leu Xaa Leu Val Phe Ile Ser Leu Leu Pro Ala Pro Phe Phe Pro  
 -10 -5 1 5  
 Thr Leu Ser Phe Pro Cys Cys Cys Val Ser Trp Leu Phe Ser Leu Ser  
 10 15 20  
 Val Xaa Val Ser Leu Arg Leu Ser Leu Xaa Val Ser Cys Leu Ser Leu  
 25 30 35  
 Trp Cys Leu Leu Val Leu Phe Leu Ser Pro Thr Leu Tyr Val Ser Asp  
 40 45 50  
 Ser Phe Cys Ser Phe Cys Val Leu Pro Ile Ala Leu Cys Pro Xaa Ala  
 55 60 65  
 Arg Ser  
 70

<210> 1239  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -54...-1

<400> 1239  
 Met Ala His Pro Cys Leu Ala Pro Ala Glu Pro Ser Thr Leu Ser Gln  
 -50 -45 -40  
 Thr Xaa His Pro Ile Gln Arg Thr Leu Thr Thr Phe Pro Gln Ala Trp  
 -35 -30 -25  
 Val Leu Thr Ser Ser Phe Ser Ile Gln Pro Gly Leu Ala Phe Leu Ala  
 -20 -15 -10  
 Ile Leu Thr Val Leu Ala Lys Pro Gly Ser Ser Xaa Trp Ser Pro Gly

-5                                  1  
Gln Phe Thr Pro His Ser Leu Leu  
                                15

```
<210> 1240
<211> 35
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -31...-1
```

```

<400> 1240
Met His Phe Pro Ile Gln Ala Thr Phe Xaa Tyr Ser Pro Thr Asp Ser
  -30                      -25                -20
Leu Cys His Leu Tyr Xaa Ser Leu Phe Ser Ser Phe Leu Cys Ser Thr
  -15                      -10                -5                1
Pro Ala Arg

```

```
<210> 1241
<211> 61
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -36..-1
```

```

<400> 1241
Met Ala Leu His Ile Leu Glu Cys Glu Arg Asn Val Cys Phe Val Ala
   -35               -30               -25
Val Arg Gln Pro Ala His Glu Ser Cys Phe Val Pro Ser Leu Val Thr
-20               -15               -10               -5
Gly Ala Leu Gln Gln Ser Gln Thr Gln His Pro Pro Trp Val Cys Pro
           1               5               10
Gln Val Gln Gly Ser Tyr Pro Ser Trp Lys Asn Arg Gly
      15               20               25

```

```
<210> 1242
<211> 58
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -32..-1
```

```

<400> 1242
Met Ser Cys Thr His Ser Ser Ser Asn Leu Gly Lys Phe Ser Val His
      -30                      -25                      -20
Arg Glu Tyr Arg Val Leu Xaa Leu Cys Asn Ser Arg Val Ser Phe Thr
      -15                      -10                      -5
Arg Xaa His Val Lys Arg Pro Pro Xaa Arg Leu Cys Val Ser Ser Lys
1      5                      10                      15
Gly Cys Leu Phe His Leu Gly Ala Gly Arg
      20                      25

```

```
<210> 1243
<211> 40
<212> PRT
<213> Homo sapiens
```

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 1243

Met Leu Lys Lys Leu Ser Ala Phe Pro Leu Leu Leu Val Ile Ile Leu  
                   -15                  -10                  -5  
 Leu Phe Gln Lys Gln Xaa Gly Leu Leu Lys Asn Tyr Xaa Ser Pro Gln  
                   1                  5                  10  
 Arg Gln Val Leu Phe Cys Asn Arg  
           15                  20

&lt;210&gt; 1244

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1244

Met Ser Tyr Phe Arg Cys Ile Phe Leu Ala Val Leu Ser Lys Ile Ser  
                   -15                  -10                  -5  
 Trp Ala Val Asn Met Cys Ser Leu Ile Ser Gly Ser Ser  
           1                  5                  10

&lt;210&gt; 1245

&lt;211&gt; 39

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -34...-1

&lt;400&gt; 1245

Met Leu Cys Ile Met Phe Gly Ile Glu Thr Asn Glu Ile Thr Lys Met  
                   -30                  -25                  -20  
 Thr Met Ser Phe Leu Leu Phe Leu Ser Ile Ser Leu Ile Thr Leu Tyr  
                   -15                  -10                  -5  
 Tyr Ser Ser Glu Ala Cys Gly  
           1                  5

&lt;210&gt; 1246

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -39...-1

&lt;400&gt; 1246

Met Cys Gln Ala Arg Ile Ala Leu Asp Arg Cys Asn Leu Arg Thr Ala  
                   -35                  -30                  -25  
 Phe Ile Leu Phe Xaa Leu Ile Leu Ser His Tyr Val Phe Xaa Leu Leu  
                   -20                  -15                  -10  
 Ala Pro Phe Leu Thr Arg Ser Ser Pro Ser Trp Asn Ser Tyr Gly Thr  
                   -5                  1                  5  
 Leu Ala Pro Glu Thr Thr Asn Ser Ser Leu Lys Phe Ser Asn Ser Asn  
   10                  15                  20                  25  
 Asn Gly Ile Ser Asp Leu Ala Xaa Leu Tyr Phe Ser His Val Xaa Lys

565

Ile Gly Ser Ala Ser Thr Met Gly Tyr Gly  
 30 35 40  
 45 50

<210> 1247  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<400> 1247  
 Met Val Lys Ser Val Ile Phe Leu Ser Phe Trp Gln Gly Met Leu Leu  
 -20 -15 -10  
 Ala Ile Leu Glu Xaa Cys Gly Ala Ile Pro Lys Ile His Ser Ala Arg  
 -5 1 5  
 Val Ser Val Gly Glu Gly Thr Val Ala Ala Gly Tyr Gln Asp Phe Ile  
 10 15 20  
 Ile Cys Val Glu Met Phe Phe Ala Ala Leu Ala Leu Arg His Ala Phe  
 25 30 35 40  
 Thr Tyr Lys Val Tyr Ala Asp Lys Arg Leu Asp Ala Gln Val Pro Thr  
 45 50 55  
 Tyr Gly Pro Tyr Gly Arg Cys Ala Pro Met Lys Ser Ile Ser Ser Ser  
 60 65 70  
 Leu Lys Glu  
 75

<210> 1248  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -86...-1

<400> 1248  
 Met Asp Met Arg Trp His Cys Glu Asn Ser Gln Thr Thr Asp Asp Ile  
 -85 -80 -75  
 Leu Val Ala Ser Ala Glu Cys Pro Ser Asp Asp Glu Asp Ile Asp Pro  
 -70 -65 -60 -55  
 Cys Glu Pro Ser Ser Gly Gly Leu Ala Asn Pro Thr Arg Ala Gly Gly  
 -50 -45 -40  
 Arg Glu Pro Tyr Pro Gly Ser Ala Glu Val Ile Arg Glu Ser Ser Ser  
 -35 -30 -25  
 Thr Thr Gly Met Val Val Gly Ile Val Ala Ala Ala Ala Leu Cys Ile  
 -20 -15 -10  
 Leu Ile Leu Leu Xaa Ala Met Tyr  
 -5 1

<210> 1249  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 1249  
 Met Ala Trp Thr Pro Leu Trp Pro Thr Leu Leu Thr Leu Cys Ile Gly

566

```

-20          -15          -10          -5
Ser Val Val Ser Ser Asp Leu Thr Gln Asp Pro Ala Val Ser Val Ala
          1          5          10
Leu Gly Gln Arg Val Arg Ile Thr Cys Gln Gly Asp Asn Leu Glu Glu
          15          20          25
Tyr Phe Ala Ser Trp Tyr Arg Gln Arg Pro Gly Gln Ala Pro Val Leu
          30          35          40
Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Xaa Arg Xaa
          45          50          55          60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Leu Thr Ile Xaa Gly Ala
          65          70          75
Gln Ala Glu Asp Xaa Ala Asp Tyr Tyr Cys Ser Xaa Arg Asp His Thr
          80          85          90
Asp Asn Arg Trp Val Phe Gly Gly Gly Thr Arg Leu Thr
          95          100          105

```

&lt;210&gt; 1250

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 1250

```

Met Glu Ala Glu Phe Tyr Met Xaa Ile Leu Thr Cys Leu Ile Phe Arg
-20          -15          -10          -5
Asn Ser Glu Gly Phe Gln Ile Xaa His Val Gln Lys Gln Gln Cys Leu
          1          5          10
Phe Lys Asn Glu Lys Val Val Val Gly Ser Cys Asn Arg Thr Ile Gln
          15          20          25
Asn Gln Gln Trp Met Trp Thr Glu Asp Glu Lys Leu Leu His Val Lys
          30          35          40
Ser Ala Leu Cys Leu Ala
          45          50

```

&lt;210&gt; 1251

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 1251

```

Met Cys Val Cys Ala Cys Ala Leu Cys Val Trp Leu Cys Val Lys Ser
          -15          -10          -5
Cys Ser Ile
          1

```

&lt;210&gt; 1252

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -21...-1

&lt;400&gt; 1252

```

Met Ile Ser Asp Val Gln His Leu Phe Ile Tyr Leu Leu Ala Phe Cys

```

-20                      -15                      -10  
 Met Pro Ser Leu Glu Lys Cys Leu Tyr Gly Ser Leu Ala His Phe Phe  
 -5                                      1                                      5                                      10  
 Phe Phe

<210> 1253  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15..-1

<400> 1253  
 Met Pro Leu Phe Arg Val Leu Phe Ser Xaa Thr Cys Ala Leu Xaa Gln  
 -15                                      -10                                      -5                                      1  
 Asp Phe Arg Met Gln Pro Cys Pro Pro Thr Pro Lys  
                                     5                                      10

<210> 1254  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24..-1

<400> 1254  
 Met Trp Tyr Val Glu Met Trp Val Ser Phe Phe Leu Leu Phe Tyr Val  
                                     -20                                      -15                                      -10  
 Leu Leu Phe Arg Asn Leu Tyr Thr His Thr His His Thr Gly  
                                     -5                                      1                                      5

<210> 1255  
 <211> 54  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -30..-1

<400> 1255  
 Met Ala Ala Arg Val Gly Ala Phe Leu Lys Asn Ala Trp Asp Lys Glu  
 -30                                      -25                                      -20                                      -15  
 Pro Val Leu Val Val Ser Phe Val Val Gly Gly Leu Gly Cys Asn Xaa  
                                     -10                                      -5                                      1  
 Ala Pro Ile Glu Pro Leu Leu Gln Val Leu Arg His Asp Gln Gln Gly  
                                     5                                      10                                      15  
 His Ala Leu Gln Leu Xaa  
                                     20

<210> 1256  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23..-1

&lt;400&gt; 1256

```

Met Gln Ala Arg Arg Trp Glu Ser Trp Met Trp Thr Cys Val Ala Pro
          -20          -15          -10
Val Tyr Pro Ala Cys Ser Gly Arg Arg Ala Xaa Ala Val Xaa Gln Xaa
          -5          1          5
Xaa Pro Arg Leu Gly Xaa Xaa Leu Pro Gly Pro Gly Xaa Glu His Leu
10          15          20          25
Ala His Val Cys Gly Leu Pro Ala Gly Glu Ala Gly Arg Gly Arg Gly
          30          35          40
Val Glu Arg Pro Gln Glu Lys Arg Ala Asp Lys Ala Val Xaa Val Arg
          45          50          55
Arg Gly Leu Gly Gly Ala Gly Leu Pro Gly Gly Asp Thr Pro Arg Gly
          60          65          70
Pro Pro Met Ser Thr Trp Pro
          75          80

```

&lt;210&gt; 1257

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 1257

```

Met Phe Leu Phe Phe Phe Gly Asn Ser Pro Cys Cys Gly Ala Thr Gly
          -10          -5          1

```

&lt;210&gt; 1258

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -25...-1

&lt;400&gt; 1258

```

Met Gly Leu Ser His His Arg Val Ser Ala Pro Ser Ser Leu Ser Leu
-25          -20          -15          -10
Ser Leu Ser Ala Ser Leu Ile Ile Ser Pro Ser Pro Ser Ala Ser Pro
          -5          1          5
Ser Leu Leu Xaa Pro Pro Xaa Arg
          10          15

```

&lt;210&gt; 1259

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -23...-1

&lt;400&gt; 1259

```

Met Phe Val Phe Leu Val Gly Thr Pro Cys Leu Ser Met Leu Leu Arg
          -20          -15          -10
Leu Val Ser Asn Ser Arg Pro Pro Val Met Arg Pro Pro Arg Pro Gly
          -5          1          5

```

&lt;210&gt; 1260

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -33...-1

&lt;400&gt; 1260

```

Met Lys Phe Thr His Phe Lys Cys Thr Ile Arg Leu Leu Leu Leu Tyr
      -30          -25          -20
Leu Gln Asn Pro Val Thr Ile Thr Ile Leu Phe Leu Ile Val Ser Met
      -15          -10          -5
Ala Leu Lys Ile Asn His Ile Pro Lys Gly
  1              5

```

&lt;210&gt; 1261

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 1261

```

Met Ser Cys Met Ser Leu Phe Pro Cys Cys Pro Ala Gln Ser Lys Asn
      -10          -5          1
Tyr Met Leu Leu Leu Phe Ile Ile Leu Leu Pro Thr Gln Phe Leu Tyr
      5              10          15
Ser Lys Leu Val Thr Ile Cys Cys Cys Phe
  20              25

```

&lt;210&gt; 1262

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 1262

```

Met Leu Val Cys Cys Thr Ile Asn Ser Ser Phe Ala Leu Gly Ile Ser
      -10          -5          1
Arg Asn Ala Ile Pro Leu Pro Ala Pro Gly
      5              10

```

&lt;210&gt; 1263

&lt;211&gt; 69

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -53...-1

&lt;400&gt; 1263

```

Met Gly Arg Gly Pro Gly Pro Leu Gln Glu Arg Ser Leu Phe Glu Xaa
      -50          -45          -40
Lys Arg Gly Ala Pro Pro Ser Ser Asn Ile Glu Asp Phe His Gly Leu
      -35          -30          -25
Leu Pro Lys Val Ile Pro Ile Cys Ala Leu Tyr Val Ile Cys Gln Phe
  -20          -15          -10

```

Ile Leu Ile Arg Ser Gly Val Asn Ile Ser Met Glu Gln Val Thr Val  
-5 1 5 10  
Val Asp Ala Ser Leu  
15

<210> 1264  
<211> 40  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -13...-1

<400> 1264  
Met Leu Tyr Cys Val Val Val Val His Ser Val Cys Cys Ala Val Tyr  
-10 -5 1  
Tyr Phe Val Ile Ile His Thr Ile Glu His Ile Thr Tyr Leu Cys Ile  
5 10 15  
His Ser Thr Ile Leu Leu Cys Val  
20 25

<210> 1265  
<211> 37  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -26...-1

<400> 1265  
Met Cys Trp Leu Arg Xaa Trp Gly Gln Ile Leu Leu Pro Val Phe Xaa  
-25 -20 -15  
Ser Leu Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly Phe  
-10 -5 1 5  
Ile His Ser Pro Met  
10

<210> 1266  
<211> 21  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -14...-1

<400> 1266  
Met Cys Gly Leu Xaa Ile Leu Cys Gly Pro Trp Leu His Ala Ala Pro  
-10 -5 1  
Pro Ser Pro Pro Arg  
5

<210> 1267  
<211> 42  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -33...-1

<400> 1267  
 Met Phe His Gly Arg Val Met Ala Met Gly Xaa Leu Thr Lys His Leu  
                   -30                  -25                  -20  
 Asn Leu Asn Ile Ser Ile Ser Leu Leu Leu Met Leu Xaa Xaa Tyr Trp  
                   -15                  -10                  -5  
 Ser Cys Trp Ile Lys Ser Pro Pro Xaa Met  
       1                                  5

<210> 1268  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -128...-1

<400> 1268  
 Met Leu Gly Arg Ser Ser Leu Leu Xaa Trp Lys Xaa Ser Pro Gly Ser  
                   -125                  -120                  -115  
 Lys Lys Leu Val Val Ala Thr Glu Lys Asn Val Ile Ala Ala Leu Asn  
                   -110                  -105                  -100  
 Ser Arg Thr Gly Glu Ile Leu Trp Arg His Val Asp Lys Gly Thr Ala  
                   -95                  -90                  -85  
 Glu Gly Ala Val Asp Ala Met Leu Leu His Gly Gln Asp Val Ile Thr  
                   -80                  -75                  -70                  -65  
 Val Ser Asn Gly Gly Arg Ile Met Arg Ser Trp Glu Thr Asn Ile Gly  
                   -60                  -55                  -50  
 Gly Leu Asn Trp Glu Ile Thr Leu Asp Ser Gly Ser Phe Gln Ala Leu  
                   -45                  -40                  -35  
 Gly Leu Val Gly Leu Gln Glu Ser Val Arg Tyr Ile Ala Val Leu Lys  
                   -30                  -25                  -20  
 Lys Thr Thr Leu Ala Leu His His Leu Ser Ser Gly His Ser Ser Gly  
                   -15                  -10                  -5  
 Trp Thr Ser Pro  
 1

<210> 1269  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -57...-1

<400> 1269  
 Met Ser Thr Thr Tyr Leu Asn Glu Asp Leu Lys Lys Lys Phe Ser Ala  
                   -55                  -50                  -45  
 Val Ile Glu Gln Val Leu Phe Ala His Leu Ser Pro Leu His Val Trp  
                   -40                  -35                  -30  
 Leu Gln Leu Arg Ser Leu Cys Glu Xaa Leu Thr Cys Ile Trp Val Arg  
                   -25                  -20                  -15                  -10  
 Phe Asn Phe Leu Ala Ser Ser Gln Ala Cys Ser Lys Cys Asn Ser Ser  
                   -5                  1                  5  
 Phe Leu Ile Met Ser Ser Ser Ser  
       10                                  15

<210> 1270  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -39...-1

&lt;400&gt; 1270

Met	Ala	Leu	Ile	Val	Leu	Gln	Leu	Thr	Phe	Gly	Ile	Gly	Tyr	Val	Thr
				-35					-30					-25	
Leu	Leu	Gln	Ile	His	Ser	Ile	Tyr	Ser	Gln	Leu	Ile	Ile	Leu	Asp	Leu
		-20					-15						-10		
Leu	Val	Pro	Val	Ile	Gly	Leu	Ile	Thr	Glu	Leu	Pro	Leu	His	Ile	Arg
	-5					1				5					
Glu	Thr	Leu	Leu	Phe	Thr	Ser	Ser	Leu	Ile	Leu	Thr	Leu	Asn	Thr	Val
10				15					20					25	
Phe	Val	Leu	Ala	Val	Lys	Leu	Lys	Trp	Phe	Tyr	Tyr	Ser	Thr	Arg	Tyr
			30						35					40	

&lt;210&gt; 1271

&lt;211&gt; 54

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 1271

Met	Arg	Val	Ala	Gly	Ala	Ala	Lys	Leu	Val	Val	Xaa	Val	Ala	Xaa	Phe
			-20					-15					-10		
Leu	Leu	Thr	Phe	Tyr	Val	Ile	Ser	Gln	Val	Phe	Glu	Ile	Lys	Met	Asp
		-5					1			5					
Ala	Ser	Leu	Gly	Asn	Leu	Phe	Ala	Arg	Ser	Ala	Leu	Asp	Thr	Ala	Ala
10				15						20					
Arg	Ser	Thr	Lys	Pro	Pro										
25				30											

&lt;210&gt; 1272

&lt;211&gt; 54

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1272

Met	His	Thr	Leu	Val	Phe	Leu	Ser	Thr	Arg	Gln	Val	Leu	Gln	Cys	Gln
-15				-10					-5					1	
Pro	Ala	Ala	Cys	Gln	Ala	Leu	Pro	Leu	Leu	Pro	Arg	Glu	Leu	Phe	Pro
		5					10					15			
Leu	Leu	Phe	Lys	Val	Ala	Phe	Met	Xaa	Lys	Lys	Thr	Val	Val	Leu	Arg
	20					25					30				
Xaa	Leu	Val	His	Thr	Arg										
	35														

&lt;210&gt; 1273

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 1273

Met Thr Val Val Ile Ser Cys Leu Val Gly Glu Cys Gly Ser Trp Lys  
                           -10                          -5                          1

&lt;210&gt; 1274

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -47...-1

&lt;400&gt; 1274

Met Cys Thr Leu Thr Asp Thr His Thr His Val Gln Val His Lys Ser  
                           -45                          -40                          -35  
 Lys Pro Cys Gln Leu Leu Ser Pro Pro Pro Pro Xaa His Gly Pro Leu  
                           -30                          -25                          -20  
 Leu Leu Pro Ile Phe Gly Leu Leu Val Pro Ser Gln Ile Phe Ser Ser  
                           -15                          -10                          -5                          1  
 Leu Leu Asn Ser Leu His Leu Gly Leu Pro Ser Phe Pro Lys Met Pro  
                           5                          10                          15  
 Leu Met Ile Phe Leu Pro Arg Trp  
                           20                          25

&lt;210&gt; 1275

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -63...-1

&lt;400&gt; 1275

Met Thr Leu Ile Leu Gly Glu Ser Ser Ser Gln Pro Gln Ile Ser Ile  
                           -60                          -55                          -50  
 Phe Leu Trp Thr Lys Val Lys Asp Leu Phe Ser Leu Met Ile Thr Trp  
                           -45                          -40                          -35  
 Thr Val Gln Met Lys Leu Thr Ser Met Trp Met Asn Leu Ile Pro Pro  
                           -30                          -25                          -20  
 Met Lys Gln Ile Leu Xaa Ser Thr Leu Ala Met Lys Ile His Ser Gln  
                           -15                          -10                          -5                          1  
 Gln Arg Phe Trp Pro Arg Val Arg Val Tyr Ser Arg Ile Tyr  
                           5                          10                          15

&lt;210&gt; 1276

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 1276

Met Tyr Lys Glu Lys Leu Val Leu Phe Leu Leu Asn Leu Phe Gln Lys  
                           -15                          -10                          -5  
 Ile Glu Glu Glu Glu Leu Phe Pro Asn  
                           1                          5

&lt;210&gt; 1277

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -48...-1

&lt;400&gt; 1277

Met Asp Ser Val Pro Ala Thr Val Pro Ser Ile Ala Ala Thr Pro Gly  
                  -45                  -40                  -35  
Asp Pro Glu Leu Val Gly Pro Leu Ser Val Leu Tyr Ala Ala Phe Ile  
                  -30                  -25                  -20  
Ala Lys Leu Leu Glu Leu Val Ala Thr Leu Pro Asp Asp Val Gln Pro  
                  -15                  -10                  -5  
Gly Pro Asp Phe Tyr Gly Xaa Xaa Trp Lys Leu Tyr Leu Ser Leu Pro  
1                                  5                                  10                                  15  
Ser Trp Glu Xaa Phe Val Cys His Phe Leu Met Glu Thr Val Leu Val  
                                  20                                  25                                  30  
Val Lys Xaa Arg Val Tyr Xaa Val  
                                  35                                  40

&lt;210&gt; 1278

&lt;211&gt; 39

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1278

Met Ala Ala Tyr Phe Ala Val Trp Ala Ser Val Ala Ser Pro Ala Ser  
                  -15                  -10                  -5  
Ile Cys Cys Gly Xaa Trp Leu Thr Gly Leu Val Arg His Glu Arg Ile  
                  1                                  5                                  10  
Glu Ala Pro Trp Ala Arg Gly  
15                                  20

&lt;210&gt; 1279

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 1279

Met Lys Thr Gln Phe Leu Ser Trp Gly Lys Phe Ser Phe Cys Phe Gly  
                  -25                  -20                  -15  
Ile Leu Leu Ile Leu Gln Leu Leu Lys Xaa Ser Leu Lys Lys Cys Arg  
                  -10                  -5                                  1  
His Gly  
                  5

&lt;210&gt; 1280

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -25...-1

&lt;400&gt; 1280

Met Leu Pro Ala Val Ala Val Ser Glu Pro Val Val Leu Arg Phe Ile  
-25 -20 -15 -10  
Leu Pro Ser Ser Trp Asp Cys Arg Cys Ala Pro Pro Leu Leu Thr Gly  
-5 1 5  
Phe Cys Ile Phe Trp Xaa Glu Thr  
10 15

&lt;210&gt; 1281

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -33...-1

&lt;400&gt; 1281

Met Asp Pro Ala Ala Pro Trp Leu Phe Trp Glu Ala Ala Ala Pro Ala  
-30 -25 -20  
Leu Lys Arg Pro Trp Leu Leu Met Val Ala Pro Arg Leu Pro Ala Gly  
-15 -10 -5  
Ala Arg Asp Ser Gly Gln Phe Pro Arg Lys Gly Gln Ala Gly Ser Pro  
1 5 10 15  
Ser Arg Gly Arg Val Arg Lys Leu Gly Gly Ala Val  
20 25

&lt;210&gt; 1282

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -31...-1

&lt;400&gt; 1282

Met Lys Met Ser Thr Pro Ser Pro Leu Ser Lys Lys Val Leu Arg Asn  
-30 -25 -20  
Gln Val Ser Arg Leu Xaa Ala Leu Leu Ser Pro Tyr Ala Phe Thr Leu  
-15 -10 -5 1  
Xaa Arg Leu Ala Ser Gly  
5

&lt;210&gt; 1283

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1283

Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys  
-15 -10 -5 1  
Ala Ile Ala Glu Glu Met Cys Xaa Gln Ala Val Val His Gly Phe Ser  
5 10 15  
Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Val Ser Val Ile Gln  
20 25 30  
Asn Thr Pro Thr Phe Ala Thr Gly Gly Arg  
35 40

<210> 1284  
 <211> 41  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 1284  
 Met Leu Ile Asp Ile Trp Ser Met Val Leu Arg Glu Asn Leu Phe Val  
           -25                  -20                  -15  
 Asn Leu Asn Leu Cys Phe Ala Tyr Thr Phe Ala Leu Tyr Ser Cys Pro  
           -10                  -5                  1                  5  
 Ala Pro Thr Arg Cys Pro Arg Pro Ser  
                           10

<210> 1285  
 <211> 73  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 1285  
 Met Leu Ser Cys Pro Trp Phe Pro Leu Ser Cys Ser Pro Ser Leu Pro  
           -15                  -10                  -5  
 Leu Ser Ile Pro Asp Cys Leu Pro Ala Phe Leu Trp Pro Leu Gly Ile  
           1                  5                  10  
 Pro Trp Pro Asp Gly Glu Gly Leu Arg Pro Ser Arg Leu Leu Arg Thr  
 15                  20                  25                  30  
 Arg Glu Asn Ile Thr Pro Leu Ser Leu Phe Ala Met Leu Ser Gly Arg  
                   35                  40                  45  
 Glu Gly Ala Pro Leu Leu Val Pro Leu  
           50                  55

<210> 1286  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -13...-1

<400> 1286  
 Met Val Val Val Ser Phe Leu Ala Ser Ser Ser Leu Pro Ala Glu Thr  
           -10                  -5                  1  
 Pro Lys Gln Gly  
           5

<210> 1287  
 <211> 145  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -107...-1

&lt;400&gt; 1287

```

Met Gly Xaa Leu Ala Leu Xaa Ala Trp Leu Gln Pro Arg Tyr Arg Lys
      -105                -100                -95
Asn Ala Tyr Leu Phe Ile Tyr Tyr Leu Ile Gln Phe Cys Gly Xaa Ser
      -90                -85                -80
Trp Ile Phe Ala Asn Met Thr Val Arg Phe Phe Ser Phe Gly Lys Asp
      -75                -70                -65                -60
Ser Met Val Asp Thr Phe Tyr Ala Ile Gly Leu Val Met Arg Leu Cys
      -55                -50                -45
Gln Ser Val Ser Leu Leu Glu Leu Leu His Ile Tyr Val Gly Ile Glu
      -40                -35                -30
Ser Asn His Leu Leu Pro Arg Phe Leu Gln Leu Thr Glu Arg Ile Ile
      -25                -20                -15
Ile Leu Phe Val Val Ile Thr Ser Arg Arg Gly Ser Pro Thr Arg Asn
      -10                -5                1                5
Met Trp Cys Val Cys Tyr Ser Ser Leu Asp Leu Trp Ile Trp Leu Xaa
      10                15                20
Thr Leu Ile Ala Xaa Xaa Ser Val Ile Gly Ile Ser Tyr Ala Val Leu
      25                30                35
Thr

```

&lt;210&gt; 1288

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1288

```

Met Asp Thr Phe Pro Ser Leu Thr Leu Thr Ala Leu Leu Val Pro Ser
      -15                -10                -5
Arg Val Gln Pro Gln
      1

```

&lt;210&gt; 1289

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 1289

```

Met Gly Leu Thr Lys Gln Tyr Leu Arg Tyr Val Ala Ser Ala Val Phe
      -20                -15                -10                -5
Gly Val Ile Gly Ser Gln Lys Gly Asn Ile Val Phe Val Thr Leu Arg
      1                5                10
Gly Glu Lys Gly Arg Tyr Val Ala Val Pro Ala Cys Glu His Val Phe
      15                20                25
Ile Xaa Asp Leu Arg Lys Gly Glu Lys Ile Leu Ile Leu Gln Gly Leu
      30                35                40
Lys Gln Glu Val Thr Cys Leu Cys Pro Ser Pro Asp Gly Leu His Leu
      45                50                55                60
Ala Val Gly Tyr

```

&lt;210&gt; 1290

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 1290

Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe Val Phe Phe Ser Val  
-20 -15 -10  
Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala  
-5 1

&lt;210&gt; 1291

&lt;211&gt; 47

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -22...-1

&lt;400&gt; 1291

Met Ser Leu Gly Leu His Ser Asn Ser Trp Val Leu Asp Pro Ala Leu  
-20 -15 -10  
Leu Leu Thr Cys Leu Thr Phe Pro Ile Tyr Lys Leu Leu Trp Val Arg  
-5 1 5 10  
Gly Gly Thr Arg Xaa Thr Leu Xaa Ala Leu His Ser Ala Arg Thr  
15 20 25

&lt;210&gt; 1292

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -60...-1

&lt;400&gt; 1292

Met Ala Ala Asn Ser Ser Gly Gln Gly Phe Gln Asn Lys Asn Arg Val  
-60 -55 -50 -45  
Ala Ile Leu Ala Glu Leu Thr Lys Arg Lys Glu Asn Tyr Leu Cys Arg  
-40 -35 -30  
Thr Ser Leu Gln Gln Ile Ile Leu Glu Leu Gly Ile Asp Thr Ile Met  
-25 -20 -15  
Trp Val Xaa Cys Xaa Phe Cys Phe Val Leu Phe Cys Phe Glu Thr Glu  
-10 -5 1  
Ser Arg Pro Val  
5

&lt;210&gt; 1293

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -35...-1

&lt;400&gt; 1293

Met Ser Ala Gly Ser Ala Thr His Pro Gly Ala Gly Gly Arg Arg Ser  
-35 -30 -25 -20  
Lys Trp Asp Gln Pro Ala Pro Ala Pro Leu Leu Phe Leu Pro Pro Ala  
-15 -10 -5  
Ala Pro Gly Gly Glu Val Thr Ser Ser Gly Gly Ser Pro Gly Xaa Thr

```

      1           5           10
Thr Ala Ala Pro Ser Gly Ala Leu Asp Ala Ala Ala Val Ala Ala
  15           20           25
Lys Ile Asn Ala Met Leu Met Ala Lys Gly Lys Leu Lys Pro Thr Gln
  30           35           40           45
Xaa Ala Ser Glu Lys Leu Gln Ala Pro Gly Lys Gly Leu Thr Ser Asn
      50           55           60
Lys Ser Lys Asp Asp Leu Val Val Ala Glu Val Glu Ile Asn Asp Val
      65           70           75
Pro Leu Thr Cys Arg Asn Leu Leu Thr Arg Gly Gln Xaa Gln Asp Glu
      80           85           90
Ile Ser Arg Leu Ser Gly Ala Ala Val Ser
  95           100

```

<210> 1294  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

```

<400> 1294
Met Ser Pro Leu Asp Gln Ala Val Ile Arg Ala Val Cys Leu Ser Gly
  -20           -15           -10
Gly Ser Cys Trp Gly Gly Val Arg Cys Leu Val Arg Gly Gly Pro Asn
  -5           1           5           10
Ile Gly Pro Ala Ala Gln Leu Leu Gly Gly Ile Pro Leu Cys Trp Pro
      15           20           25
Pro Ala Val Thr Ala Gly Glu Val Lys Leu
      30           35

```

<210> 1295  
 <211> 19  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

```

<400> 1295
Met Asn Ser Phe His Phe Ile Xaa Phe Leu Pro Phe Pro Trp Ala Glu
  -15           -10           -5           1
Xaa Ala Gln

```

<210> 1296  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -29...-1

```

<400> 1296
Met Gly Trp His Ser His Ser Ser Gln Gly Val Xaa Ala Met Pro Leu
      -25           -20           -15
Leu Leu Ser Thr His Thr Trp Thr Asp Thr Ala Leu Ala Phe Ser Thr
      -10           -5           1
His Thr His
  5

```

<210> 1297  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 1297  
 Met Xaa Ala Val Arg Asn Ala Gly Ser Trp Phe Leu Arg Ser Trp Thr  
           -20                  -15                  -10  
 Trp Pro Gln Thr Ala Gly Arg Val Val Ala Arg Xaa Pro Ala Gly Thr  
           -5                  1                  5                  10  
 Ile Cys Thr

<210> 1298  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 1298  
 Met Cys Ala Leu Phe Ile Leu Val Ser Ile Ser Leu Phe Tyr Ala Leu  
           -15                  -10                  -5                  1  
 Phe Ile Ser Pro Ser Ile Gln  
                   5

<210> 1299  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -53...-1

<400> 1299  
 Met Tyr Leu Val Cys Thr Thr Cys Thr Trp Cys Val Phe Ser Glu Met  
           -50                  -45                  -40  
 Phe Val His Gly Leu Asn Ile Thr Gln Leu Val Leu Ser Gln Leu Asp  
           -35                  -30                  -25  
 Tyr Phe Phe His Ser Asn Leu Thr Asn Leu Val Leu Tyr Phe Leu Val  
           -20                  -15                  -10  
 His Leu Leu Phe Ser Leu Ser Leu Phe Met Pro Leu Thr  
           -5                  1                  5

<210> 1300  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -78...-1

<400> 1300  
 Met Lys Leu Lys Leu Tyr Leu Cys Ile Leu Gly Pro Trp Gly Cys Xaa  
           -75                  -70                  -65

**PCT/IB99/00712**

Xaa	Lys	Val	Pro	Leu	Ile	Gly	Phe	Leu	Lys	Arg	Ile	Xaa	Xaa	Tyr	Xaa
		-60					-55					-50			
Leu	Thr	Val	Leu	Lys	Pro	Xaa	Ser	Leu	Xaa	Ser	Xaa	Ser	Ala	Gly	Leu
	-45					-40					-35				
Val	Pro	Ser	Glu	Asp	Ser	Lys	Lys	Glu	Ser	Val	Ser	Cys	Leu	Ser	Pro
-30					-25					-20					-15
Arg	Phe	Trp	Trp	Trp	Leu	Gly	Ser	Leu	Xaa	Val	Thr	Trp	Leu	Ile	His
			-10						-5					1	
Ala	Ser	Leu	Gln	Ser	Leu	Ser	Pro	Phe	Ser	His	Ala	Ile	Phe	Ser	Cys
	5						10					15			
Val	Ser	Val	Phe	Ser	Phe	Ala	Tyr	Lys	Asp	Thr	Ser	His	Ile	Glu	Leu
	20					25				30					
Gly	Pro	Ala	Leu	Ile	Thr	Ser	Ser	Gln	Leu	Pro	Leu	Gln	Gly	Thr	Asn
35					40					45					50
Phe	Gln	Ile	Met	Ser	His	Ser	His	Val	Ala						
				55					60						

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<222> -33...-1
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<221> SIGNAL  
<222> -27...-1
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<221> SIGNAL
<222> -31...-1
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<400> 1303
Met Asp Ser Asn Lys Lys Leu Val Leu Ser Ile Thr Gly Asn Thr Val
  -30                      -25                      -20
Trp Ile Leu Thr Thr Leu Glu Ser Leu Ala Gly Ser Val Xaa Ser Glu
-15                      -10                      -5                      1

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Gln Asp Leu Ser Ala Tyr  
5

<210> 1304  
<211> 55  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> -47...-1

<400> 1304  
Met Thr Cys Met Leu Ala Cys Arg Cys Ser Leu Xaa Gly Pro Gln Asp  
-45 -40 -35  
Phe Arg Phe Cys Ser Val Phe Ser Leu Leu Lys Leu Gly Asn Phe  
-30 -25 -20  
Tyr Phe Ser Phe Xaa Xaa Cys Leu Phe Leu Xaa Leu Xaa Xaa Ser Glu  
-15 -10 -5 1  
Met Glu Ser His Ser Phe Ser  
5

<210> 1305  
<211> 113  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -65...-1

<400> 1305  
Met Glu Asp Val Glu Ala Arg Phe Ala His Leu Leu Gln Pro Ile Arg  
-65 -60 -55 -50  
Asp Leu Thr Lys Asn Trp Glu Val Asp Val Ala Ala Gln Leu Gly Glu  
-45 -40 -35  
Tyr Leu Glu Glu Leu Asp Gln Ile Cys Ile Ser Phe Asp Glu Gly Lys  
-30 -25 -20  
Thr Thr Met Asn Phe Ile Glu Ala Ala Leu Leu Ile His Gly Ser Ala  
-15 -10 -5  
Cys Val Tyr Ser Lys Lys Val Glu Tyr Leu Tyr Ser Leu Val Tyr Gln  
1 5 10 15  
Ala Leu Asp Phe Ile Ser Gly Lys Arg Arg Ala Lys Gln Leu Ser Ser  
20 25 30  
Val Gln Glu Asp Arg Ala Asn Gly Val Ala Ala Pro Gly Ser Pro Gly  
35 40 45  
Gly

<210> 1306  
<211> 20  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> -15...-1

<400> 1306  
Met Phe Val Ser Tyr Leu Ile Leu Thr Leu Leu His Val Gln Thr Ala  
-15 -10 -5 1  
Val Leu Ala Arg  
5

<210> 1307  
<211> 60  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> -25...-1

<400> 1307  
Met Pro Glu Ala Ala Leu Phe Leu Phe Phe Leu Phe Ile Phe Leu Leu  
-25 -20 -15 -10  
Tyr Phe Lys Phe Trp Gly Thr Cys Ala Glu Arg Ala Gly Leu Leu His  
-5 1 5  
Arg Tyr Thr Arg Ala Met Glu Val Cys Cys Thr His Gln Pro Ser Ser  
10 15 20  
Thr Leu Gly Ile Ser Pro Asn Ala Leu Leu Pro Leu  
25 30 35

<210> 1308  
<211> 30  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> -23...-1

<400> 1308  
Met Arg Met Gly Thr Arg Ala Ser Pro Pro Leu Cys Met His Leu Ser  
-20 -15 -10  
Ile His Pro Xaa Xaa Cys Ala Cys Ile Cys Pro Ser Ile Gln  
-5 1 5

<210> 1309  
<211> 38  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> -36...-1

<400> 1309  
Met Tyr Pro Arg Val Trp Gly Cys Phe Gln Leu Leu His Xaa Leu Xaa  
-35 -30 -25  
Xaa Thr Arg Thr Thr Gly Lys Xaa Val Cys Val Cys Val Cys Val Cys  
-20 -15 -10 -5  
Val Cys Val Cys Val Cys  
1

<210> 1310  
<211> 100  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -14...-1

<400> 1310  
Met Ala Ala Val Val Leu Ala Ala Thr Arg Leu Leu Arg Gly Ser Gly  
-10 -5 1

Ser Trp Gly Cys Ser Arg Leu Arg Phe Gly Pro Pro Ala Tyr Arg Arg  
           5                          10                          15  
 Phe Ser Ser Gly Gly Ala Tyr Pro Asn Ile Pro Leu Ser Ser Pro Leu  
       20                          25                          30  
 Pro Gly Val Pro Lys Pro Val Phe Ala Thr Val Asp Gly Gln Glu Lys  
       35                          40                          45                          50  
 Phe Glu Thr Lys Val Thr Thr Leu Asp Asn Gly Leu Arg Val Ala Ser  
                           55                          60                          65  
 Gln Asn Lys Phe Gly Gln Phe Cys Thr Val Gly Ile Leu Ile Asn Ser  
                           70                          75                          80  
 Gly Ser Arg Tyr  
           85

<210> 1311  
 <211> 59  
 <212> PRT  
 <213> Homo sapiens

<220>  
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<400> 1311  
 Met Tyr Cys Leu Xaa Cys Val Glu Lys Ile Ala Lys Ala Leu Tyr Leu  
       -25                          -20                          -15                          -10  
 Ser Leu Asn Leu Tyr Phe Ala Asn Ser Leu Tyr Tyr Met Cys Val Cys  
                           -5                          1                          5  
 Ser Tyr Ile Tyr Phe Tyr Leu Xaa Ile Tyr Xaa Tyr Xaa Leu Ile Lys  
           10                          15                          20  
 Xaa Xaa Ser Tyr Tyr Val Ala Gln Thr Gly Leu  
       25                          30

<210> 1312  
 <211> 36  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -29...-1

<400> 1312  
 Met Cys Gln Leu Arg Arg Gly Leu Gly Lys Arg Pro Leu Ser Glu Ala  
                           -25                          -20                          -15  
 Ser Ala Val Phe Leu Thr Ala Val Phe Ser Ser His Ser Trp Leu Val  
                           -10                          -5                          1  
 Gly Pro Arg Tyr  
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<210> 1313  
 <211> 33  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> -31...-1

<400> 1313  
 Met Ser Val Arg Ser Thr Trp Cys Arg Ala Gln Phe Asn Ser Trp Val  
       -30                          -25                          -20  
 Ser Leu Leu Thr Phe Cys Leu Ile Asp Leu Ser Asn Val Asp Ser Gly  
       -15                          -10                          -5                          1

Xaa

<210> 1314  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> -53...-1

<400> 1314  
 Met Val Ser Gly Val Pro Ser Gly Leu Gly Lys Ser Ala Arg Pro Arg  
                   -50                  -45                  -40  
 Gly Arg Arg Ala Arg Lys Leu Leu Pro Ala Pro Arg Ala Ala Pro Arg  
                   -35                  -30                  -25  
 Thr Ala Pro Asp Tyr Pro Gly Pro Leu Arg Leu Thr Trp Leu Val Ala  
                   -20                  -15                  -10  
 Ala Gly Leu Glu Gly Arg Val His Leu Ala Asp Thr Ser Ser Gly Arg  
                   -5                  1                  5                  10  
 Lys Thr Trp Pro Gly Cys Gly His Gln Trp Lys Trp Lys Ala Leu Leu  
                   15                  20                  25  
 Ile Leu Val Arg Ala Phe Pro Ala  
                   30                  35

<210> 1315  
 <211> 37  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> -31...-1

<400> 1315  
 Met Gly Gly Cys Val Xaa Trp Arg Phe Leu Gly His Ser Ser Ala Leu  
                   -30                  -25                  -20  
 Arg Thr Val Cys Ser Ser Leu Arg Ser Xaa Arg Pro Cys Trp Cys Asp  
                   -15                  -10                  -5                  1  
 Gly Leu Arg Leu Arg  
                   5

<210> 1316  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -51...-1

<400> 1316  
 Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln  
                   -50                  -45                  -40  
 Pro Pro Gly Asn Ser Ser Ile Pro Ser Asp Leu Ala Ser Ser Ser Gly  
                   -35                  -30                  -25                  -20  
 Ser Thr Leu Tyr Arg Cys Ser Thr Cys Leu Leu Arg Ala Leu Ser Ser  
                   -15                  -10                  -5  
 Glu Leu Cys Ala Pro Arg Gly Cys His Ser Pro His His Val Ser Arg  
                   1                  5                  10  
 Ile Ser Trp Thr Leu Ser Val Ser Ser His Gly Pro Val Cys Gly Cys  
                   15                  20                  25  
 Trp Ala Phe Arg Phe His Asn Pro His Gly Leu Leu Ser Ser Arg Ser

30 35 40 45  
 His Leu Ser Xaa Trp Leu His Ser Ala Gly  
 50 55

<210> 1317  
 <211> 59  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 1317  
 Met Val Val Val Ser Ala Phe Ile Tyr Leu Phe Phe Glu Thr Gly Ser  
 -20 -15 -10  
 Pro Ser Val Ala Gln Ser Gly Val Gln Trp Cys Asp Leu Gly Leu Leu  
 -5 1 5 10  
 Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser Leu Leu  
 15 20 25  
 Gly Xaa Xaa Asp Cys Arg Arg Ala Pro Pro Gly  
 30 35

<210> 1318  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> -24...-1

<400> 1318  
 Met Phe Val Ser Xaa Thr Xaa Phe Phe Phe Xaa Leu Xaa Phe Leu Gly  
 -20 -15 -10  
 Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala Asn Trp Asn Phe  
 -5 1 5  
 Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe Tyr Phe Gly Ala  
 10 15 20  
 Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp Leu His Cys Asn  
 25 30 35 40  
 Thr Thr Ile Thr Xaa Gln Pro Leu Leu Ser Asp Asn Gln Tyr Asn Ile  
 45 50 55  
 Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr Ala Cys Tyr Gly  
 60 65 70  
 Cys Ser Leu Gly Leu Ala Leu  
 75

<210> 1319  
 <211> 41  
 <212> PRT  
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<220>  
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 <222> -26...-1

<400> 1319  
 Met Ser Ser Glu Ile Phe Xaa Xaa Xaa Xaa Ile Ala Tyr Ala Xaa Tyr  
 -25 -20 -15  
 Leu Leu Val Gly Leu Phe Pro Leu Lys Cys His Xaa Ser Xaa Phe Ser  
 -10 -5 1 5  
 Lys Xaa Gln Ile Ser Ser Phe Val Glu

10

15

<210> 1320  
<211> 63  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> -18...-1

<400> 1320  
Met Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg Leu Ala Ser Ala  
                  -15                  -10                  -5  
Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly Ala Ala Ser Leu  
          1                  5                  10  
Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr Ser Tyr Leu Pro  
15                  20                  25                  30  
Gly Tyr Val Xaa Lys Thr Ser Leu Ser Ser Pro Pro Trp Pro Arg  
                  35                  40                  45

<210> 1321  
<211> 24  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> -18...-1

<400> 1321  
Met Leu Ile Ala Ala Cys Ile Cys Ser Cys Leu Phe Phe Ser Gln Tyr  
                  -15                  -10                  -5  
Leu Xaa Xaa Ser Asn Pro Ala Ala  
          1                  5

<210> 1322  
<211> 30  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -16...-1

<400> 1322  
Met Lys Cys Trp Val Leu Ser Tyr Met Trp Gln Ser Ala Ser Leu Gly  
          -15                  -10                  -5  
Phe Ser Asn Arg Ile Lys Ser Xaa Leu Arg Pro Pro Ala Gly  
1                  5                  10

<210> 1323  
<211> 101  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -69...-1

<400> 1323  
Met Ser Val Gly Leu Cys Phe Leu Ile Trp Gln Met Gly Ile Met Leu  
                  -65                  -60                  -55

Leu Pro Arg Glu Cys Trp Lys Val Lys Asp Ser Lys Lys Tyr Lys Ser  
                   -50                  -45                  -40  
 Cys Arg Glu Ser Val Leu Pro Ala Gln Ala Cys Thr Gly Glu Ser Pro  
                   -35                  -30                  -25  
 Val Leu Ser Gly Val Arg Val Leu Gly Ile Arg Leu Ser Cys Val Leu  
                   -20                  -15                  -10  
 Ser His Leu Gln Ala Trp Asp Ser Trp Asp Asn Gln Lys Val Cys Tyr  
                   -5                  1                  5                  10  
 Leu Gly Ala Pro Cys Phe Gly Lys Arg Leu Ser Pro Thr Thr Trp Leu  
                   15                  20                  25  
 Thr Phe Trp Val Gly  
                   30

<210> 1324  
 <211> 43  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> -14...-1

<400> 1324  
 Met Phe Ala Phe Leu Ala Gly Cys Ser Gly Ser Cys Leu Trp Ser Arg  
                   -10                  -5                  1  
 His Phe Gly Arg Leu Arg Arg Ala Ala Pro Leu Ser Pro Glu Phe Glu  
                   5                  10                  15  
 Thr Gly Leu Gly Asn Met Val Glu Pro Gln Trp  
                   20                  25

<210> 1325  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> -17...-1

<400> 1325  
 Met Pro Thr Tyr Phe Leu Phe Val Pro His Leu Ile Ser Cys Asn Trp  
                   -15                  -10                  -5  
 Cys Glu Pro Arg Gly Asn Asn Pro Gln Ile Pro Leu Leu Ala Ile His  
                   1                  5                  10                  15  
 Thr Arg Lys Lys Asn Gln His Phe Ile Thr  
                   20                  25

<210> 1326  
 <211> 59  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> -27...-1

<400> 1326  
 Met Leu Trp Thr Ser Phe Gln Asn Pro Leu Gln Val Val Leu Leu Thr  
                   -25                  -20                  -15  
 Ser Val Ser Leu Xaa Xaa Xaa Xaa Xaa Xaa Gly Ser Val Arg Ile Xaa  
                   -10                  -5                  1                  5  
 Leu Ser His Trp Ser Ser Ser Ala Phe Phe Phe Leu Ile Xaa Xaa Xaa  
                   10                  15                  20

Xaa Leu Ser His Val Thr Lys Gln Met His Leu  
25 30

<210> 1327  
<211> 31  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -14...-1

<400> 1327  
Met Leu Thr Cys Leu Cys Gly Cys Phe Ile Val Leu Leu Val Cys Val  
-10 -5 1  
Leu Lys Cys Val Phe Val Val Ala Ser Asn Gly Leu Phe Phe Pro  
5 10 15

<210> 1328  
<211> 40  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -29...-1

<400> 1328  
Met Val Val Ser Phe Ala Val Gln Lys Leu Phe Ser Leu Ile Arg Ser  
-25 -20 -15  
His Leu Ser Ile Leu Ala Phe Val Ala Ile Ala Phe Gly Val Leu Asp  
-10 -5 1  
Met Lys Ser Leu Pro Thr Pro Gly  
5 10

<210> 1329  
<211> 104  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -65...-1

<400> 1329  
Met Gly Gly Arg Lys Met Ala Thr Asp Glu Glu Asn Val Tyr Gly Leu  
-65 -60 -55 -50  
Glu Glu Asn Ala Gln Ser Arg Gln Glu Ser Thr Arg Arg Leu Ile Leu  
-45 -40 -35  
Val Gly Arg Thr Gly Ala Gly Lys Ser Ala Thr Gly Asn Ser Ile Leu  
-30 -25 -20  
Gly Gln Arg Arg Phe Phe Ser Arg Leu Gly Ala Thr Ser Val Xaa Arg  
-15 -10 -5  
Ala Cys Thr Thr Xaa Ser Arg Arg Trp Asp Lys Cys His Val Glu Val  
1 5 10 15  
Val Xaa Leu Gly His Xaa Xaa Xaa Gly Lys Cys Pro Arg Gln Ile Leu  
20 25 30  
Ala Val Arg Arg Glu Val Thr Ala  
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<210> 1330  
<211> 80  
<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -31...-1

<400> 1330

Met Gln Leu Gln Val Leu Gly Arg Pro Gln Gly Ala Pro Gln Leu Ala  
-30 -25 -20  
Pro Gln Ala Leu Ala Leu Thr Xaa Thr Leu Leu Pro Ala Pro Gly Glu  
-15 -10 -5 1  
His Asp Ser Pro Met Xaa Ile Gly Gln Phe Pro Xaa Asn Pro Pro Ser  
5 10 15  
Glu His Pro Gly Ala Ser Pro Arg Arg Xaa Xaa Thr Gly Trp Xaa Pro  
20 25 30  
Gln Ser Trp Asp Arg Arg Val Ser Pro Ala Glu Ala Glu Thr Arg Arg  
35 40 45

<210> 1331

<211> 45

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -41...-1

<400> 1331

Met Gly Val Tyr Thr Cys Pro Ile Phe Val His Tyr Tyr Glu Asn His  
-40 -35 -30  
Gly Pro Thr Pro Ser Phe Xaa Ala Phe Ile Ser Phe His Leu Phe Thr  
-25 -20 -15 -10  
Leu Gly Phe Leu Cys Ser Leu Cys Pro His Pro His Gly  
-5 1

<210> 1332

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 1332

Met Lys Lys Ser Val Ser Cys Cys Ser Ser Leu Trp Val Ser Leu Ser  
-15 -10 -5  
Lys Asp Glu Asn Ala Glu Met  
1 5

<210> 1333

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30...-1

<400> 1333

Met Leu Leu Pro Leu Ala Met Ala Gly Arg Cys Tyr Thr Ala Lys His  
-30 -25 -20 -15  
Ser Thr Val Leu Leu Ser Gly Ser Pro Arg Ala Val Val Ser Ala Val

Val Met Val Gly Thr Gly Cys  
5

-5

1

<210> 1334  
<211> 26  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> -19...-1

<400> 1334  
Met Pro Ser Cys Cys Tyr Leu Arg Ala Phe Leu Leu Ser Val Pro Leu  
-15 -10 -5  
Gly Lys Gly Ser Ala Leu Lys Asp Pro Val  
1 5

<210> 1335  
<211> 101  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -24...-1

<400> 1335  
Met Val Ala Asp Lys Glu Val Gln Thr Arg Thr Leu Leu Leu Ser Ser  
-20 -15 -10  
Leu Trp Ile Val Cys Cys Leu His Leu Asp Ser Leu Ile Ser Xaa Lys  
-5 1 5  
Tyr Pro Leu His Ala Ile Arg Arg Tyr Leu Ser Thr Leu Arg Asn Gln  
10 15 20  
Arg Ala Glu Glu Gln Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu  
25 30 35 40  
Asn Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu  
45 50 55  
Pro Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly  
60 65 70  
Leu Lys Gln Cys Glu  
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<210> 1336  
<211> 20  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> -14...-1

<400> 1336  
Met His Ile Cys Leu Phe Phe Ser Phe Ser Xaa Xaa Phe Xaa Leu Phe  
-10 -5 1  
Phe Phe Phe Phe  
5

<210> 1337  
<211> 45  
<212> PRT  
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<220>  
<221> SIGNAL  
<222> -19...-1

<400> 1337  
Met Trp Leu Pro Cys Gln Ile Leu Ala Arg Leu Cys Arg Met Gln Thr  
                  -15                  -10                  -5  
Cys Trp Cys Leu Ser Phe Pro Thr Ser Ser Phe Thr Glu Ser Val Met  
                  1                  5                  10  
Arg Ser Leu Gly Glu Cys Pro Arg Lys Arg Trp Gly Gly  
          15                  20                  25

<210> 1338  
<211> 110  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -84...-1

<400> 1338  
Met Xaa Lys Leu Xaa Ser Asn Pro Ser Glu Lys Gly Thr Lys Pro Pro  
                  -80                  -75                  -70  
Ser Val Glu Asp Gly Phe Gln Thr Val Pro Leu Ile Thr Pro Leu Glu  
                  -65                  -60                  -55  
Val Asn His Leu Gln Leu Pro Ala Pro Glu Lys Val Ile Val Lys Thr  
                  -50                  -45                  -40  
Arg Thr Glu Tyr Gln Pro Glu Gln Lys Asn Lys Gly Lys Phe Arg Val  
          -35                  -30                  -25  
Pro Lys Ile Ala Glu Phe Thr Val Thr Ile Leu Val Ser Leu Ala Leu  
          -20                  -15                  -10                  -5  
Ala Phe Leu Ala Cys Ile Val Phe Leu Val Val Tyr Lys Ala Phe Thr  
                  1                  5                  10  
Tyr Asp His Ser Cys Pro Glu Asp Ser Ser Xaa Ser Thr Gly  
          15                  20                  25

<210> 1339  
<211> 51  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -21...-1

<400> 1339  
Met Phe Xaa Ala Ala Ala Gly Val Glu Val Leu Ser Leu Leu Phe Xaa  
          -20                  -15                  -10  
Cys Ile Tyr Trp Gly Gln Tyr Ala Thr Asp Gly Ile Gly Asn Glu Ser  
          -5                  1                  5                  10  
Val Lys Ile Leu Ala Lys Leu Leu Phe Ser Ser Ser Phe Leu Ile Phe  
                  15                  20                  25  
Leu Leu Met  
          30

<210> 1340  
<211> 35  
<212> PRT  
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<220>

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 1340

Met Leu Thr Gly Arg Phe Leu Gly Gly Ser Gln Gly Phe Phe Leu Ser  
 -25 -20 -15  
 Phe Leu Ser Phe Phe Phe Phe Ser Phe Phe Leu Phe Leu Xaa Phe Phe  
 -10 -5 1 5  
 Phe Phe Phe

&lt;210&gt; 1341

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -28...-1

&lt;400&gt; 1341

Met Phe Ile Xaa Xaa Xaa Met Lys Gln Xaa Phe His Ile Ile Asp Phe  
 -25 -20 -15  
 Val Phe Met Ser Lys Leu Leu Leu Phe Ser Phe Ser Phe Leu Xaa Lys  
 -10 -5 1  
 Ala Arg Met Xaa Thr Ala Ala Pro Gly  
 5 10

&lt;210&gt; 1342

&lt;211&gt; 37

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1342

Met Val Thr Pro Val His Ile Leu Thr Ala Val Leu Pro Leu Val Ser  
 -15 -10 -5  
 His Gln Gln Asn His Leu Gly Gly Arg Phe Ala Ser Leu Gly Ser Ser  
 1 5 10  
 Gly Ile Arg His Gly  
 15

&lt;210&gt; 1343

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1343

Met Leu Ile Leu His Leu Ala Thr Leu Leu Asn Leu Phe Ile Ser Ser  
 -15 -10 -5 1  
 Asn Ser Phe

&lt;210&gt; 1344

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 1344  
 Met Pro Leu Ala Ser Phe Gly Pro Phe Arg Ser Ser Cys Phe Ala Ala  
 -15 -10 -5 1  
 Arg Ser Ile Ile Trp Lys Ser Gly Arg Gln Gly  
 5 10

<210> 1345  
 <211> 36  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 1345  
 Met Glu Thr Trp Asn Gly Thr Ser Ile Ile Val Ala His Leu Xaa Ser  
 -30 -25 -20  
 Phe Ser Phe Leu Leu Ser Phe Leu Ser Phe Arg Ser Pro Leu Cys His  
 -15 -10 -5 1  
 His Pro Leu Gly  
 5

<210> 1346  
 <211> 26  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1346  
 Met Gln Phe Leu Ser Leu Ile Phe Ala Ser Cys Ser Ser Thr Thr Pro  
 -10 -5 1  
 Leu Pro Leu Xaa Gln Cys Cys Thr Leu Pro  
 5 10

<210> 1347  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -53...-1

<400> 1347  
 Met Val Thr Ser Lys Ser Arg Gly Pro Xaa Val Gln Thr Leu Gly His  
 -50 -45 -40  
 Ala Gly Asn Leu Arg Ser Leu Arg Glu Trp Pro Asp Leu Cys Cys Leu  
 -35 -30 -25  
 Arg Leu Phe Val Pro Asp His Thr Val Leu Ala Leu Val Cys His Ser  
 -20 -15 -10  
 Ala Ser Ile Ser Val Phe Pro Ser Gln Val Thr Cys Arg Leu Pro Arg  
 -5 1 5 10  
 Thr Gly Ser His Pro Ile Cys Val Ile Ser Gln Gly Ala Phe His Asp  
 15 20 25  
 Pro His Pro Asn

30

<210> 1348  
 <211> 53  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 1348  
 Met Pro Arg Ser Ile Asp Xaa Lys Ala Leu Ile Trp Thr Val Arg Leu  
           -25                  -20                  -15  
 Val Val Leu Phe Ala Ser Pro Xaa Val Arg Pro Ala Ser Ser Met Ser  
           -10                  -5                  1                  5  
 Ser Arg Leu Leu Leu Pro Xaa Leu His Tyr Ser Asp Trp Thr Cys Trp  
                           10                  15                  20  
 Leu Pro Glu Arg Arg  
                   25

<210> 1349  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -54...-1

<400> 1349  
 Met Thr Ser Leu Leu Thr Thr Pro Ser Pro Arg Glu Glu Leu Met Thr  
                           -50                  -45                  -40  
 Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp Gly Ala  
                   -35                  -30                  -25  
 Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu Thr Leu  
           -20                  -15                  -10  
 Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn Lys Gly  
           -5                  1                  5                  10  
 Ser Tyr Val Xaa Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala Ile Val  
                   15                  20                  25  
 Gln Met Glu Xaa Xaa Leu Ala Lys Gly Ser Glu  
           30                  35

<210> 1350  
 <211> 50  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 1350  
 Met Thr Lys Ala Xaa Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala Leu  
           -15                  -10                  -5  
 Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val Leu Gln  
           1                  5                  10  
 Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser Asp Trp Leu  
 15                  20                  25                  30  
 Cys Trp

<210> 1351

<211> 36  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 1351  
 Met Ala Gln Leu Ile Met Trp Leu Lys Asn Gln Leu Ile Leu Leu Gly  
                   -20                  -15                  -10  
 Ile Phe Arg Gly Ile Arg His Gln Ile Tyr Leu Ile Arg Thr Leu Gln  
               -5                          1                          5  
 Ile Arg Gln Trp  
 10

<210> 1352  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -30...-1

<400> 1352  
 Met Gly Pro Val Pro Gly Ala Ala Ala Gly Val Xaa Pro Xaa Xaa Gly  
 -30                  -25                  -20                  -15  
 Glu Leu Ala Xaa Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Val Ser  
                   -10                          -5                          1  
 Ile Thr Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly  
               5                          10                          15  
 Pro Glu Trp Ile Gly Xaa Ile Asp His Ser Gly Asp Thr Asp Tyr Asn  
       20                          25                          30  
 Pro Ser Leu Gln Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn  
 35                          40                          45                          50  
 Gln Phe Ser Leu Arg Leu Leu Ser Val Ser Ala  
                           55                          60

<210> 1353  
 <211> 39  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -36...-1

<400> 1353  
 Met Trp Phe Gln Thr Arg Ser Cys Gly His His Asp Pro Val Gly Ile  
       -35                          -30                          -25  
 Thr Gly Val Thr Lys Val Ile Leu Pro Leu Phe Leu Cys Pro Leu Gly  
 -20                          -15                          -10                          -5  
 Met Val Glu Thr Ser Phe Gly  
                           1

<210> 1354  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

&lt;222&gt; -109...-1

&lt;400&gt; 1354

```

Met Ser Tyr Val Val Thr Lys Thr Lys Ala Ile Asn Gly Lys Tyr His
                    -105                    -100                    -95
Arg Phe Leu Gly Arg His Phe Pro Arg Phe Tyr Val Leu Tyr Thr Ile
                    -90                    -85                    -80
Phe Met Lys Gly Leu Gln Met Leu Trp Ala Asp Ala Lys Lys Ala Arg
                    -75                    -70                    -65
Arg Ile Lys Thr Asn Met Trp Lys His Asn Ile Lys Phe His Gln Leu
                    -60                    -55                    -50
Pro Tyr Arg Glu Met Glu His Leu Arg Gln Phe Arg Gln Asp Val Thr
                    -45                    -40                    -35                    -30
Lys Cys Leu Phe Leu Gly Ile Ile Ser Ile Pro Pro Phe Ala Asn Tyr
                    -25                    -20                    -15
Leu Val Phe Leu Leu Met Tyr Leu Phe Pro Arg Gln Leu Leu Ile Arg
                    -10                    -5                    1

```

&lt;210&gt; 1355

&lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 1355

```

Met Tyr Asn Tyr Tyr Phe Leu Ser Leu Pro Ser Phe Leu Cys Thr Cys
                    -15                    -10                    -5
Cys Gln Phe Phe Pro His Asp Pro Ile Ser Ser Gln Tyr Ser Ser Pro
                    1                    5                    10
Gln Gly Lys Pro Cys Gln Val Thr Tyr Lys Phe Leu Phe Ile Leu Leu
                    15                    20                    25
Gly His Val Tyr Pro Arg Asp Gly Gly
30                    35

```

&lt;210&gt; 1356

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -79...-1

&lt;400&gt; 1356

```

Met Gln Gly Gly Asn Ser Gly Val Arg Lys Arg Glu Glu Glu Gly Asp
                    -75                    -70                    -65
Gly Ala Gly Ala Val Ala Ala Pro Pro Ala Ile Asp Phe Pro Ala Glu
                    -60                    -55                    -50
Gly Pro Asp Pro Glu Tyr Asp Glu Ser Asp Val Pro Ala Xaa Ile Gln
                    -45                    -40                    -35
Val Leu Lys Glu Pro Leu Gln Gln Pro Thr Phe Pro Phe Ala Val Ala
                    -30                    -25                    -20
Asn Gln Leu Leu Leu Val Ser Leu Leu Glu His Leu Ser His Val His
                    -15                    -10                    -5                    1
Glu

```

&lt;210&gt; 1357

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<220>  
<221> SIGNAL  
<222> -17...-1

<400> 1357  
Met Val Phe Tyr Cys Phe Ala Leu Cys Ile Ile Leu Ile Cys Val Met  
          -15                  -10                  -5  
Ser Cys Arg His Leu  
          1

<210> 1358  
<211> 65  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -43...-1

<400> 1358  
Met Leu Trp Glu Thr Asp Leu Ser Thr Asn Lys Thr Pro Val Ser Cys  
                  -40                  -35                  -30  
Thr Ala Gly Ser Ala Cys Ala Leu Ser Leu Leu Gln Phe Pro Val Leu  
                  -25                  -20                  -15  
Ile Thr Gln Leu Cys Leu Gly Lys Gly Gln Ser Glu Pro Ile Gly Pro  
          -10                  -5                  1                  5  
Leu Gln Asp Phe Val Ser Leu Glu Ser Thr Ser His Phe Tyr Ser Phe  
                  10                  15                  20  
Phe

<210> 1359  
<211> 32  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -20...-1

<400> 1359  
Met Thr Arg Arg Arg Thr Ser Leu Trp Cys Cys Ser Pro Ser Ser Arg  
-20                  -15                  -10                  -5  
Thr Ser Ser Ser Leu Ser Trp Arg Met Gly Ser Gln Ile Arg Pro Ser  
                  1                  5                  10

<210> 1360  
<211> 20  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -18...-1

<400> 1360  
Met Ala Phe Tyr Leu Trp Cys Phe His Ala Val Phe Phe Thr Val Cys  
                  -15                  -10                  -5  
Val Cys Val Arg  
          1

<210> 1361  
<211> 60

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -33...-1

&lt;400&gt; 1361

```

Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
      -30                -25                -20
His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
      -15                -10                -5
Cys Phe Arg Glu His Arg Val Gly Gly Lys Val Ile Asp Glu Gln His
  1           5           10           15
Pro Lys Ala Glu Glu Ser Phe Leu Val Gln Glu Gly
      20                25

```

&lt;210&gt; 1362

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 1362

```

Met Ser Phe Ser Ser Ser Leu Pro Pro Ser Leu Pro Pro Ser Leu Ala
      -25                -20                -15
Ser Phe Leu Leu Leu Thr Phe Leu Pro Ser Leu Pro Arg
      -10                -5                1

```

&lt;210&gt; 1363

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -46...-1

&lt;400&gt; 1363

```

Met Arg Ala Gln Gly Leu Ser Cys Gly Tyr Pro Ala Arg Pro Leu Gln
      -45                -40                -35
Pro Phe Leu Glu His Leu Ala Gly Ser Gly Ile Thr Lys Arg Thr Ala
      -30                -25                -20                -15
Pro Gly Cys Ala Pro Leu Arg Trp Val Pro Gln Ile Arg Gly Cys Pro
      -10                -5                1
Leu Thr Arg Leu Ala Gln Arg Gly Ala Asp Thr Arg Thr Arg Glu Asn
      5                10                15
Leu Phe Tyr Ser Arg Phe Pro Gly Leu Gln Leu Pro Ala Ala Xaa Xaa
      20                25                30
Ser Ala Ser Ala Leu Ser Leu Cys Thr Pro Arg Ser Pro Pro Leu Pro
      35                40                45                50
Leu Pro Leu Pro Ile Asn Ser Pro Gly
      55

```

&lt;210&gt; 1364

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> SIGNAL  
<222> -37...-1

<400> 1364

Met Ala Ala Ser Ser Thr Ser His Leu Lys Asn Lys Thr Lys Thr Phe  
-35 -30 -25  
Leu Ala Pro Met Thr Asn Cys His Ser Ile Ser Phe Leu Pro Phe Gln  
-20 -15 -10  
Ala Ser Ile Phe Gly Lys Thr Arg Leu Gln Ser Leu Arg Pro Ser His  
-5 1 5 10  
Pro Tyr Pro His  
15

<210> 1365

<211> 43

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39...-1

<400> 1365

Met Pro Lys Asp Ala Asp Leu Ala Phe Ser Ala Ser Leu Phe Glu Arg  
-35 -30 -25  
Ala Glu Ser Leu Tyr Thr Leu Ile Ser Lys Phe Xaa Ser Cys Xaa Cys  
-20 -15 -10  
Val Ser Thr Leu Ala Tyr Thr Lys Gly Arg Gly  
-5 1

<210> 1366

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 1366

Met Phe Val Asn Arg Thr Cys Phe Asn Ser Ser Phe Pro Ile Trp Met  
-25 -20 -15  
Pro Phe Leu Phe Leu Thr Leu Phe His Cys Leu Gly Arg Arg  
-10 -5 1

<210> 1367

<211> 63

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37...-1

<400> 1367

Met Xaa Gly Ser Ser Arg Xaa Xaa Gly Leu Gln Ile Thr Ala Ser Arg  
-35 -30 -25  
Thr Gly Lys Val Tyr Pro Ala Cys His Phe Leu Xaa Ala Val Ser Ala  
-20 -15 -10  
Ser Ser Ser Xaa Ala Cys Leu Trp Tyr Arg Pro Ile Ala Arg Arg Pro  
-5 1 5 10  
Ala Gly Pro Gly Gly Ser Leu Ser Ser Ala Gln Val His Pro Ala  
15 20 25

<210> 1368  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 1368  
 Met Ile Leu Phe Asp His Leu His Cys Ser Ala Ser Gly Val Thr Phe  
           -25                  -20                  -15  
 Trp Leu Leu Cys Arg Ile Cys Thr Phe Gly Phe His Gly Phe Ser Lys  
       -10                  -5                  1                  5  
 Tyr Thr Val Ser Arg Gly Thr Gln Gln Gly Ala Gly Xaa Xaa Xaa Gly  
                   10                  15                  20  
 Leu His Gln Asn Trp Glu Gln Trp Arg Gly Leu Val Gly Lys Ser Ser  
           25                  30                  35  
 Ser Ala Ala Val Val Phe Cys Leu Thr Phe Asp Leu Val Thr Ser Phe  
       40                  45                  50  
 Gln Leu Ala Ser Ala Ile Glu Ser Thr His Phe His Ala Gly Arg Asp  
  55                  60                  65                  70  
 Gly Ser His Leu

<210> 1369  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -29...-1

<400> 1369  
 Met Glu Leu Ser Leu Pro Pro Ser Met Cys Asp Tyr Pro Xaa Phe Cys  
                   -25                  -20                  -15  
 Leu Leu Leu Phe Pro Ala Ser Leu Arg Leu Leu Cys Val His Pro  
           -10                  -5                  1

<210> 1370  
 <211> 27  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 1370  
 Met Asp Gln Lys Pro Leu Phe Thr Val Gly Cys Ala Gly Leu Ala Gly  
       -20                  -15                  -10                  -5  
 Ser Cys Arg Gly Ile Ser Phe Leu Arg Thr Arg  
                   1                  5

<210> 1371  
 <211> 45  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

&lt;400&gt; 1371

```

Met Ser Val Asn Xaa Ile Phe Ile Phe Tyr Phe Ile Leu Leu Leu Leu
      -20          -15          -10
Ile Gln Asp Leu Thr Met Ser Pro Thr Ala Gly Met Gln Trp His Asn
      -5          1          5
His Gly Pro Pro Gln Ala Leu Pro Cys Pro Leu Arg Xaa
10          15          20

```

&lt;210&gt; 1372

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -45...-1

&lt;400&gt; 1372

```

Met Ser Phe Leu Asn Val Asp Ile Thr Asp Cys Leu Tyr Asn Pro Ser
-45          -40          -35          -30
Val Cys Pro Val Ala Gln Ser Ser Leu Thr Cys Asp Phe Ile Asp Gly
      -25          -20          -15
Ile Cys Leu Gly Ser Pro Leu Ala Glu Cys Leu Leu Gly Xaa Xaa Xaa
      -10          -5          1
Xaa Ile Xaa Gly Ile Asn Xaa Xaa Cys Phe Pro Cys Gly Val Lys Cys
      5          10          15
Ala Gly Val Val Leu Gly Leu Ser Thr Leu Trp Tyr Val Val
20          25          30

```

&lt;210&gt; 1373

&lt;211&gt; 49

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -37...-1

&lt;400&gt; 1373

```

Met Lys Val Gly Lys Asp Ser Leu Glu Ser Leu Pro Ser Leu Cys Glu
      -35          -30          -25
Lys His Ile Gly Pro Ser Gly Leu Phe Thr Phe Leu Ser Pro Ser Phe
      -20          -15          -10
His Ser Val His Leu Ser Glu Leu Asn Glu Leu Tyr Thr Ile Ala Ala
-5          1          5          10
Gly

```

&lt;210&gt; 1374

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -17...-1

&lt;400&gt; 1374

```

Met Glu Ser Lys Val Leu Ile Ser Ala Ser Leu Leu Arg Ala Ser Gln
      -15          -10          -5
Leu Lys Ile Lys Xaa Asn Lys Met Thr Asn Phe Leu Ile Leu
      1          5          10

```

<210> 1375  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<400> 1375  
 Met Ala Ala Ser Val Leu Asn Thr Val Leu Arg Arg Leu Pro Met Leu  
                           -20                          -15                          -10  
 Ser Leu Phe Arg Gly Ser His Xaa Xaa Phe Arg Phe Pro Ser Arg Leu  
                           -5                                  1                          5  
 Phe Ala Pro Lys Leu Pro Leu Arg Lys Ile Leu Cys Pro Gln Phe Pro  
   10                          15                          20  
 Phe Leu Leu Ile Arg Met Ser Pro Gly Asn Ile Trp Asn Gln Lys Asn  
 25                          30                          35                          40  
 Thr Arg Ser Asp Met Val Leu Ala Pro Ser Gly Leu Thr Thr Ala Ala  
                           45                          50                          55  
 Thr Thr Arg Val Val Tyr Pro His Ser Gly Leu Gly Arg His Val Phe  
                           60                          65                          70  
 Val Gly Ile Lys Leu Leu Gly Ile Pro Ala Pro Ser Val Glu Ile Thr  
           75                          80                          85  
 Ser Cys Met Leu Thr Leu  
           90

<210> 1376  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 1376  
 Met Lys Ser Asn Leu Thr Leu Leu Thr Cys Leu Xaa Leu Xaa Gly Gly  
                           -15                          -10                          -5  
 Glu Gly Trp Lys Gly Ala Ala Val Cys Phe Glu Thr Val Glu Gln Phe  
   1                                  5                          10  
 Cys Ser Leu Arg Lys Trp His Val Thr Tyr Leu Xaa Lys Asp Ser Gly  
 15                          20                          25                          30  
 Leu Cys Gln Gln Gln Glu Lys Leu Tyr Thr Lys Phe Leu Val Cys Ile  
                           35                          40                          45  
 Lys Gly Ala Ser Asn Glu Glu Ile Lys Lys Thr Tyr  
           50                          55

<210> 1377  
 <211> 24  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1377  
 Met Leu Ala Ser Pro Cys Val Leu Val Gln Gly Ser Gly Xaa Ser Leu  
                           -10                          -5                          1  
 Val Arg Thr Pro Trp Cys Pro Glu  
           5                          10

<210> 1378  
<211> 46  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -19...-1

<400> 1378  
Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Ile Thr Ile Ile Tyr  
                  -15                  -10                  -5  
Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys  
                  1                  5                  10  
Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His  
          15                  20                  25

<210> 1379  
<211> 53  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -39...-1

<400> 1379  
Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser  
                  -35                  -30                  -25  
Ile Phe Gly Tyr Lys Xaa Arg Gly Gly Val Pro Ser Leu Ile Ala Gly  
                  -20                  -15                  -10  
Leu Phe Val Gly Cys Leu Ala Gly Tyr Xaa Ala Tyr Arg Val Ser Asn  
          -5                  1                  5  
Asp Lys Arg Asp Val  
10

<210> 1380  
<211> 68  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -19...-1

<400> 1380  
Met Glu Gly Val Ala Xaa Xaa Thr Phe Leu Ala Ala Xaa Arg Arg Leu  
                  -15                  -10                  -5  
Val Thr Gly Gln Thr Ser Pro Arg Gly Thr Trp Cys Leu Tyr Pro Gly  
                  1                  5                  10  
Phe Cys Arg Ser Val Ala Cys Ala Met Pro Cys Cys Ser His Arg Ser  
          15                  20                  25  
Cys Arg Glu Asp Pro Gly Thr Ser Glu Ser Arg Glu Met Val Arg Val  
30                  35                  40                  45  
Arg Asp His Gly

<210> 1381  
<211> 37  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL

&lt;222&gt; -21...-1

&lt;400&gt; 1381

Met Thr Gly Gln Phe Thr Lys Glu Ile Gly Leu Ile Gly Leu Thr Val  
-20 -15 -10  
Pro Cys Gly Trp Gly Ser Leu Ile Thr Met Ala Glu Gly Arg Glu Glu  
-5 1 5 10  
Gln Val Thr Ser Gly  
15

&lt;210&gt; 1382

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 1382

Met His Leu Gly Phe Ile Leu Ser Phe His Gly Leu Ile Ala Asn Phe  
-10 -5 1  
Phe Phe Cys Leu Asn Ala Pro Ala  
5 10

&lt;210&gt; 1383

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 1383

Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile  
-20 -15 -10 -5  
Gly Ala Gly Ala Ala Thr Val Tyr Thr Asp  
1 5

&lt;210&gt; 1384

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -38...-1

&lt;400&gt; 1384

Met Glu Ser His Ser Val Ala Gln Ala Arg Met Arg Xaa Xaa Asn Leu  
-35 -30 -25  
Ser Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Pro Xaa Ser Cys Leu  
-20 -15 -10  
Ser Leu Leu Ser Asn Xaa Asp Tyr Arg His Ala Pro Pro Phe Leu Ala  
-5 1 5 10  
Asn Phe Xaa Ile Phe His Arg Asp Gly Val Ser Pro  
15 20

&lt;210&gt; 1385

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -55...-1

&lt;400&gt; 1385

Met	Phe	His	Gly	Ile	Pro	Ala	Thr	Pro	Gly	Ile	Gly	Ala	Pro	Gly	Asn
-55					-50					-45					-40
Lys	Pro	Glu	Leu	Tyr	Glu	Val	Arg	Gln	His	Gly	Arg	Ala	Val	Cys	Gly
			-35					-30						-25	
Gly	Glu	Asp	Asn	Ala	Ser	Pro	Gly	Glu	Gly	Leu	His	Gln	Gly	Leu	Cys
			-20					-15					-10		
Leu	Pro	Gln	Arg	Val	His	Cys	Ser	Leu	Leu	Pro	Ala	Pro			
	-5						1				5				

&lt;210&gt; 1386

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -22...-1

&lt;400&gt; 1386

Met	Pro	His	Ser	Phe	Val	Ser	Cys	Asn	Leu	Phe	Leu	Ser	Val	Leu	Asn
	-20						-15					-10			
Phe	Leu	Phe	Leu	Leu	Ser	Phe	Ser	Thr							
	-5					1									

&lt;210&gt; 1387

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 1387

Met	Ala	Val	Phe	Leu	Gln	Lys	Arg	Lys	His	Thr	Met	Arg	His	His	Leu
	-25				-20					-15					
Leu	Leu	Ser	Thr	Leu	Ala	Thr	Ile	Ala	Gly	Asn	Ile	Tyr	Arg		
-10				-5					1						

&lt;210&gt; 1388

&lt;211&gt; 47

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -26...-1

&lt;400&gt; 1388

Met	Ala	Asp	Ser	Glu	Ala	Leu	Pro	Ser	Leu	Ala	Gly	Asp	Pro	Val	Ala
	-25				-20					-15					
Val	Glu	Ala	Leu	Leu	Arg	Ala	Val	Phe	Gly	Val	Val	Val	Asp	Glu	Ala
-10			-5				1						5		
Ile	Gln	Lys	Gly	Thr	Ser	Val	Ser	Gln	Lys	Val	Cys	Xaa	Trp	Lys	
			10					15					20		

&lt;210&gt; 1389

<211> 87  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -36...-1

<400> 1389  
Met Arg Leu Ala Met Val Gln Leu Val Leu Asn Asn Leu Lys Thr Phe  
-35 -30 -25  
Tyr Pro Phe Ala Asp His Asp Leu Ala Glu Leu Pro Val Ser Ser Pro  
-20 -15 -10 -5  
Leu Cys His Ala Val Leu Lys Thr Leu Gln Cys Trp Glu Gln Val Leu  
1 5 10  
Leu Arg Arg Leu Glu Ile His Gly Gly Pro Pro Gln Asn Tyr Ile Ala  
15 20 25  
Ser His Thr Ala Xaa Xaa Ser Leu Ser Ala Gly Pro Ala Ile Leu Arg  
30 35 40  
His Lys Ala Leu Leu Glu Pro  
45 50

<210> 1390  
<211> 51  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -20...-1

<400> 1390  
Met Phe Lys Leu Phe Leu Phe Leu Phe Ile Leu Xaa Tyr Phe Xaa Xaa  
-20 -15 -10 -5  
Tyr Thr Leu Ser Ser Gly Ile Tyr Val Gln Asn Val Gln Val Cys Tyr  
1 5 10  
Ile Gly Ile His Met Pro Trp Trp Phe Ala Ala Pro Met Asn Leu Ser  
15 20 25  
Ser Ala Leu  
30

<210> 1391  
<211> 29  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -21...-1

<400> 1391  
Met Ile Tyr Ser Arg Ser Leu Glu Leu Ile Pro Leu Leu Ser Glu Ile  
-20 -15 -10  
Leu Tyr Ala Leu Ala Asn Ile Ser Pro Ile Pro Gln Thr  
-5 1 5

<210> 1392  
<211> 18  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL

<222> -16...-1

<400> 1392

Met Val His Val Ile Phe Tyr Phe Val Leu Phe Leu Gly Ile Met Thr  
-15 -10 -5

Gln Arg

1

<210> 1393

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 1393

Met His Lys Phe Phe Arg His Phe Tyr Ser Asp Phe Leu Ile Tyr Phe  
-25 -20 -15 -10

Phe Gln Leu His Ser Cys Cys His Asp Lys Val Thr Ala Xaa Arg Ala  
-5 1 5

Tyr Xaa His Tyr Ser Ser Leu Leu Thr Pro Tyr Leu Ser Gln His Pro  
10 15 20

Cys Pro His Pro Gly  
25

<210> 1394

<211> 121

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 1394

Met Ala Ala Leu Gly Ser Pro Ser His Thr Phe Arg Gly Leu Leu Arg  
-25 -20 -15

Glu Leu Arg Tyr Leu Ser Ala Ala Thr Gly His Pro Ile Ala Thr Pro  
-10 -5 1 5

Arg Pro Ile Gly Thr Xaa Val Lys Ala Phe Arg Ala His Arg Val Thr  
10 15 20

Ser Glu Lys Leu Cys Arg Ala Gln His Glu Leu His Phe Gln Ala Ala  
25 30 35

Thr Tyr Leu Cys Leu Leu Arg Xaa Ser Gly Asn Met Trp Pro Tyr Ile  
40 45 50

Arg Asn Phe Met Ala Arg Val Ser Ala Arg Trp Arg Ser Leu Leu Ala  
55 60 65 70

Trp Trp Val Ser Ser Cys Pro Ile Ser Leu Glu Gly Arg Ala Gly Ser  
75 80 85

His Glu His Gly Glu Tyr Pro Trp Met  
90 95

<210> 1395

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

&lt;400&gt; 1395

Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met Leu Gly Val  
-25 -20 -15  
Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Ala Ala Val  
-10 -5 1

&lt;210&gt; 1396

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1396

Met Ala Glu Gly Ala Leu Ser Phe Leu Cys Ser Leu Ser Gln Asn Ala  
-15 -10 -5  
Leu Asn Ile Ser Leu Ile Ser Arg Lys  
1 5

&lt;210&gt; 1397

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 1397

Met Tyr Pro Ser Phe Leu Leu Cys Phe Thr Leu Val Gly Thr Gln Leu  
-15 -10 -5  
Arg Asn Ser Ser Leu Ala Met  
1 5

&lt;210&gt; 1398

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1398

Met Glu Ser Cys Thr Val Gly Cys Ala Thr Ala Ser Ser Trp Gly Cys  
-15 -10 -5 1  
Thr Ser Arg

&lt;210&gt; 1399

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -43...-1

&lt;400&gt; 1399

Met Ala Met Ser Phe Glu Trp Pro Trp Gln Tyr Arg Phe Pro Pro Phe  
-40 -35 -30  
Phe Thr Leu Gln Pro Asn Val Asp Thr Arg Gln Lys Gln Leu Ala Ala

-25                      -20                      -15  
 Trp Cys Ser Leu Val Leu Ser Phe Cys Arg Leu His Lys Gln Ser Ser  
   -10                      -5                      1                      5  
 Met Thr Val Met Glu Ala Gln Glu Ser Pro Leu Phe Asn Asn Val Lys  
                          10                      15                      20  
 Leu Gln Arg Lys Leu Pro Val  
                          25

<210> 1400  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1400  
 Met Arg Leu His Val His Ser Leu Ser Pro Phe Ser Phe Ala Cys Leu  
                          -10                      -5                      1  
 Pro Phe Leu Ser Pro Pro Leu  
                          5

<210> 1401  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 1401  
 Met Leu His Phe Xaa Tyr Met Ile Xaa Val Cys Leu Glu Arg Met Cys  
   -25                      -20                      -15  
 Ile Leu Gln Leu Leu Ser Ala Val Leu Tyr Arg Phe  
 -10                      -5                      1

<210> 1402  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -30...-1

<400> 1402  
 Met Ser Ser Glu Pro Pro Pro Pro Gln Pro Pro Thr His Gln Ala  
 -30                      -25                      -20                      -15  
 Ser Val Gly Leu Leu Asp Thr Pro Leu Gly Ala Val Ser Ala His His  
                          -10                      -5                      1  
 Pro Leu Cys  
                          5

<210> 1403  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 1403  
Met Phe Leu Asp His Val Arg Phe Leu Thr Ser Ile Ser Phe Leu Ala  
-20 -15 -10 -5  
Leu Val Leu Trp Asn Val Phe Leu Asn Ser Thr Arg Leu  
1 5

<210> 1404  
<211> 26  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -19...-1

<400> 1404  
Met Arg Glu Lys Pro Gln Pro Ala Leu Leu Thr Ser Ser Glu Leu Pro  
-15 -10 -5  
Ala Leu Ala Ser Gln Ile His Cys Arg Val  
1 5

<210> 1405  
<211> 38  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -26...-1

<400> 1405  
Met Pro His Asn His Leu Glu Gly Asp Ala Leu Leu Arg Val Pro Val  
-25 -20 -15  
Leu Cys Ile Trp Arg Ala Trp Leu Arg Ala Glu Val Gly Gly Arg Ala  
-10 -5 1 5  
Pro Leu Pro Gly Arg Met  
10

<210> 1406  
<211> 27  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -22...-1

<400> 1406  
Met Lys Asn Thr Leu Tyr Tyr Asn Phe Cys Leu Phe Trp Ile Xaa Leu  
-20 -15 -10  
Pro Pro His Thr Cys Thr His Thr Asp Thr His  
-5 1 5

<210> 1407  
<211> 53  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -35...-1

&lt;400&gt; 1407

Met Cys Leu Asn Pro Ala Cys Ser Gly Pro Leu Ser Leu Arg Ser Pro  
 -35 -30 -25 -20  
 Arg Leu Pro Pro Leu Phe Cys Thr Phe Leu Ser Leu Ser Leu His Pro  
 -15 -10 -5  
 Trp Gly Gly Phe Phe Leu Cys Ala Trp Ile Ser Xaa Phe Leu Pro Trp  
 1 5 10  
 Val Cys Val Xaa Ala  
 15

&lt;210&gt; 1408

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -89...-1

&lt;400&gt; 1408

Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr Pro  
 -85 -80 -75  
 Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val  
 -70 -65 -60  
 Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp  
 -55 -50 -45  
 Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu Ala  
 -40 -35 -30  
 Ser Asp Phe Phe Leu Lys His Pro Asp Lys Asp Val Arg Leu Leu Val  
 -25 -20 -15 -10  
 Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro  
 -5 1 5  
 Tyr Thr Ser Pro Lys  
 10

&lt;210&gt; 1409

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1409

Met Xaa Ser Cys Glu Ile Ala Trp Thr Ala Thr Pro Ser Ser Ala Ala  
 -15 -10 -5  
 Phe Ala Gln Ala Phe Pro Thr Ala Cys Asn  
 1 5

&lt;210&gt; 1410

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -25...-1

&lt;400&gt; 1410

Met Cys His Tyr Leu Trp Lys Lys Leu Tyr Ser Thr Leu Leu Tyr Ile  
 -25 -20 -15 -10  
 Leu Ser Arg Ser Ser Gly Arg Arg Gly Lys Asn Leu Ile Thr Ala Val

Ala Ser Arg Ala Gly Asn Leu Gly Val Trp Thr Glu Lys Gly  
 10 15 20

<210> 1411  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 1411  
 Met Xaa Ser His Arg Leu Phe Gly Cys Phe Pro Ser Asp Leu Ser Arg  
 -25 -20 -15  
 Met Val Leu Leu Ser Ser Ala Leu Leu Ser Thr Glu Asn  
 -10 -5 1

<210> 1412  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 1412  
 Met Arg Pro Ser His Ser Ser Ala Tyr Leu Cys Leu His Leu Cys Ala  
 -20 -15 -10  
 Phe Ser Thr Glu Gly Trp Met Asn Arg Leu Ser Ser Ser Leu Arg Leu  
 -5 1 5 10  
 Ala Pro Leu Pro Leu Tyr Pro Phe Cys Leu Pro Ser Asn Ser Pro  
 15 20 25

<210> 1413  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1413  
 Met Trp Ser Arg Leu Val Trp Leu Gly Leu Arg Ala Pro Leu Gly Gly  
 -15 -10 -5  
 Arg Gln Gly Phe Thr Ser Lys Ala Asp Pro Gln Gly Ser Gly Arg Ile  
 1 5 10 15  
 Thr Ala Ala Val Ile Glu His Leu Glu Arg Leu Ala Leu Val Asp Phe  
 20 25 30  
 Gly Ser Arg Glu Ala Val Ala Arg Leu Glu Lys Ala Ile Ala Phe Ala  
 35 40 45  
 Asp Arg Leu Arg Ala Val Asp Thr Asp Gly Val Glu Pro Met Glu Ser  
 50 55 60  
 Val Leu Glu Asp Arg Cys Leu Tyr Leu Arg Ser Asp Asn Val Val Glu  
 65 70 75 80  
 Gly Asn Cys Ala Asp Glu Leu Leu Gln Asn Ser His Arg Val Val Glu  
 85 90 95  
 Glu Tyr Phe Val Ala Pro Pro Gly Asn Ile Ser  
 100 105

<210> 1414  
<211> 83  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -81...-1

<400> 1414  
Met Ala Pro Pro Val Arg Tyr Cys Ile Pro Gly Glu Arg Leu Cys Asn  
-80 -75 -70  
Leu Glu Glu Gly Ser Pro Gly Ser Gly Thr Tyr Thr Arg His Gly Tyr  
-65 -60 -55 -50  
Ile Phe Ser Ser Leu Xaa Gly Cys Leu Met Lys Ser Ser Glu Asn Gly  
-45 -40 -35  
Ala Leu Pro Val Val Ser Val Val Arg Glu Thr Glu Ser Gln Leu Leu  
-30 -25 -20  
Pro Asp Val Gly Ala Ile Val Thr Cys Lys Ser Leu Ala Ser Ile His  
-15 -10 -5  
Ala Leu Pro  
1

<210> 1415  
<211> 80  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -60...-1

<400> 1415  
Met Val Gly Asn Gln Gly Pro Gln Pro Pro Phe Pro Met Glu Pro  
-60 -55 -50 -45  
Thr Met Ala Gln Tyr Gln Ala Ile Ser Lys His Leu Pro Lys Val Cys  
-40 -35 -30  
Gln Glu Pro His Leu Pro Arg Gly His Leu Gln Pro Gln Gln His Arg  
-25 -20 -15  
Leu Leu Val Ala Arg Leu His Met Ala Ser Leu Ala Arg Arg Cys Thr  
-10 -5 1  
Glu Trp Ala Lys Leu His Cys Ser Asp Ala Arg Leu Pro Trp Val Ser  
5 10 15 20

<210> 1416  
<211> 35  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -28...-1

<400> 1416  
Met Lys Pro Gln Thr Leu Ala Val Ser Val Thr Val Leu Lys Asp Gly  
-25 -20 -15  
Val Ala Gly Val Cys Phe Phe Arg Arg Ser Asp Ala Ser Glu Val Ser  
-10 -5 1  
Ser Phe Trp  
5

<210> 1417  
<211> 47

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -43...-1

&lt;400&gt; 1417

Met	Val	Val	Leu	Ile	Cys	Leu	Ser	Leu	Met	Ile	Ser	Asn	Thr	Glu	Leu
			-40					-35					-30		
Phe	Phe	Ile	Arg	Phe	Leu	Thr	Ala	Cys	Met	Pro	Ser	Phe	Glu	Lys	Cys
		-25				-20				-15					
Leu	Phe	Leu	Ser	Phe	Ala	His	Phe	Leu	Met	Gly	Arg	Thr	His	Arg	
	-10					-5				1					

&lt;210&gt; 1418

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -22...-1

&lt;400&gt; 1418

Met	Ser	Ser	Leu	Tyr	Ile	Leu	Asp	Ile	Ser	Leu	Leu	Ser	Asp	Ile	Leu
		-20				-15				-10					
Phe	Ala	Asn	Ile	Phe	Ser	His	Ser	Trp	Asp	Val	Phe	Pro	Leu	Ser	Phe
	-5				1				5				10		
Leu	Phe	Phe	Ser												

&lt;210&gt; 1419

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -84...-1

&lt;400&gt; 1419

Met	Gly	Gln	Gly	Ala	Arg	Gly	Trp	His	Arg	Glu	Pro	Gly	Leu	Gly	Leu
			-80				-75					-70			
Arg	His	Ser	Pro	Arg	Arg	Leu	Ser	Gly	Ala	Leu	His	Leu	Glu	Ala	Gly
		-65				-60				-55					
Cys	Asp	Arg	Asn	Ala	Thr	Thr	Val	Arg	Pro	Leu	Arg	Ala	Lys	Xaa	Gly
	-50				-45				-40						
Asp	Ala	Leu	Pro	Glu	Glu	Ile	Arg	Glu	Pro	Ala	Leu	Arg	Asp	Ala	Gln
	-35				-30				-25						
Trp	Val	Arg	Asp	Gln	Leu	Ala	Ser	Ser	Leu	Leu	Ile	Ile	Leu	Leu	Pro
	-20			-15					-10				-5		
Asn	Thr	Gln	Asp	Leu	Arg	Ile	Gln	Lys	Asp	Pro	Thr	Pro	Gly	Pro	
		1				5						10			

&lt;210&gt; 1420

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -48...-1

<400> 1420  
 Met Arg Lys Arg Lys Ile Ser Val Cys Gln Gln Thr Trp Ala Leu Leu  
                   -45                  -40                  -35  
 Cys Lys Asn Phe Leu Lys Lys Trp Arg Met Lys Arg Glu Ser Leu Met  
                   -30                  -25                  -20  
 Glu Trp Leu Asn Ser Leu Leu Leu Leu Cys Leu Tyr Ile Tyr Pro  
                   -15                  -10                  -5  
 His Ser His Gln Val Asn Xaa Xaa Ser Ser Leu Leu Thr Met Asp Leu  
 1                  5                  10                  15  
 Gly Arg Val Asp Xaa Xaa Asn Glu Ser Arg Phe Ser Val Val Tyr Thr  
                   20                  25                  30  
 Pro Val Thr Asn Thr Thr Pro  
                   35

<210> 1421  
 <211> 33  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -30...-1

<400> 1421  
 Met Cys Thr Cys Leu Cys Val Cys Leu Tyr Met Tyr Asn Met Gln Phe  
 -30                  -25                  -20                  -15  
 Leu Xaa Phe Val Phe Val Cys Xaa Leu Leu Lys Cys Met Ser Val Pro  
                   -10                  -5                  1  
 Leu

<210> 1422  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 1422  
 Met Ala Ala Ser Ala Ala Ala Glu Leu Gln Ala Ser Gly Gly Pro  
                   -30                  -25                  -20  
 Arg His Pro Val Cys Leu Leu Val Leu Gly Met Ala Gly Ser Gly Lys  
 -15                  -10                  -5                  1  
 Thr Thr Phe Val Gln Arg Leu Thr Gly His Leu His Ala Gln Gly Thr  
                   5                  10                  15  
 Pro Pro Tyr Val Ile Asn Leu Asp Pro Ala Val His Glu Val Pro Xaa  
                   20                  25                  30  
 Pro Ala Asn Ile Asp Ile Arg Asp Thr Val Lys Tyr Lys Glu Val Met  
                   35                  40                  45  
 Lys Gln Tyr Gly Leu Gly Pro Asn Gly Gly Ile Val Thr Ser Leu Asn  
 50                  55                  60                  65  
 Leu Phe Xaa Thr Arg Phe Asp Gln Val Met Lys Leu Leu Arg Arg Pro  
                   70                  75                  80  
 Arg Thr Cys Pro Asn Met Cys  
                   85

<210> 1423  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 1423

Met Tyr Ala Cys Ala Met Leu Val Leu Leu Thr His Gly Leu Ile His  
 -20 -15 -10 -5  
 Tyr Ser Phe Thr His His Leu His Tyr Val Phe Ile Leu Ile Leu Pro  
 1 5 10  
 Leu Pro Pro Pro Pro Gln  
 15

&lt;210&gt; 1424

&lt;211&gt; 45

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 1424

Met Gly Phe Leu Gly Ser Pro Arg Gln Arg Asn Ser Met Cys Leu Leu  
 -20 -15 -10  
 Leu Asp Val Ser Ser Xaa Lys Ser Thr Asp Asn Xaa Xaa Xaa Xaa Xaa  
 -5 1 5  
 Leu Ile Ile Tyr Tyr Leu Ile Thr Arg Lys Gly Pro Gly  
 10 15 20

&lt;210&gt; 1425

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -43...-1

&lt;400&gt; 1425

Met Ser Cys Gln Xaa Xaa Leu Ala Xaa Thr Leu Thr Trp Leu Met Ile  
 -40 -35 -30  
 Arg Gly Arg His Pro Tyr Leu Thr Arg Arg Ser Ala Arg Asn Phe Asn  
 -25 -20 -15  
 Ile Phe Leu Ala Ala Pro Ser Pro Val Trp Gln Pro Gln Arg Thr Arg  
 -10 -5 1 5  
 Arg Pro Gln

&lt;210&gt; 1426

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -34...-1

&lt;400&gt; 1426

Met Cys Pro Ala Trp Leu Pro Cys Trp Thr Ala Gln Thr Glu His Leu  
 -30 -25 -20  
 Asp Arg Tyr Arg Lys Phe His Gln Met Ala Leu Xaa Pro Gly Thr Ser  
 -15 -10 -5  
 Arg Ala Gln Ala Leu Leu Tyr Asn Glu Val Leu Glu Arg Phe Met Phe  
 1 5 10  
 Thr Arg Leu

15

&lt;210&gt; 1427

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -18...-1

&lt;400&gt; 1427

Met Asn Val Met Lys Arg Ile Cys Thr Phe Leu Leu Pro Ser His Ser  
                   -15                  -10                  -5  
 Thr Ser Gly Pro Leu Cys Cys Ser Asn Ala His Leu Pro Ala Thr Ser  
           1                  5                  10  
 Ser Thr Leu Lys His Cys Arg Ala Trp Arg Glu Ala  
 15                  20                  25

&lt;210&gt; 1428

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -121...-1

&lt;400&gt; 1428

Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly  
           -120                  -115                  -110  
 Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val Phe Lys Met Ala  
 -105                  -100                  -95                  -90  
 Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu  
                   -85                  -80                  -75  
 Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu  
                   -70                  -65                  -60  
 Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr  
                   -55                  -50                  -45  
 Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys  
                   -40                  -35                  -30  
 Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr  
 -25                  -20                  -15                  -10  
 Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp  
                   -5                  1                  5  
 Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser  
           10                  15                  20  
 Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Xaa Ala  
 25                  30                  35  
 Phe Thr  
 40

&lt;210&gt; 1429

&lt;211&gt; 63

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -38...-1

&lt;400&gt; 1429

Met Ala Glu Ile Thr Asn Ile Arg Pro Ser Phe Asp Val Ser Pro Val

```
<220>  
<221> SIGNAL  
<222> -26...-1
```

&lt;400&gt; 1433

Met Phe Leu Ile Leu Gly Lys Phe Ser Arg Val Met Gly Leu Pro Leu  
-25 -20 -15  
Ala Cys Phe Ser Leu Phe Gly Xaa Leu Pro Gln Gly Leu Leu Ile  
-10 -5 1 5

&lt;210&gt; 1434

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 1434

Met Val Ala Leu Gly Gln Leu Ala Xaa Leu Pro Gly Xaa Xaa His Gly  
-15 -10 -5  
Gly Leu Ser Ala Val Thr Val Val Leu Pro Ile Leu Leu Cys  
1 5 10

&lt;210&gt; 1435

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1435

Met Pro Val Ser Phe Val Cys Leu Leu Phe Arg Asn Val Tyr Ser Asn  
-15 -10 -5 1  
Leu Leu Pro Ser Phe Phe  
5

&lt;210&gt; 1436

&lt;211&gt; 64

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -27...-1

&lt;400&gt; 1436

Met Gly Ser Gly Gly Asp Ser Leu Leu Gly Gly Arg Gly Ser Leu Pro  
-25 -20 -15  
Leu Leu Leu Pro Ala His His Gly Arg His Gly Ser Gly Leu Pro Ala  
-10 -5 1 5  
Pro Asp Pro Ser Pro Pro Gly Pro Ala Val Pro Gly Pro Trp Pro  
10 15 20  
Cys Gln Asp Glu Leu Pro Ser Leu Arg Pro Ala Thr Ser His His Phe  
25 30 35

&lt;210&gt; 1437

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -25...-1

&lt;400&gt; 1437

Met Ala Val Gly Gly Thr Ala Val Ile Thr Arg Arg Leu Leu Gly Arg  
 -25 -20 -15 -10  
 Ser Gly Phe Ser Phe Gln Val Ser Gly Trp Gly Trp Gly Glu Arg Val  
 -5 1 5  
 Asp Asp Phe Leu Phe Ser Ser Gly Ile Asp Gly  
 10 15

&lt;210&gt; 1438

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -21...-1

&lt;400&gt; 1438

Met Arg His His Val Arg Xaa Pro Ala Leu Ser Ser Leu Ala His His  
 -20 -15 -10  
 Pro Arg Thr Ser Gly Gln Lys Arg Glu Pro Ile Ala Pro Ala Gln Leu  
 -5 1 5 10  
 Ser Pro

&lt;210&gt; 1439

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -73...-1

&lt;400&gt; 1439

Met Leu Ile Leu Asn Gly Phe Arg Gly His Ala Thr Asp Ser Val Lys  
 -70 -65 -60  
 Asn Ser Met Glu Ser Met Asn Thr Asp Met Val Ile Ile Pro Gly Gly  
 -55 -50 -45  
 Leu Thr Ser Gln Leu Gln Val Leu Asp Val Val Val Tyr Lys Pro Leu  
 -40 -35 -30  
 Asn Asp Ser Val Arg Ala Gln Tyr Ser Asn Trp Leu Leu Ala Gly Asn  
 -25 -20 -15 -10  
 Leu Ala Leu Ser Pro Thr Gly Asn Ala Lys Lys Pro Pro Leu Gly Leu  
 -5 1 5  
 Phe Leu Glu Trp Val Met Val Ala Trp Asn Ser Ile Ser Ser Glu Ser  
 10 15 20  
 Ile Val Gln Gly Xaa Lys Glu Val Pro Tyr Leu Xaa Gln Leu Gly Gly  
 25 30 35  
 Gly Arg Arg  
 40

&lt;210&gt; 1440

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -25...-1

&lt;400&gt; 1440

Met Ile Cys Thr Thr Val Tyr Ile Thr Met Ala Pro Tyr Cys Leu Ser

```

-25          -20          -15          -10
Asn Cys Leu Leu Xaa Xaa Ser Trp Gly Leu His Leu Tyr Arg Phe Leu
          -5          1          5
Ala Pro

```

```
<210> 1441
<211> 16
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -14...-1
```

```

<400> 1441
Met Val Ser Leu Cys Val Ala Ala Leu Phe Pro Leu Gln Ala Tyr Gly
          -10                      -5                      1

```

```
<210> 1442
<211> 28
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -24...-1
```

```

<400> 1442
Met Leu Ser Ile Phe Ser Phe Phe Cys Arg Pro Phe Val Tyr Leu Leu
      -20      -15      -10
Leu Arg Asn Leu Xaa Ser Tyr Ser Leu Pro Thr Thr
      -5      1

```

```
<210> 1443
<211> 94
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -77..-1
```

```

<400> 1443
Met Phe Pro Val Ser Ser Gly Cys Phe Gln Glu Gln Gln Glu Thr Asn
      -75                      -70                      -65
Lys Ser Leu Pro Arg Ser Ala Ser Thr Pro Glu Thr Arg Thr Lys Phe
      -60                      -55                      -50
Thr Gln Asp Asn Leu Cys Xaa Ala Gln Arg Glu Arg Leu Asp Ser Ala
-45                      -40                      -35                      -30
Asn Leu Trp Val Leu Val Asp Cys Ile Leu Arg Asp Thr Ser Glu Asp
      -25                      -20                      -15
Leu Gly Leu Gln Cys Asp Ala Val Asn Leu Ala Phe Gly Arg Arg Cys
      -10                      -5                      1
Glu Glu Leu Glu Asp Ala Arg His Lys Leu Gln Xaa His Leu
      5                      10                      15

```

```
<210> 1444
<211> 20
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL
```

&lt;222&gt; -15...-1

&lt;400&gt; 1444

Met Pro Leu Val His Ser Phe Leu Trp Leu Ser Ser Ile Leu Tyr Ile  
 -15 -10 -5 1  
 Tyr His Leu Arg  
 5

&lt;210&gt; 1445

&lt;211&gt; 56

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 1445

Met Ile Ser Asn Gly Lys Phe Phe Cys Phe Phe Xaa Val Phe Xaa Phe  
 -20 -15 -10  
 Xaa Phe Leu Xaa Arg Xaa Leu Xaa Xaa Xaa Pro Arg Leu Glu Cys Asn  
 -5 1 5  
 Gly Lys Xaa Ser Ala His Xaa Asn Leu Arg Leu Leu Ser Xaa Ser Asn  
 10 15 20  
 Ser Leu Ala Ser Ala Pro Arg Gly  
 25 30

&lt;210&gt; 1446

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -90...-1

&lt;400&gt; 1446

Met Glu Asp Ser Ala Ser Ala Ser Leu Ser Ser Ala Ala Ala Thr Gly  
 -90 -85 -80 -75  
 Thr Ser Thr Ser Thr Pro Ala Ala Pro Thr Ala Arg Lys Gln Leu Asp  
 -70 -65 -60  
 Lys Glu Gln Val Arg Lys Ala Val Asp Ala Leu Leu Thr His Cys Lys  
 -55 -50 -45  
 Ser Arg Lys Asn Asn Tyr Gly Leu Leu Asn Glu Asn Glu Ser Leu  
 -40 -35 -30  
 Phe Leu Met Val Val Leu Trp Lys Ile Pro Ser Lys Glu Leu Arg Val  
 -25 -20 -15  
 Arg Leu Thr Leu Pro His Ser Ile Arg Ser Asp Ser Glu Asp Ile Cys  
 -10 -5 1 5  
 Xaa Phe Thr Lys Asp  
 10

&lt;210&gt; 1447

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 1447

Met Asn Ala Glu Gly Ala Ser Pro Gly Lys Glu Thr Asn Thr Gly Thr

Met Ser Leu Pro Pro Phe Phe His Pro Ser Pro Ala Pro Ser Leu Ala  
-30 -25 -20 -15  
Pro Pro Pro Ser Leu Phe Leu Ser Leu Pro Pro Ser Leu Ser Pro Pro  
-10 -5 1  
Leu Pro Ala Arg

5

<210> 1451  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -13...-1

<400> 1451  
 Met Phe Phe Leu Cys Gly Phe Leu Tyr Leu Cys Phe Ile Ser Phe Phe  
                   -10                  -5                  1  
 Phe Phe  
       5

<210> 1452  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -42...-1

<400> 1452  
 Met Lys Ala Gly Pro Cys Ser Cys Gln Glu Gly Gly Arg Gln Trp Ala  
           -40                  -35                  -30  
 His Gly Ser Val Pro Leu Gln Pro Thr Ala Arg Leu Ala Ala Leu Gly  
       -25                  -20                  -15  
 Ile Phe Leu Cys Pro Gly Glu Thr Leu Ser Ala Ser Leu His Trp Asn  
 -10                  -5                  1                  5  
 Pro Ile Gly

<210> 1453  
 <211> 53  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 1453  
 Met Leu Ser Gln Ser Phe Gln Lys Asn Lys Thr Asn Leu Leu Cys Leu  
                   -20                  -15                  -10  
 Thr Phe Gln Arg Cys Gln Ser Tyr Asn Trp Leu Asn Ile Phe Glu Ala  
       -5                  1                  5  
 Thr Tyr Met Thr Thr Leu Phe Ile Ser Val Ile Xaa Thr Asn Phe Leu  
 10                  15                  20                  25  
 Lys Arg Tyr Leu Leu  
                   30

<210> 1454  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

&lt;400&gt; 1454

Met Phe Leu Phe Cys Trp Glu Lys Ser Pro Arg Met Gln Leu Leu Gly  
 -25 -20 -15 -10  
 Cys Met Val Leu Tyr Asp Cys Phe Ser Phe Lys Lys Leu Pro Gly  
 -5 1 5

&lt;210&gt; 1455

&lt;211&gt; 47

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -30...-1

&lt;400&gt; 1455

Met Ser Phe Ile Ser Val Ile Phe Pro Leu Ile Leu Leu Asn Arg Phe  
 -30 -25 -20 -15  
 Ser Phe Val Cys Phe Phe His Val Phe Tyr Cys Val Phe Cys Asn Val  
 -10 -5 1  
 Ser Ser Leu Phe Ser Tyr Gln Phe Leu Leu His Phe Cys Asp Asp  
 5 10 15

&lt;210&gt; 1456

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -31...-1

&lt;400&gt; 1456

Met His Glu Tyr Leu Pro Arg Asn Phe His Asp Phe Asn Ser Pro Asn  
 -30 -25 -20  
 Ser Lys Leu Gly Met Gly Met Gly Phe Phe Ser Gly Val Lys Ser Trp  
 -15 -10 -5 1  
 Ile Gly Gly

&lt;210&gt; 1457

&lt;211&gt; 83

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -36...-1

&lt;400&gt; 1457

Met Ala Ser Xaa Val Pro Val Lys Asp Lys Lys Leu Leu Glu Val Lys  
 -35 -30 -25  
 Leu Gly Glu Leu Pro Ser Trp Ile Leu Met Arg Asp Phe Ser Pro Ser  
 -20 -15 -10 -5  
 Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys  
 1 5 10  
 Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser Gly Ile Thr Met Val Leu  
 15 20 25  
 Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys  
 30 35 40  
 His Glu Ser  
 45

&lt;210&gt; 1458

<211> 24  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -18...-1

<400> 1458  
Met Val Ile Ser Ala Gly Ala Leu Leu Trp Met Ala Trp Asp Gly Gln  
          -15                  -10                  -5  
Leu Ser Arg Pro Glu Gly Ala Arg  
          1                          5

<210> 1459  
<211> 31  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -18...-1

<400> 1459  
Met Val His Cys Asn Leu Glu Leu Leu Gly Ser Ser Tyr Asn Pro Ile  
          -15                  -10                  -5  
Ser Ala Ser Pro Val Ala Arg Thr Ile Ser Cys Pro Ala Ile Val  
          1                          5                  10

<210> 1460  
<211> 127  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -88...-1

<400> 1460  
Met Leu Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu Arg  
          -85                  -80                  -75  
Leu Val Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Lys Thr Glu Leu  
          -70                  -65                  -60  
Ala Gln Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly Lys  
          -55                  -50                  -45  
Asp Glu Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp Tyr  
          -40                  -35                  -30                  -25  
Leu Val Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu Leu  
                  -20                  -15                  -10  
Ala Arg Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly Leu  
          -5                          1                  5  
Ala Glu Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln Ser  
          10                  15                  20  
Glu Val Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Pro Ser  
25                          30                          35

<210> 1461  
<211> 54  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL

<222> -43...-1

<400> 1461

Met Arg Gly Trp Xaa Ala Pro Ala Trp Arg Xaa Leu Xaa Thr Arg Arg  
-40 -35 -30  
Leu Pro Met Gly Ser Arg His Gly Ala Ser Pro Ala Ser Ala Val Trp  
-25 -20 -15  
Cys Leu Xaa Leu Lys Leu Val Pro Ala Leu Cys Ile Ser Gly Leu Thr  
-10 -5 1 5  
Leu Gly Ile Gln Gly Phe  
10

<210> 1462

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34...-1

<400> 1462

Met Tyr Phe Lys Thr Thr Thr Xaa Xaa His Ser Ala His Met Leu Leu  
-30 -25 -20  
Gln Ile Cys Phe Phe Arg Leu Thr Ile Leu Xaa Phe His Asp Asn Thr  
-15 -10 -5  
Trp Gly Ser Thr Ser Phe Ser Xaa Val Ala Ala Met Leu Phe His Tyr  
1 5 10  
Arg  
15

<210> 1463

<211> 26

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 1463

Met Ser Ser Asn Ile Gln Arg Leu Gly Phe Pro Leu Leu Phe Leu Phe  
-20 -15 -10  
Phe Leu Phe Leu Phe Phe Phe Phe Phe  
-5 1

<210> 1464

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -67...-1

<400> 1464

Met Cys Asp Ala Phe Val Gly Thr Trp Lys Leu Val Ser Ser Glu Asn  
-65 -60 -55  
Phe Asp Asp Tyr Met Lys Glu Val Gly Val Gly Phe Ala Thr Arg Lys  
-50 -45 -40  
Val Ala Gly Met Ala Lys Pro Asn Met Ile Ile Ser Val Asn Gly Asp  
-35 -30 -25 -20  
Val Ile Thr Ile Pro His Leu Val Leu Pro Leu Pro Met Leu Pro Thr

Ser Asn Arg Lys Arg  
 1

-10

-5

<210> 1465  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 1465  
 Met Phe Leu Tyr Arg Ser Phe Gly Gly Gln Leu Leu Ser Phe Leu Leu  
 -20 -15 -10  
 Gly Thr Tyr Leu Gly Arg Arg Glu Val Ala Gly Pro Gln His Gly Gln  
 -5 1 5 10  
 Phe Ser Lys

<210> 1466  
 <211> 19  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1466  
 Met Xaa Gly Phe Phe Cys Leu Cys Ala Phe Asn Ser Phe Leu Leu Ser  
 -15 -10 -5  
 Pro Glu Gly  
 1

<210> 1467  
 <211> 68  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -66...-1

<400> 1467  
 Met Ile Phe Pro His Cys Met Tyr Cys Leu Glu Cys Ile Thr Lys Asn  
 -65 -60 -55  
 Gly Leu Leu Gly Leu Lys Val Leu Pro Leu Tyr Gly Ile Met Leu Ile  
 -50 -45 -40 -35  
 Phe Phe Pro Lys Val Val Tyr Asn Asn Gln Pro Leu His Tyr Lys Ser  
 -30 -25 -20  
 Val Met Val Phe Gln Leu Thr Ser Phe Leu Ser Ile Xaa Ile Phe Val  
 -15 -10 -5  
 Asn Pro Thr Arg  
 1

<210> 1468  
 <211> 79  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

&lt;222&gt; -54...-1

&lt;400&gt; 1468

```

Met Val Ser Met Ser Phe Lys Arg Asn Arg Ser Asp Arg Phe Tyr Ser
      -50      -45      -40
Thr Arg Cys Cys Gly Cys Cys His Val Arg Xaa Gly Thr Ile Ile Leu
      -35      -30      -25
Gly Thr Trp Tyr Met Val Val Asn Leu Leu Met Ala Xaa Leu Leu Thr
      -20      -15      -10
Val Glu Val Thr His Pro Asn Ser Met Pro Ala Val Asn Ile Gln Tyr
      -5      1      5      10
Glu Val Ile Gly Asn Tyr Tyr Ser Ser Glu Arg Met Ala Asp Asn
      15      20      25

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&lt;210&gt; 1469

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -31...-1

&lt;400&gt; 1469

```

Met Ala Ala Ala Thr Leu Thr Ser Lys Leu Tyr Ser Leu Leu Phe Arg
      -30      -25      -20
Arg Thr Ser Thr Phe Ala Leu Thr Ile Xaa Arg Xaa Xaa Ser Cys Ser
      -15      -10      -5      1
Ser Xaa Ala Pro Ser Ile Lys Ala Arg Thr Leu Ser Thr Thr Ser
      5      10      15
Thr Arg Gly Ser Cys Gly Asn Thr Ser Ser Thr Ser Met Arg Thr Ser
      20      25      30
Ser Ser Leu Glu Ala Pro Ile Gln Ala Arg Arg Thr Arg Ser Thr Gln
      35      40      45
Gln Leu Phe Ala Gln Ser Trp Ser Leu Ser Xaa Lys Met Met
      50      55      60

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&lt;210&gt; 1470

&lt;211&gt; 83

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -41...-1

&lt;400&gt; 1470

```

Met Lys Ala Ile Lys Lys Ser Leu Thr Glu Glu Glu Tyr Leu Tyr Leu
      -40      -35      -30
Asp Phe Ser His Gln Thr Glu Gly Cys Ile Phe Pro Leu His Thr Ser
      -25      -20      -15      -10
Val Thr Leu Phe Leu Leu Ser Tyr Cys Asp Cys Lys Ile Phe Lys Ile
      -5      1      5
Cys Leu Val Val Thr Lys Glu Val Ser Arg Asp Xaa Ser Leu Leu Arg
      10      15      20
Asp Asp Leu Ile Gln Asp Val Glu Ile Gln Ile Ile Ser Arg Gln Glu
      25      30      35
Leu Pro Pro
      40

```

&lt;210&gt; 1471

&lt;211&gt; 20

&lt;212&gt; PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 1471

Met Phe Leu Cys Val Cys Tyr Phe Ile Arg Lys Ser Thr Ser Phe Phe  
                    -10                    -5                    1  
Ser Ile Ser Ser  
                    5

<210> 1472

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45...-1

<400> 1472

Met Gly Lys Pro Arg Gly Gly Glu Met Leu Glu Val Val Lys Thr Val  
-45                    -40                    -35                    -30  
Ser Thr Phe Thr Leu Gly Gly Trp Lys Gly Thr Ala Pro Val Ser Cys  
                    -25                    -20                    -15  
Ala Trp Trp Leu Leu Pro Val Trp Lys Leu Gly Gly Gln Leu Glu  
                    -10                    -5                    1  
Arg Arg Lys Asn Pro Lys Glu Tyr Cys Leu Gly Ser Trp Val Trp Leu  
5                    10                    15  
Ser Pro Gln Leu Ala Pro Arg  
20                    25

<210> 1473

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 1473

Met Leu Ile Phe Thr Phe Ile Ser Thr Leu Leu Phe Val Phe Leu Gly  
-15                    -10                    -5  
Val Val  
1

<210> 1474

<211> 47

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37...-1

<400> 1474

Met Glu Val Leu Ser Xaa Pro Asn Ser Phe Gln Thr Gln Ala Leu Trp  
-35                    -30                    -25  
Asp Ser Leu His Ser Pro Gly Val Pro Gly Ser Gly Leu Cys Ser Met  
-20                    -15                    -10  
Ala Ala Val Gln Ala Gly Asn Gln Ala Ile Tyr Ser Ala Ser Gly

-5 1 5 10

<210> 1475  
<211> 47  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -42...-1

<400> 1475  
Met Gln Ala Thr Ala Ser Gln Pro Ile His Phe Phe Xaa Ser Ser Pro  
-40 -35 -30  
Gln Ala Pro Arg His His Ser Gly His Pro Val Pro Leu Leu Leu Thr  
-25 -20 -15  
Gln Ala Gly Phe Pro Arg Arg Gly Glu Ala Ala Pro Pro Leu Leu  
-10 -5 1 5

<210> 1476  
<211> 34  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -30...-1

<400> 1476  
Met Arg Gly Xaa Asn Xaa Val Phe Arg Val Phe Ser Glu Ser Leu Lys  
-30 -25 -20 -15  
Gly Leu Cys Thr Phe Thr Leu Asn Leu Thr Ala Val Arg Thr Ile Xaa  
-10 -5 1  
Leu Asp

<210> 1477  
<211> 40  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -32...-1

<400> 1477  
Met Gly Arg Ile Ile' Pro Met Val Glu Lys Ala Asp Thr Ala Gln Lys  
-30 -25 -20  
Phe Gln Gly Arg Leu Thr Ile Ser Thr Xaa Leu Ser Thr Ser Xaa Xaa  
-15 -10 -5  
Phe Met Glu Leu Ser Ser Leu Arg  
1 5

<210> 1478  
<211> 112  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -67...-1

<400> 1478  
Met Asn Leu Val Ile Cys Val Leu Leu Leu Ser Ile Trp Lys Asn Asn

-65                      -60                      -55  
 Cys Met Thr Thr Asn Gln Thr Asn Gly Ser Ser Thr Thr Gly Asp Lys  
      -50                      -45                      -40  
 Pro Val Glu Ser Met Gln Thr Lys Leu Asn Tyr Leu Arg Arg Asn Leu  
      -35                      -30                      -25                      -20  
 Leu Ile Leu Val Gly Ile Ile Ile Met Val Phe Val Phe Ile Cys Phe  
                              -15                      -10                      -5  
 Cys Tyr Leu His Tyr Asn Cys Leu Ser Asp Asp Ala Ser Lys Ala Gly  
                              1                      5                      10  
 Met Val Lys Lys Lys Gly Ile Ala Ala Lys Ser Ser Lys Thr Ser Phe  
                              15                      20                      25  
 Ser Glu Ala Lys Thr Ala Ser Gln Cys Ser Ser Glu Thr Gln Thr Gly  
 30                               35                               40                               45

&lt;210&gt; 1479

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -28...-1

&lt;400&gt; 1479

Met Gln Ile Ser Ala Ala Ser Leu Asn Phe Ser Ser Lys Asn Gly Ile  
                              -25                      -20                      -15  
 Phe Phe Ser Leu Thr Leu Ser Gly Cys Lys Phe Ser Lys Leu Leu Cys  
                              -10                      -5                      1  
 Pro Phe Gly  
 5

&lt;210&gt; 1480

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -52...-1

&lt;400&gt; 1480

Met Ile Phe Glu Pro Val Val Leu Lys Pro Val Phe Leu Asn Ile Phe  
                              -50                      -45                      -40  
 Phe Phe Ser His His Val Phe Thr Val Phe Phe Ser Gly Ser His Val  
                              -35                      -30                      -25  
 Asp Ile Leu Ser Arg Thr Val Leu Val Trp Asp Cys Leu Leu Pro Pro  
                              -20                      -15                      -10                      -5  
 Pro Ser Phe Phe Leu Leu Leu Ser Ser Ser Xaa Ser Xaa Leu Leu  
                              1                      5                      10  
 Leu Xaa Xaa Ser Ser Ser Ser Arg  
                              15                      20

&lt;210&gt; 1481

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -14...-1

&lt;400&gt; 1481

Met Leu Val Pro Leu Leu Ser His Leu Leu Phe Lys Phe Thr Trp Pro

Lys Xaa Ser Gln  
5

-5

1

<210> 1482  
<211> 70  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -49..-1

<400> 1482  
Met Asp Arg Asn Pro Ser Pro Pro Pro Pro Gly Arg Asp Lys Glu Glu  
-45 -40 -35  
Glu Glu Glu Val Ala Gly Gly Asp Cys Ile Gly Ser Thr Val Tyr Ser  
-30 -25 -20  
Lys His Trp Leu Phe Gly Val Leu Ser Gly Leu Xaa Gln Xaa Val Ser  
-15 -10 -5  
Pro Gly Lys His Gln Asn Leu Gly Ser Xaa Xaa Glu Glu Gln Leu Thr  
1 5 10 15  
Glu Leu Asp Glu Arg Asn  
20

<210> 1483  
<211> 37  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -23..-1

<400> 1483  
Met Lys Leu Ser Leu Ala Gly Tyr Glu Ile Leu Gly Cys His Phe Phe  
-20 -15 -10  
Ser Leu Ala Leu Leu Asn Thr Gly Pro Gln Tyr Leu Leu Ala Tyr Arg  
-5 1 5  
Val Ser Ala Glu Arg  
10

<210> 1484  
<211> 48  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -40..-1

<400> 1484  
Met Ala Thr Ser Val Gly His Arg Cys Leu Gly Leu Leu His Gly Val  
-40 -35 -30 -25  
Ala Pro Trp Arg Ser Ser Leu His Pro Cys Glu Ile Thr Ala Leu Ser  
-20 -15 -10  
Gln Ser Leu Gln Pro Leu Arg Lys Leu Pro Phe Arg Ala Ser Xaa Thr  
-5 1 5

<210> 1485  
<211> 126  
<212> PRT  
<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -49...-1

&lt;400&gt; 1485

```

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
              -45              -40              -35
Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
              -30              -25              -20
Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
              -15              -10              -5
Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
      1              5              10              15
Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser
              20              25              30
Glu Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln
              35              40              45
Gly Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val
              50              55              60
Gln Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp
      65              70              75

```

&lt;210&gt; 1486

&lt;211&gt; 55

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 1486

```

Met Ala Ala Val Thr Val Thr Val Thr Lys Thr Ala Ala Ala Ala Thr
              -25              -20              -15
Ala Phe Asn Lys Ala Val Trp Phe Thr Pro Cys Ser Cys Gln Glu Val
              -10              -5              1
Ser Ser Arg Leu Pro Ala Arg Thr Ala Ala Thr Arg Gln Asp Arg Ala
      5              10              15
Asp Lys Lys Glu Arg Pro Cys
20              25

```

&lt;210&gt; 1487

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -19...-1

&lt;400&gt; 1487

```

Met Leu Gln Phe Glu Lys Pro Gly Ser Ala Ile Cys Leu Trp His Ser
              -15              -10              -5
Thr Leu Gly Gly Xaa Gly Gly Arg Glu Ile Xaa Ser Leu Arg Pro Ala
      1              5              10
Cys Gly
      15

```

&lt;210&gt; 1488

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 1488  
 Met Leu Ile Ser Tyr Leu Ala Ile Leu Leu Lys Trp Val Ser Asn Ser  
                   -15                  -10                  -5  
 Lys Ser Phe Leu Val Lys Ala Ser  
           1                          5

<210> 1489  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 1489  
 Met Lys Leu Gln Thr Leu Ala Phe Trp Ser Ala Tyr Val Pro Cys Gln  
 -15                  -10                  -5                  1  
 Thr Gln Asp Arg Asp Ala Pro Arg Leu Thr Leu Glu Gln Ile Asp Leu  
                   5                  10                  15  
 Ile Arg Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser  
           20                  25                  30  
 Ala Lys Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val  
           35                  40                  45  
 Glu Gly Gly His Ser Leu Asp Asn Ser Leu Ser Arg  
 50                  55                  60

<210> 1490  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 1490  
 Met Pro Ala Cys Leu Ser Ser Phe Val Ile Pro Ser Leu Leu Ser Pro  
                   -10                  -5                  1  
 Ser Ser Pro Pro Ser Ile Gly  
           5

<210> 1491  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1491  
 Met Val Val Ser Phe Ala Gly Ser Cys Thr Ile Leu Gly Ala Ser Ser  
           -15                  -10                  -5  
 His Ser Phe Pro Ile Glu Val Ser Leu Phe Pro Val Asp Cys Gly Phe  
 1                  5                  10                  15  
 Leu Leu

<210> 1492  
 <211> 32  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 1492  
 Met Cys Cys Pro Gly Trp Asn Ala Val Ser Gln Ser Trp Leu Ala Ala  
 -20 -15 -10 -5  
 Pro Ser Thr Ser Trp Val Gln Glu Ile Leu Val Leu Gln Pro Pro Gly  
 1 5 10

<210> 1493  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -54...-1

<400> 1493  
 Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr  
 -50 -45 -40  
 Val Pro Leu Lys Xaa Xaa Xaa Val Asp Asp Asp Ser Lys Ile Trp  
 -35 -30 -25  
 Ser Xaa Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe  
 -20 -15 -10  
 Leu Xaa Xaa Val Ser Gly Thr Xaa Asp Val Phe Phe Arg Gln Ile Leu  
 -5 1 5 10  
 Ala Leu Thr Gly Trp  
 15

<210> 1494  
 <211> 45  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1494  
 Met Asp Ala Ser His Ser His Leu Ser Leu Val Gly His Ser Arg Ala  
 -15 -10 -5  
 Cys Gly Val Thr Ser Arg Pro His Ala Arg His Arg Gly Arg Cys Leu  
 1 5 10 15  
 Gly Pro Cys Ser Arg Ser Gly Pro Arg Leu Cys Ser Ala  
 20 25

<210> 1495  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400> 1495

Met Gly Ser Asn Ala Val Val Trp His Thr Lys Pro Ser Leu Leu Asn  
                                   -30                                  -25                                  -20  
 His Pro Ala Ser Ser Leu Ile Ser His Asp Pro Trp Pro Arg Gly Ala  
                                   -15                                  -10                                  -5  
 Phe Ala Leu Ser Cys Pro Ser Ala Ser Phe Met Leu Phe Ser Ser Leu  
                                   1                                  5                                  10  
 Gln Cys Pro Phe Pro Tyr Xaa Xaa Thr Glu Cys Asn Xaa  
 15                                  20                                  25

<210> 1496  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 1496  
 Met Lys Glu Asp Gly Ala Cys Leu Phe Arg Ala Val Ala Asp Gln Val  
                                   -15                                  -10                                  -5  
 Tyr Gly Asp Gln Asp Met His Glu Val Val Arg Lys His Xaa Met Asp  
                                   1                                  5                                  10  
 Tyr Leu Met Lys Asn Ala Asp Tyr Phe Ser Xaa Tyr Val Thr Glu Asp  
 15                                  20                                  25                                  30  
 Phe Thr Thr Tyr Ile Xaa Arg Lys  
                                   35

<210> 1497  
 <211> 24  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 1497  
 Met Val His Leu Ile Leu Thr Glu Val Leu Ile Met Ile Xaa Glu Ala  
                                   -20                                  -15                                  -10  
 Xaa Asn Val Trp Cys Gly Asp Ser  
 -5                                  1

<210> 1498  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -47...-1

<400> 1498  
 Met Tyr His Asn Leu Phe Ala Leu Leu Ile Asp Ile His Val Val  
                                   -45                                  -40                                  -35  
 Leu Val Phe Tyr Cys Leu Asp Leu Leu Met Ile His Ile Phe Tyr Cys  
                                   -30                                  -25                                  -20  
 Lys Tyr Cys Leu Xaa Phe Gly Ile Leu Ala Ser Glu Val Tyr Ser Trp  
 -15                                  -10                                  -5                                  1  
 Asn Ile Tyr

<210> 1499  
 <211> 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 1499

Met	Glu	Ser	Pro	Ser	Arg	Ala	Gly	Gly	Val	Xaa	Leu	Xaa	Lys	Ala	Ala
				-25					-20					-15	
Ser	Pro	Leu	Cys	Ser	Xaa	Ser	Ser	Gly	Tyr	Cys	Xaa	Ala	Phe	Pro	Arg
			-10					-5					1		
Arg	Ser	Ala	Arg	Arg	His	Leu	His	Pro	Gly	His	Gly				
	5					10					15				

&lt;210&gt; 1500

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -25...-1

&lt;400&gt; 1500

Met	Trp	Arg	Tyr	Val	Ser	Arg	Leu	Ser	Ser	Val	Pro	Leu	Ile	Ser	Leu
-25					-20					-15				-10	
Ser	Val	Leu	Met	Pro	Val	Gln	His	Ser	Pro	Asp	Phe	Cys	Ser	Phe	Ile
			-5					1				5			
Val	Ser	Thr	Val	Ile	Pro	Trp	Phe	Pro	Trp	Gly	Ile	Gly	Ser	Arg	Thr
	10					15					20				
Leu	Met	Asp	Ile	Lys	Ile	Leu	Gly	Cys	Ser	Ser	Pro	Gly			
	25					30					35				

&lt;210&gt; 1501

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -30...-1

&lt;400&gt; 1501

Met	Asp	Val	Ser	Cys	Lys	Ile	Leu	Tyr	Asn	Val	Ile	Glu	Lys	Phe	Cys
-30				-25					-20					-15	
Asn	Asn	Leu	Leu	Lys	Leu	Ser	Ser	His	Ser	Pro	Thr	Cys	Ala	Cys	Lys
			-10					-5					1		

Leu

&lt;210&gt; 1502

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -20...-1

&lt;400&gt; 1502

Met	Ile	Phe	Lys	Asp	Val	Phe	Ser	His	Leu	Ser	Gly	Ser	Ser	Leu	Gln
-20				-15					-10					-5	
Leu	Cys	Val	Ala	Gln	Phe	Leu	Xaa	Leu	Ser	Ala	Val	Asp			

1

5

<210> 1503  
 <211> 50  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -44...-1

<400> 1503  
 Met Lys Leu Thr Lys Asn Ile Leu Xaa Val Ile Ile Gly Cys Phe Lys  
                             -40                            -35                            -30  
 Leu Ile Ala Tyr Lys Asn Ser Val Leu Tyr Phe Tyr Ser Asn Phe Ser  
                             -25                            -20                            -15  
 Phe Ser Phe Leu Phe Phe Phe Phe Leu Ser Phe Phe Phe Phe Phe  
                             -10                            -5                            1  
 Phe Phe  
 5

<210> 1504  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -87...-1

<400> 1504  
 Met Asn Asn Gln Lys Gln Xaa Xaa Pro Thr Leu Ser Gly Gln Arg Phe  
                             -85                            -80                            -75  
 Lys Thr Arg Lys Arg Asp Glu Lys Glu Arg Phe Asp Pro Thr Gln Phe  
                             -70                            -65                            -60  
 Gln Asp Cys Ile Ile Gln Gly Leu Thr Glu Thr Gly Thr Asp Leu Glu  
                             -55                            -50                            -45                            -40  
 Ala Val Ala Lys Phe Leu Asp Ala Ser Gly Ala Lys Leu Asp Tyr Arg  
                             -35                            -30                            -25  
 Arg Tyr Ala Glu Thr Leu Phe Asp Ile Leu Val Ala Gly Xaa Met Leu  
                             -20                            -15                            -10  
 Ala Pro Gly Gly Thr Leu Ala Asp Asp Met Met Xaa  
                             -5                            1                            5

<210> 1505  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17...-1

<400> 1505  
 Met Ala Asp Ser Leu Glu Ile Lys Leu Pro Phe Leu Pro Phe Ala Gln  
                             -15                            -10                            -5  
 Gln Ile Asp Ile Lys Ser Cys Phe Tyr Phe Phe Phe Xaa Asn Xaa Xaa  
                             1                            5                            10                            15  
 Phe Pro Arg

<210> 1506  
 <211> 115  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -35...-1

&lt;400&gt; 1506

```

Met Asp Arg Lys Trp Thr Trp Lys Arg Gly Gln Arg Ser His Leu Glu
-35          -30          -25          -20
Ser Gly Gln Ala Ala Pro Ala Thr Ala Ala Thr Ala Ala Ser Ala
          -15          -10          -5
Thr Thr Gly Ala Ser Val Trp Arg Ser Thr Met Gly Xaa Leu Cys Asp
          1          5          10
Cys Thr Xaa Xaa Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val Ser
          15          20          25
Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu Pro
30          35          40          45
Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr Thr
          50          55          60
Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr Thr
          65          70          75
Gln Ala Pro
          80

```

&lt;210&gt; 1507

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -43...-1

&lt;400&gt; 1507

```

Met Ala Pro Gln Met Tyr Glu Phe His Leu Pro Leu Ser Pro Glu Glu
          -40          -35          -30
Leu Leu Lys Ser Gly Gly Val Asn Gln Tyr Val Val Gln Glu Val Leu
          -25          -20          -15
Ser Ile Lys His Leu Pro Pro Gln Leu Arg Ala Phe Gln Ala Ala Phe
          -10          -5          1          5
Arg Ala Gln Gly Pro Leu Ala Met Leu Gln His Phe Asp Thr Ile Tyr
          10          15          20
Ser Ile Leu His His Phe Arg Ser Ile Asp
          25          30

```

&lt;210&gt; 1508

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -15...-1

&lt;400&gt; 1508

```

Met Ala Ala Val Gln Val Val Gly Ser Trp Pro Ser Val Gln Pro Arg
-15          -10          -5          1
Glu Ala Pro Arg Glu Ala Ile Pro Glu Arg Gly Asn Gly Phe Arg Leu
          5          10          15
Leu Ser Ala Arg Leu Cys Ala Leu Arg Pro Asp Asp Ser Ser Ser Ala
          20          25          30
Arg Thr Glu Ile His Leu Xaa Phe Asp Gln Leu Ile Ser Glu Asn Tyr
          35          40          45

```

Ser Glu Gly Ser Gly Val Ala Pro Glu Asp Val Ser Ala Leu Leu Val  
 50 55 60 65  
 Gln Ala Cys Gly

<210> 1509  
 <211> 48  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -30...-1

<400> 1509  
 Met Phe His Gly Cys His Ile Leu Ser Phe Leu Arg Ile Ser Thr Arg  
 -30 -25 -20 -15  
 Gly Phe Leu Phe Phe Leu Gln Phe Ser Phe Pro Leu Tyr Tyr Leu Phe  
 -10 -5 1  
 Arg Xaa Xaa Phe Pro Gln Ser Phe Met Leu Glu Ala Phe Val Arg Cys  
 5 10 15

<210> 1510  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 1510  
 Met Tyr Arg His Ser Lys Gln Arg Asn Asn Val Pro Cys Leu Val Leu  
 -25 -20 -15  
 Tyr Ala Pro Trp Val Pro Pro Leu Leu Leu Ala Phe Trp Gly Trp Trp  
 -10 -5 1 5  
 Leu Leu Glu Gln Gly Leu Phe Phe Phe Phe  
 10 15

<210> 1511  
 <211> 137  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -50...-1

<400> 1511  
 Met Gly Asp Pro Ser Lys Gln Asp Ile Leu Thr Ile Phe Lys Arg Leu  
 -50 -45 -40 -35  
 Arg Ser Val Pro Thr Asn Lys Val Cys Phe Asp Cys Gly Ala Lys Asn  
 -30 -25 -20  
 Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val Phe Leu Cys Ile Asp Cys  
 -15 -10 -5  
 Ser Gly Ser His Arg Ser Leu Gly Val His Leu Ser Phe Ile Arg Ser  
 1 5 10  
 Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe Gln Leu Arg Cys Met Gln  
 15 20 25 30  
 Val Gly Gly Asn Ala Ser Ala Ser Ser Phe Phe His Gln His Gly Cys  
 35 40 45  
 Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn Ser Arg Ala Ala Gln Leu  
 50 55 60  
 Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser Gln Ala Thr Arg Lys His

65 70 75  
Gly Thr Asp Leu Trp Leu Asp Ser Cys  
80 85

<210> 1512  
<211> 26  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -22...-1

<400> 1512  
Met Pro Leu Pro Pro Asn Gln Ser Pro Leu Leu Leu His Leu Val Phe  
-20 -15 -10  
His Gln Arg Thr Leu Ile Ser Leu Pro Pro  
-5 1

<210> 1513  
<211> 21  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -13...-1

<400> 1513  
Met Phe Leu Thr Phe Phe Phe Cys Thr Gln Val His Gly Pro Ser Ile  
-10 -5 1  
Leu Asp Ser Pro Ala  
5

<210> 1514  
<211> 56  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -14...-1

<400> 1514  
Met Val Thr Leu Trp Ile Phe Gln Phe Phe Leu Cys Leu Thr Cys Lys  
-10 -5 1  
Ala Tyr Asn Leu Arg Asn Cys Asn Asp Gly Lys Gly Xaa Xaa Ser Xaa  
5 10 15  
Val Leu Gly Leu Glu Gln Xaa Leu Pro Glu Ser Ala Gly Met Val Xaa  
20 25 30  
Phe Leu Gly Leu Lys His Arg Trp  
35 40

<210> 1515  
<211> 37  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -14...-1

<400> 1515

```

<400> 1518
Met Asn Glu Ala Met Ala Thr Asp Ser Pro Arg Arg Pro Ser Arg Cys
1          5          10          15
Thr Gly Gly Val Val Val Arg Pro Gln Ala Val Thr Glu Gln Ser Tyr
20          25          30
Met Glu Ser Val Val Thr Phe Leu Gln Asp Val Val Pro Gln Ala Tyr
35          40          45

```

Ser Gly Thr Pro Leu Thr Glu Glu Lys Glu Lys Ile Val Trp Val Arg  
 50 55 60  
 Phe Glu Asn Ala Asp Leu Asn Asp Thr Ser Arg Asn Leu Glu Phe His  
 65 70 75 80  
 Glu Ile His Ser Thr Gly Ser Glu Pro Pro Leu Leu Ile Met Ile Gly  
 85 90 95  
 Tyr Ser Asp Gly Met Gln Val Trp Ser Ile Pro Ile Xaa Gly Glu Xaa  
 100 105 110  
 Lys Ser Ser Ser Leu Phe Asp Met Ala Gln Phe Glu Arg Leu Glu Ser  
 115 120 125  
 Cys Leu Leu His  
 130

&lt;210&gt; 1519

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1519

Met Pro Val Thr Arg Ala Ser Gln Pro Arg Lys Pro Ser Ser Ala Gln  
 1 5 10 15  
 Gln Gln Lys Ala Ala Leu Leu Xaa Asn Asn Thr Ala Leu Gln Ser Val  
 20 25 30  
 Ser Leu Arg Ser Lys Thr Thr Ile Arg Glu Arg Pro Ser Ser  
 35 40 45

&lt;210&gt; 1520

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1520

Met Asn Gly Phe Gly Arg Leu Glu His Phe Ser Gly Ala Val Tyr Glu  
 1 5 10 15  
 Gly Gln Phe Lys Asp Asn Met Phe His Gly Leu Gly Thr Tyr Thr Phe  
 20 25 30  
 Pro Asn Gly Ala Lys Tyr Thr Gly Ile  
 35 40

&lt;210&gt; 1521

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1521

Met Ala Lys Ile Ala Lys Thr His Glu Asp Ile Glu Ala Gln Ile Arg  
 1 5 10 15  
 Glu Ile Gln Gly Lys Lys Ala Ala Leu Asp Glu Ala Gln Gly Val Gly  
 20 25 30  
 Leu Asp Ser Thr Gly Tyr Tyr Asp Gln Glu Ile Tyr Gly Gly Ser Asp  
 35 40 45  
 Ser Arg Phe Ala Gly Tyr Val Thr Ser Ile Ala Ala Thr Glu Leu Glu  
 50 55 60  
 Asp Asp Asp Asp Tyr Ser Ser Ser Thr Ser Leu Leu Gly Gln Lys  
 65 70 75 80  
 Lys Pro Gly Tyr His Ala Pro Val Ala Leu Leu Asn Asp Ile Pro Gln  
 85 90 95  
 Ser Thr Glu Gln Tyr Asp Pro Phe Ala Glu His Arg Pro Pro Lys Ile  
 100 105 110  
 Ala Asp Arg Glu Asp Glu Tyr Lys Lys His Arg Arg Thr Met Ile Ile  
 115 120 125  
 Ser Gln Ser  
 130

&lt;210&gt; 1522

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1522

```

Met Pro Ile Asn Lys Ser Glu Lys Pro Glu Ser Cys Asp Asn Val Lys
1           5           10           15
Val Val Val Arg Cys Arg Pro Leu Asn Glu Arg Glu Lys Ser Met Cys
          20           25           30
Tyr Lys Gln Ala Val Ser Val Asp Glu Met Arg Gly Thr Ile Thr Val
          35           40           45
His Lys Thr Asp Ser Ser Asn Glu Pro Pro Lys Thr Phe Thr Phe Asp
          50           55           60
Thr Val Phe Gly Pro Glu Ser Lys Gln Leu Asp Val Tyr Asn Leu Thr
65           70           75           80
Ala Arg

```

&lt;210&gt; 1523

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1523

```

Met Pro Asn Arg Gly Gly Asn Gly Leu Ala Pro Gly Glu Asp Arg Phe
1           5           10           15
Lys Pro Val Val Pro Trp Pro His Val Glu Gly Val Glu Val Asp Leu
          20           25           30
Glu Ser Ile Arg Arg Ile Asn Lys
          35           40

```

&lt;210&gt; 1524

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1524

```

Met Ser Leu Trp Leu Cys Phe Gln Cys Pro Leu Gly Val Ser Lys Ser
1           5           10           15
Asn Lys Lys Arg Ile Asn Leu Cys Asn Gly Phe Trp Asn Glu Lys Ile
          20           25           30
Lys Asn Arg
          35

```

&lt;210&gt; 1525

&lt;211&gt; 47

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1525

```

Met Gly Thr His Val Phe Ala Ile Asn Lys Arg Thr Tyr Val Ile Ser
1           5           10           15
Arg Asp Arg Glu Leu Ser Thr Ala Lys Pro Xaa Cys Ser Ser Leu Leu
          20           25           30
Thr Ala Pro Val Leu Cys Tyr Trp Arg Ala Cys Pro Leu Gln Thr
          35           40           45

```

&lt;210&gt; 1526

&lt;211&gt; 56

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1526

```

Met Phe Cys Phe Leu Phe Ser Trp Trp Leu Arg Gly Gly Leu His Val
1           5           10           15
Leu Leu Asn Thr Cys Leu Tyr Val Pro Tyr Gly Tyr Leu Ser Leu Ile
          20           25           30
Cys Leu Leu Cys Leu Trp Tyr Leu Asn Leu Tyr Lys Phe Ser Ile Phe
          35           40           45
Phe Ser Phe Leu Ser Phe Phe Phe

```

50

55

&lt;210&gt; 1527

&lt;211&gt; 55

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1527

```

Met Thr Thr Thr Ser Lys His Ala Ala Tyr Cys Leu Lys Gly Ser Cys
1           5           10           15
Leu Xaa Gln Ala Arg Val Gln Trp Pro Leu Lys Xaa Thr Thr Ala Ser
          20           25           30
Asn Phe Trp Ala Gln Val Ile Leu Ser Leu Pro Val Val Phe Val Asp
          35           40           45
Cys Leu Met Glu Xaa His Gly
          50           55

```

&lt;210&gt; 1528

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1528

```

Met Glu Gly Gly Gly Ile Pro Leu Glu Thr Leu Lys Glu Glu Ser
1           5           10           15
Gln Ser Arg His Val Leu Pro Ala Ser Phe Glu Val Asn Ser Leu Gln
          20           25           30
Lys Ser Asn Trp Gly Phe Leu Leu Thr Gly Leu Val Gly Gly Thr Leu
          35           40           45
Val Ala Val Tyr Ala Val Ala Thr Pro Phe Val Thr Pro Ala Leu Arg
          50           55           60
Lys Val Cys Leu Pro Phe Val Pro Ala Thr Met Lys Gln Ile Glu Asn
          65           70           75           80
Val Val Lys Met Leu Arg Cys Arg Arg Gly Ser Leu Val Asp Ile Gly
          85           90           95
Ser Gly Asp Gly Arg Ile Val Ile Ala Ala Lys Lys Gly Phe Xaa
          100          105          110
Ala Val Gly Tyr Glu Leu Asn Pro Trp
          115          120

```

&lt;210&gt; 1529

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1529

```

Met Ala Thr Pro Leu Ala Val Asn Ser Ala Ala Ser Leu Trp Gly Pro
1           5           10           15
Tyr Lys Asp Ile Trp His Lys Val Gly Asn Ala Leu Trp Arg Arg Gln
          20           25           30
Pro Glu Ala Val Xaa Leu Leu Asp Lys Ile Leu Lys Lys His Lys Pro
          35           40           45
Asp Phe Ile Ser Leu Phe Lys Asn Pro Pro Lys Asn Val Gln Gln His
          50           55           60
Glu Lys Val Gln Lys Ala Ser Thr Glu Gly Val Ala Ile Gln Gly Gln
          65           70           75           80
Gln Gly Thr Arg Leu Leu Pro Glu Gln Leu Ile Lys Glu Ala Phe Ile
          85           90           95
Leu Ser Asp Leu Phe Asp Ile Gly Glu Leu Ala Ala Val Glu Leu Leu
          100          105          110
Leu Ala Gly Glu His Gln Gln Pro His Phe Pro Gly Leu Thr Arg Gly
          115          120          125
Leu Val Ala Val Leu Leu Tyr Trp Asp Gly Lys Arg Cys Ile Ala Asn
          130          135          140
Ser Leu Lys Ala Leu Ile Gln Ser Arg Arg
          145          150

```

<210> 1530  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1530  
 Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala Glu Val Pro Arg  
 1 5 10 15  
 Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr Glu Glu Arg  
 20 25 30  
 Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp Phe Arg Ser Val  
 35 40 45  
 Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly Leu Ile Ser Lys  
 50 55 60  
 Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile Pro Lys Leu Ile  
 65 70 75 80  
 Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu Ser Tyr Val Lys  
 85 90 95  
 Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser Pro Leu Gly Glu  
 100 105 110  
 Ala Leu Arg Ser Gly Gln Ala Arg Arg Ser Ser Pro Pro  
 115 120 125

<210> 1531  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1531  
 Met His Met Ser Lys Leu Ile Asn Leu Tyr Thr Ser Xaa Met Cys Asn  
 1 5 10 15  
 Leu Leu Xaa Ile His Leu Xaa Xaa Ile Ser Cys Leu Xaa Asn Asn Lys  
 20 25 30  
 Xaa Thr Leu  
 35

<210> 1532  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1532  
 Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala Val Pro Ser Asp Ser  
 1 5 10 15  
 Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr Glu Tyr Leu Leu His  
 20 25 30  
 Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu Ser Glu Ile Arg Trp  
 35 40 45  
 Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly Phe Leu His Ser Trp  
 50 55 60  
 Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala Pro Glu Arg Arg Glu  
 65 70 75 80  
 Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe His Asp Tyr Ser Ala  
 85 90 95  
 Ala Ala Ala Pro Ser Pro Val Leu Gly Asn Ile Pro Pro Gly Asp  
 100 105 110

<210> 1533  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1533  
 Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly Asp  
 1 5 10 15  
 Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp Asp Thr

20 25 30  
 Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys Ile Arg  
 35 40 45  
 Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp Asp Thr  
 50 55 60  
 Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr Arg Gly  
 65 70 75 80  
 Ala His Gly Ile Ile Val Val Tyr Asp Val Thr Asp Gln Glu Ser Tyr  
 85 90 95  
 Ala Xaa Val Lys Gln Trp Leu Gln Glu Ile Asp  
 100 105

&lt;210&gt; 1534

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1534

Met Asn Ser Lys Ala Xaa Lys Ser Ser Thr Ala Asn Gln Gly Asp Gly  
 1 5 10 15  
 Asp Glu Glu Xaa Val Gly Arg Xaa Glu Xaa Ser Val Gly Glu Phe  
 20 25 30

&lt;210&gt; 1535

&lt;211&gt; 48

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1535

Met Leu Tyr Ser Thr Leu Lys His Thr Leu Gln Tyr Val Ile Ile Asn  
 1 5 10 15  
 Cys Gly His His Ala Val Gln Lys Ile Ser Lys Thr Tyr Ser Ser Cys  
 20 25 30  
 Leu Thr Glu Xaa Leu Tyr Pro Leu Pro Asn Ile Ser Pro Ile Pro Pro  
 35 40 45

&lt;210&gt; 1536

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1536

Met Asn Asp Glu Val Asn Pro Arg Arg Val Leu Glu Leu Met Gly Ser  
 1 5 10 15  
 Glu Val Thr Gln Ile Ala Cys Gly Arg Gln His Thr Leu Xaa Phe Val  
 20 25 30  
 Pro Ser Ser Gly Leu Ile Tyr Ala Phe Gly Cys Gly Ala Arg Gly Gln  
 35 40 45  
 Leu Gly Thr Gly His Thr Cys Asn Val Lys Cys Pro Ser Pro Val Lys  
 50 55 60  
 Gly Tyr Trp Ala Ala His Ser Gly Gln Leu Ser Ala Arg Ala Asp Arg  
 65 70 75 80  
 Phe Lys Tyr His Ile Val Lys Gln Ile Phe Ser Gly Gly Asp  
 85 90

&lt;210&gt; 1537

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1537

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Val Pro Trp Gly  
 1 5 10 15  
 Pro Asn His Cys Asp Lys  
 20

&lt;210&gt; 1538

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1538

Met Gly Asp Asn Pro Phe Gln Pro Lys Ser Asn Ser Lys Met Ala Glu  
1 5 10 15  
Leu Phe Met Glu Cys Glu Glu Glu Leu Glu Pro Trp Gln Lys Lys  
20 25 30  
Val Lys Glu Val Glu Asp Asp Asp Glu Pro Ile Phe Val Gly  
35 40 45  
Glu Ile Ser Ser Ser Lys Pro Ala Ile Ser Asn Ile Leu Asn Arg Val  
50 55 60  
Asn Pro Ser Ser Tyr Ser Arg Gly Leu Lys Asn Gly Ala Leu Ser Arg  
65 70 75 80  
Gly Ile Thr Ala Ala Phe Lys Pro Thr Ser Gln His Tyr Thr  
85 90

&lt;210&gt; 1539

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1539

Met Val Thr Gln Ala Gln Gln Glu Ile Thr Val Gln Gln Leu Met Ala  
1 5 10 15  
His Leu Asp Ala Ile Arg Lys Asp Met Val Ile Leu Glu Lys Ser Glu  
20 25 30  
Phe Ala Asn Leu Arg Ala Glu Asn Glu Lys Met Lys Ile Glu Leu Asp  
35 40 45  
Gln Val Lys Gln Gln Leu Met His Glu Thr Ser Xaa Ile Arg Ala Asp  
50 55 60  
Asn Lys Leu  
65

&lt;210&gt; 1540

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1540

Met Lys Phe Gly Asn Val Arg Met Xaa Ser Ile Gln Ile Phe Ile Val  
1 5 10 15  
Ser Ile Trp Ser Phe Phe Leu Phe Tyr Gly Lys Tyr Thr Tyr Ile Arg  
20 25 30  
Leu Ile Leu Ser Gln Gly  
35

&lt;210&gt; 1541

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1541

Met Thr Phe Asp Leu Ser Val Phe Ser Thr Leu Ser Asp His Phe Tyr  
1 5 10 15  
Ser Ser Ser Leu Ser Asn Thr Ala Arg Asn Leu Tyr Ile Cys Leu Phe  
20 25 30  
His Ile Thr  
35

&lt;210&gt; 1542

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1542

Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu

1 5 10 15  
 Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser  
 20 25

<210> 1543

<211> 128

<212> PRT

<213> Homo sapiens

<400> 1543

Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys  
 1 5 10 15  
 Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn  
 20 25 30  
 Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly  
 35 40 45  
 Pro Asn Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe  
 50 55 60  
 Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His  
 65 70 75 80  
 Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu  
 85 90 95  
 Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu  
 100 105 110  
 Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val  
 115 120 125

<210> 1544

<211> 33

<212> PRT

<213> Homo sapiens

<400> 1544

Met Ala Asn Arg Tyr Thr Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu  
 1 5 10 15  
 Leu Ser Leu Ser Pro Asp Val Thr Leu Thr His Phe Ala His Cys Asn  
 20 25 30  
 Leu

<210> 1545

<211> 68

<212> PRT

<213> Homo sapiens

<400> 1545

Met Met Glu Glu Ser Gly Ile Glu Thr Thr Pro Pro Gly Thr Pro Pro  
 1 5 10 15  
 Pro Asn Pro Ala Gly Leu Ala Ala Thr Ala Met Ser Ser Thr Pro Val  
 20 25 30  
 Pro Leu Ala Ala Thr Ser Ser Phe Ser Ser Pro Asn Val Ser Ser Met  
 35 40 45  
 Glu Ser Phe Pro Pro Leu Ala Tyr Ser Thr Pro Gln Pro Pro Leu Pro  
 50 55 60  
 Pro Val Arg Pro  
 65

<210> 1546

<211> 50

<212> PRT

<213> Homo sapiens

<400> 1546

Met Leu Cys Leu Thr Glu Gly Ala Lys Asp Glu Cys Asn Val Val Glu  
 1 5 10 15  
 Val Val Ala Arg Asn His Asp His Gln Glu Ile Ala Val Pro Val Ala  
 20 25 30  
 Xaa Leu Lys Leu Ser Cys Gln Pro Met Leu Ser Leu Asp Asp Phe Gln

35 40 45  
 Leu Gln  
 50  
 <210> 1547  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1547  
 Met Pro Thr Val Ser Val Lys Arg Asp Leu Leu Phe Gln Ala Leu Gly  
 1 5 10 15  
 Arg Thr Tyr Thr Asp Glu Glu Phe Asp Glu Leu Cys Phe Glu Phe Gly  
 20 25 30  
 Leu Glu Leu Asp Glu Ile Thr Ser Glu Lys Glu Ile Ile Ser Lys Glu  
 35 40 45  
 Gln Gly Asn Val Lys Ala Ala Gly Ala Ser Asp Val Val Leu Tyr Lys  
 50 55 60  
 Ile Asp Val Pro Ala Asn Arg Tyr Asp Leu Leu Cys Leu Glu Gly Leu  
 65 70 75 80  
 Val Arg Gly Leu Gln Val Phe Lys Glu Arg Ile Lys Ala Pro Val Tyr  
 85 90 95  
 Lys Arg Val Met Pro Asp Gly Lys Ile Gln Lys Leu Ile Ile Thr Glu  
 100 105 110  
 Glu Thr Ala Lys Ile Arg Pro Phe Ala Val Ala Ala Val Leu Arg Asn  
 115 120 125  
 Ile Lys Phe Thr Lys Asp Arg Tyr Asp Ser Phe  
 130 135

<210> 1548  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1548  
 Met Phe Ser Glu Glu Leu Trp Leu Glu Asn Glu Lys Lys Cys Ala Val  
 1 5 10 15  
 Val Arg Lys Ser Lys Gln Gly Arg Lys Arg Gln Glu Leu Leu Ala Val  
 20 25 30  
 Ala Phe Gly Val Lys Val His Thr Phe Arg Gly Pro His Trp Cys Glu  
 35 40 45  
 Tyr Cys Ala Asn Phe Met Trp Gly Leu Ile Ala Gln Gly Val Arg Cys  
 50 55 60  
 Ser Asp Cys Gly Leu Asn Val  
 65 70

<210> 1549  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1549  
 Met Val Val Phe Met Thr Tyr Val Thr Leu Pro Phe Phe Phe Ser Phe  
 1 5 10 15  
 Ile Ser Ser Leu Leu Ser Phe Phe Phe Leu Phe Leu Leu  
 20 25

<210> 1550  
 <211> 50  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1550  
 Met Gln Glu Leu Phe Leu Lys Phe Val Asp Glu Asn Trp Glu Gly Ser  
 1 5 10 15  
 Leu Lys Ser Lys Tyr Val Arg Gly Ser Asp Pro Val Leu Lys Leu Leu  
 20 25 30

Met	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Gly	Asp	Lys	Gly
			-10					-5					1		
Asp	Gly	Gly	Arg	Gln	Thr	Ile	Trp	Gly	Trp	Leu	Leu	Ala	Ala	Ser	Ala
	5				10					15					
Gly	Ala	Gly	Asp	Gly	Ala	Gly	Gly	Pro	Val	Cys	Pro	Cys	Ala	Leu	Leu
20					25					30					35

Leu Leu Leu Pro Pro Gly Trp Leu Asp  
40

<210> 1555  
<211> 95  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -18...-1

<400> 1555  
Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys  
-15 -10 -5  
Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr  
1 5 10  
Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu  
15 20 25 30  
Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln  
35 40 45  
Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met  
50 55 60  
Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn  
65 70 75

<210> 1556  
<211> 95  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -31...-1

<400> 1556  
Met Val Ala Met Ala Ala Gly Pro Ser Gly Cys Leu Val Pro Ala Phe  
-30 -25 -20  
Gly Leu Arg Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe  
-15 -10 -5 1  
Gly Ala Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser  
5 10 15  
Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu  
20 25 30  
Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe  
35 40 45  
Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly  
50 55 60

<210> 1557  
<211> 101  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -32...-1

<400> 1557  
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu  
-30 -25 -20  
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly  
-15 -10 -5

Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met  
 1 5 10 15  
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu  
 20 25 30  
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn  
 35 40 45  
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Lys  
 50 55 60  
 Lys Ser Arg Lys Pro  
 65

<210> 1558  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -51...-1

<400> 1558  
 Met Gln Ala Gln Ala Pro Val Val Val Thr Gln Pro Gly Val Gly  
 -50 -45 -40  
 Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys Asp  
 -35 -30 -25 -20  
 Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe Pro  
 -15 -10 -5  
 Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu Cys  
 1 5 10  
 Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly Ile  
 15 20 25  
 Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro His  
 30 35 40 45  
 Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala Met  
 50 55 60  
 Arg Thr Phe

<210> 1559  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<400> 1559  
 Met Asp Lys Ser Leu Leu Leu Glu Leu Pro Ile Leu Leu Cys Cys Phe  
 -20 -15 -10  
 Arg Ala Leu Ser Gly Ser Leu Ser Met Arg Asn Asp Ala Val Asn Glu  
 -5 1 5  
 Ile Val Ala Val Lys Asn Asn Phe Pro Val Ile Glu Ile Val Arg Cys  
 10 15 20  
 Arg Met Cys His Leu Gln Phe Pro Gly Glu Lys Cys Ser Arg Gly Arg  
 25 30 35 40  
 Gly Ile Cys Thr Ala Thr Thr Glu Glu Ala Cys Met Val Gly Arg Met  
 45 50 55  
 Phe Lys Arg Asp Gly Asn Pro Trp Leu Thr Phe Met Gly Cys Leu Lys  
 60 65 70  
 Asn Cys Ala Asp Val Lys Gly Ile Arg Trp Ser Val Tyr Leu Val Asn  
 75 80 85  
 Phe Arg Cys Xaa Arg Ser His Asp Leu Cys Asn Glu Asp Leu  
 90 95 100

<210> 1560  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1560  
 Met Asp Leu Leu Trp Ile Leu Pro Ser Leu Trp Leu Leu Leu Leu Gly  
           -15                          -10                          -5  
 Gly Pro Ala Cys Leu Lys Thr Gln Glu His Pro Ser Cys Pro Gly Pro  
                           5  10                          15  
 Arg Glu Leu Glu Ala Ser Lys Val Val Leu Leu Pro Ser Cys Pro Gly  
                           20  25                          30  
 Ala Pro Gly Ser Pro Gly Glu Lys Gly Ala Pro Gly Pro Gln Gly Pro  
                           35  40                          45  
 Pro Gly Pro Pro Gly Lys Met Gly Pro Lys Gly Glu Pro Gly Asp Pro  
                           50  55                          60  
 Val Asn Leu Leu Arg Cys Gln Glu Gly Pro Arg Asn Cys Arg Glu Leu  
   70  75                          80  
 Leu Ser Arg Ala Pro Pro  
   85

<210> 1561  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 1561  
 Met Glu Ser Pro Ser Xaa Ser Ala Val Val Leu Pro Ser Thr Pro Gln  
                           -15  -10                          -5  
 Ala Ser Ala Asn Pro Ser Ser Pro Tyr Thr Asn Ser Ser Arg Lys Gln  
                           1  5  10  
 Pro Met Ser Ala Thr Leu Arg Glu Arg Leu Arg Lys Thr Arg Phe Ser  
           15  20  25  
 Phe Asn Ser Ser Xaa Asn Val Val Asn Val Leu Lys  
           30  35  40

<210> 1562  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 1562  
 Met Asp Phe Trp Leu Trp Pro Leu Tyr Phe Leu Pro Val Ser Gly Ala  
           -15                          -10                          -5  
 Leu Arg Ile Leu Pro Glu Val Lys Val Glu Gly Glu Leu Gly Gly Ser  
           1  5  10                          15  
 Val Thr Ile Lys Cys Pro Leu Pro Glu Met His Val Arg Ile Tyr Leu  
                           20  25                          30  
 Cys Arg Glu Met Ala Gly Ser Gly Thr Cys Gly Thr Val Val Ser Thr  
           35  40  45

Thr Asn Phe Ile Xaa Ala Glu Tyr Lys Gly Arg Val Thr Leu Arg Ala  
 50 55 60  
 Ile Pro Thr Gln Glu Ser Val Pro Ser Gly Gly Asn Thr Ala Asp Arg  
 65 70 75 80  
 Lys

<210> 1563  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400> 1563  
 Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala Val Ala  
 -30 -25 -20  
 Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val  
 -15 -10 -5  
 Tyr Ser Xaa Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu  
 1 5 10  
 Leu Ser Xaa Leu Leu Ser Xaa Ala Phe Leu Leu Val Arg Xaa Leu Pro  
 15 20 25 30  
 Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn Pro Ser  
 35 40 45  
 Xaa Xaa

<210> 1564  
 <211> 48  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17...-1

<400> 1564  
 Met Ala Gln Leu Trp Leu Ser Cys Phe Leu Leu Pro Ala Leu Val Val  
 -15 -10 -5  
 Ser Val Ala Ala Asn Val Ala Pro Xaa Phe Leu Ala Asn Met Thr Ser  
 1 5 10 15  
 Val Ile Leu Pro Glu Asp Cys Leu Trp Val Pro Arg Pro Ser Gly Trp  
 20 25 30

<210> 1565  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400> 1565  
 Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala Val Ala  
 -30 -25 -20  
 Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val  
 -15 -10 -5  
 Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu  
 1 5 10  
 Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro  
 15 20 25 30

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Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn Pro Cys  
 35 40 45  
 Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile  
 50 55 60  
 Val Met Met Lys Asn Arg Arg Ser Ser  
 65 70

<210> 1566  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19..-1

<400> 1566  
 Met Val Ala Trp Arg Ser Ala Phe Leu Val Cys Leu Ala Phe Ser Leu  
 -15 -10 -5  
 Ala Thr Leu Val Gln Arg Gly Ser Gly Asp Phe Asp Asp Phe Asn Leu  
 1 5 10  
 Glu Asp Ala Val Lys Glu Thr Ser Ser Val Lys Gln Pro Trp Asp His  
 15 20 25  
 Thr Thr Thr Thr Thr Thr Asn Arg Pro Gly Thr Thr Arg Ala Pro Ala  
 30 35 40 45  
 Lys Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala Leu Asp Asp Gln  
 50 55 60  
 Asp Asp Gly Arg Arg Asn Arg Val  
 65

<210> 1567  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -53..-1

<400> 1567  
 Met Ala Asp Pro Asp Pro Arg Tyr Pro Arg Ser Ser Ile Glu Asp Asp  
 -50 -45 -40  
 Phe Asn Tyr Gly Ser Ser Val Ala Ser Ala Thr Val His Ile Arg Met  
 -35 -30 -25  
 Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu  
 -20 -15 -10  
 Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr  
 -5 1 5 10  
 Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser  
 15 20 25  
 Leu Gly Leu Ile Phe Ala Leu Xaa Leu Asn Arg His Lys Tyr Pro Leu  
 30 35 40  
 Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Glu Ala Leu Thr Val  
 45 50 55  
 Ala Val Val Val Thr Val Leu  
 60 65

<210> 1568  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<220>

&lt;221&gt; SIGNAL

&lt;222&gt; -55...-1

&lt;400&gt; 1568

Met Ser Ser Gln Lys Gly Asn Val Ala Arg Ser Arg Pro Gln Lys His  
 -55 -50 -45 -40  
 Gln Asn Thr Phe Ser Phe Lys Asn Asp Lys Phe Asp Lys Ser Val Gln  
 -35 -30 -25  
 Thr Lys Ser Met Asn Asn Leu Ser Phe Ser Glu Leu Cys Cys Leu Phe  
 -20 -15 -10  
 Cys Cys Pro Pro Cys Pro Gly Lys Ile Ala Ser Lys Leu Ala Phe Leu  
 -5 1 5  
 Pro Pro Asp Pro Thr Tyr Thr Leu Met Cys Asp Glu Ser Gly Ser Val  
 10 15 20 25  
 Gly Leu Tyr Ile Cys Leu Asn Glu Gln Thr Gly Ser Ile Leu Leu Glu  
 30 35 40  
 Lys Lys Met Leu Leu Ser Val Ser  
 45

&lt;210&gt; 1569

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -62...-1

&lt;400&gt; 1569

Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu Thr  
 -60 -55 -50  
 Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu Ile Asn  
 -45 -40 -35  
 Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser Leu Ala Val  
 -30 -25 -20 -15  
 Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala Gly Leu Leu Val  
 -10 -5 1  
 Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg Val Leu Glu Met Tyr  
 5 10 15  
 Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp Ser Pro Ser Phe Ser Leu  
 20 25 30  
 Leu Gln Ser Ala His Pro Gly Glu His Leu Ala Gln Gly Ala Ser Arg  
 35 40 45 50  
 Leu Gln Ser Cys Arg Pro Asn Ser Pro Gly Ser Ala Ser Xaa  
 55 60

&lt;210&gt; 1570

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -56...-1

&lt;400&gt; 1570

Met Ala Pro Thr Lys Pro Ser Phe Gln Gln Asp Pro Ser Arg Arg Glu  
 -55 -50 -45  
 Arg Leu Gln Ala Leu Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser  
 -40 -35 -30 -25  
 Arg Arg Gly Lys Glu Asn Phe Glu Phe Tyr Glu Leu Ala Lys Leu Leu  
 -20 -15 -10  
 Pro Leu Pro Ala Ala Ile Thr Ser Gln Leu Asp Lys Ala Ser Ile Ile

```

      -5      1      5
Arg Leu Thr Ile Ser Tyr Leu Lys Met Arg Asp Phe Ala Asn Gln Gly
  10      15      20
Asp Pro Pro Trp Asn Leu Arg Met Glu Gly Pro Pro Pro Asn Thr Ser
 25      30      35      40
Val Lys Val Ile Gly Ala Gln Arg Arg Arg Ser Pro Ser Ala Leu Ala
      45      50      55
Ile Glu Val Phe Glu Ala His Leu Gly Ser His Ile Leu Gln Ser Trp
      60      65      70
Met Ala Leu Tyr Leu His
      75

```

<210> 1571  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

```

<400> 1571
Met Glu Glu Leu Gln Asp Gln Ala Leu Leu Ser Val Cys Ser Thr Asp
-20      -15      -10      -5
Val Thr Thr Ala His Ala Trp Leu Thr Val Leu Val
      1      5

```

<210> 1572  
 <211> 28  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

```

<400> 1572
Met Glu Glu Leu Gln Asp Gln Ala Leu Leu Ser Val Cys Ser Thr Asp
-20      -15      -10      -5
Val Thr Thr Ala His Ala Trp Leu Thr Val Leu Val
      1      5

```

<210> 1573  
 <211> 47  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -45...-1

```

<400> 1573
Met Val Gly Arg Val Arg Val Cys Arg Lys Tyr Pro Pro Thr Thr Leu
-45      -40      -35      -30
Trp Glu Gly Ala Arg Gly His Arg Gln Ile Ser Val Ser Pro Trp Asn
      -25      -20      -15
Ile Cys Cys Ala Ala Ala Ala Ala Ala Gly Ser Arg Ile
      -10      -5      1

```

<210> 1574  
 <211> 137  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -52...-1

<400> 1574  
 Met Lys Arg Leu Glu Ala Lys Tyr Ala Pro Leu His Leu Val Pro Leu  
           -50                          -45                          -40  
 Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg Glu Gly  
           -35                          -30                          -25  
 Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met Phe Glu  
           -20                          -15                          -10                          -5  
 Val Ile Leu Thr Arg Ile Arg Ser Tyr Leu Gln Asp Pro Ile Trp Arg  
                           1                          5                          10  
 Gly Pro Pro Pro Thr Asn Gly Val Met His Val Asp Glu Cys Val Glu  
                           15                          20                          25  
 Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile Pro Val  
           30                          35                          40  
 Gly Thr Asn Glu Phe Thr Ala Glu Gln Cys Phe Gly Asp Gly Leu Asn  
           45                          50                          55                          60  
 Trp Ala Gly Ser Pro Xaa Leu Ser Cys Xaa Ala Ser Ser Val Ala Leu  
                           65                          70                          75  
 Thr Cys Ser Thr Ser Val Thr Thr Cys  
                           80                          85

<210> 1575  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -71...-1

<400> 1575  
 Met Ala Leu Val Pro Cys Gln Val Leu Arg Met Ala Ile Leu Leu Ser  
           -70                          -65                          -60  
 Tyr Cys Ser Ile Leu Cys Asn Tyr Lys Ala Ile Glu Met Pro Ser His  
           -55                          -50                          -45                          -40  
 Gln Thr Tyr Gly Gly Ser Trp Lys Phe Leu Thr Phe Ile Asp Leu Val  
                           -35                          -30                          -25  
 Ile Gln Ala Val Phe Phe Gly Ile Cys Val Leu Xaa Asp Leu Ser Ser  
           -20                          -15                          -10  
 Leu Leu Thr Arg Gly Ser Gly Asn Gln Glu Gln Glu Arg Gln Leu Lys  
           -5                          1                          5  
 Lys Leu Ile Ser Leu Arg Asp Trp Met Leu Ala Val Leu Ala Phe Leu  
           10                          15                          20                          25  
 Leu Gly Phe Leu Leu  
                           30

<210> 1576  
 <211> 79  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -69...-1

<400> 1576  
 Met Ala Thr His His Leu Gly Leu Pro Ala Ser Gln Pro Leu Pro Gly  
                           -65                          -60                          -55  
 Ile Leu Ser Arg Ala Pro Ser Leu Pro Pro Arg Ser Pro Ala Thr Arg

-50 -45 -40  
 Ser Arg Val Ser Ser Pro Trp Gly Glu Ser Ser Ser Ser Leu Leu Phe  
 -35 -30 -25  
 Pro Asp Cys His Ile Ser Phe Pro Ala Leu Thr Gly Ser Gln Leu Leu  
 -20 -15 -10  
 Gly Asp Thr Ile Pro Arg Pro His Leu Pro Pro Thr Ala Ala Cys  
 -5 1 5 10

<210> 1577  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -35...-1

<400> 1577  
 Met Thr Pro Ser Arg Leu Pro Trp Leu Leu Ser Trp Val Ser Ala Thr  
 -35 -30 -25 -20  
 Ala Trp Arg Ala Ala Arg Ser Pro Leu Leu Cys His Ser Leu Arg Lys  
 -15 -10 -5  
 Thr Ser Ser Ser Gln Gly Gly Lys Ser Glu Leu Val Lys Gln Ser Leu  
 1 5 10  
 Lys Lys Pro Lys Leu Pro Glu Gly Arg Phe Asp Ala Pro Glu Asp Ser  
 15 20 25  
 His Leu Glu Lys Glu Pro Leu Glu Lys Phe Pro Asp Asp Val Xaa Pro  
 30 35 40 45  
 Val Thr Lys Glu Lys Gly Gly Pro Arg Gly Pro Glu Pro Thr Arg Tyr  
 50 55 60  
 Gly Asp Trp Glu Arg Lys Gly Arg Cys Ile Asp Phe  
 65 70

<210> 1578  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -51...-1

<400> 1578  
 Met Glu Lys Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln  
 -50 -45 -40  
 Gly Leu Thr Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr  
 -35 -30 -25 -20  
 Arg Leu Lys Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser  
 -15 -10 -5  
 Ile Leu Gly Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe  
 1 5 10  
 Ala Val Phe Tyr Thr Leu Gly Asn Leu Ala Ala Leu Xaa Val His Ala  
 15 20 25  
 Xaa  
 30

<210> 1579  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

&lt;222&gt; -93...-1

&lt;400&gt; 1579

```

Met Cys Glu Asn Gln Glu Glu Pro Ala Gly Ser Val Cys Cys His Arg
      -90                      -85                      -80
Val Ser Ala Cys Arg Gly Gly Thr Pro Gly Gly Gly Arg Gly Gln Ser
      -75                      -70                      -65
His Cys Arg Gly Pro Asp Trp Glu Asn Asn Asp Met Ala Gly Ala Ser
      -60                      -55                      -50
Leu Gly Ala Arg Phe Tyr Arg Gln Ile Lys Arg His Pro Gly Ile Ile
      -45                      -40                      -35                      -30
Pro Met Ile Gly Leu Ile Cys Leu Gly Met Gly Ser Ala Ala Leu Tyr
      -25                      -20                      -15
Leu Leu Arg Leu Ala Leu Arg Ser Pro Asp Val Trp Leu Gly Gln Lys
      -10                      -5                      1
Glu Gln Pro Gly Ala Leu Glu Pro Pro Glu Pro Gln
      5                      10                      15

```

&lt;210&gt; 1580

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -16...-1

&lt;400&gt; 1580

```

Met Ala Ala Ala Gly Leu Ala Leu Leu Xaa Arg Arg Val Ser Ser Ala
      -15                      -10                      -5
Leu Lys Ser Ser Arg Ser Leu Ile Thr Pro Gln Val Pro Ala Cys Thr
1      5                      10                      15
Gly Phe Phe Leu Ser Leu Leu Pro Lys Ser Thr Pro Asn Val Thr Ser
      20                      25                      30
Phe His Gln Tyr Arg Leu Leu His Thr Thr Leu Ser Arg Lys Gly Leu
      35                      40                      45
Glu Glu Phe Phe Asp Asp Pro Lys Asn Trp Gly Gln Glu Lys Val Lys
      50                      55                      60
Ser Gly Ala Ala Trp Thr Cys Gln Gln Leu Arg Asn Lys Ser Asn Glu
      65                      70                      75                      80
Asp Leu His Lys Leu Trp Tyr Val Leu Leu Lys Glu Arg Asn Met Leu
      85                      90                      95
Leu Thr Leu Glu Gln Glu Ala Lys Arg Gln Arg Leu Pro Met Pro Ser
      100                      105                      110
Pro Glu Arg Leu Asp Arg
      115

```

&lt;210&gt; 1581

&lt;211&gt; 64

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1581

```

Met Asn Glu Ser Lys Pro Gly Asp Ser Gln Asn Leu Ala Cys Val Phe
1      5                      10                      15
Cys Arg Lys His Asp Asp Cys Pro Asn Lys Tyr Gly Glu Lys Lys Thr
      20                      25                      30
Lys Glu Lys Trp Asn Leu Thr Val His Tyr Tyr Cys Leu Met Ser
      35                      40                      45
Ser Gly Ile Trp Gln Arg Gly Lys Glu Glu Glu Gly Val Met Val Phe
      50                      55                      60

```

&lt;210&gt; 1582

&lt;211&gt; 79

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1582

Met Ala Val Ala Arg Ala Gly Val Leu Gly Val Gln Trp Leu Gln Arg  
1 5 10 15  
Ala Ser Arg Asn Val Met Pro Leu Gly Ala Arg Thr Ala Ser His Met  
20 25 30  
Thr Lys Asp Met Phe Pro Gly Pro Tyr Pro Arg Thr Pro Glu Glu Arg  
35 40 45  
Ala Ala Ala Ala Lys Lys Tyr Asn Met Arg Val Glu Asp Tyr Glu Pro  
50 55 60  
Tyr Pro Asp Asp Gly Met Gly Tyr Gly Asp Leu Phe Leu Xaa Val  
65 70 75

&lt;210&gt; 1583

&lt;211&gt; 66

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1583

Met Glu Val Asp Ala Pro Gly Val Asp Gly Arg Asp Gly Leu Arg Glu  
1 5 10 15  
Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln Asn Phe Asp Val Arg Pro  
20 25 30  
Gln Ser Gly Ala Asn Gly Leu Pro Lys His Ser Tyr Trp Leu Asp Leu  
35 40 45  
Trp Leu Phe Ile Leu Phe Asp Val Val Val Phe Leu Phe Val Tyr Phe  
50 55 60  
Leu Pro  
65

&lt;210&gt; 1584

&lt;211&gt; 45

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1584

Met Tyr Val Tyr Val Cys Val Trp Val Cys Val Tyr Thr Val Glu Ser  
1 5 10 15  
Lys Leu Glu Asn Ser Ser Ile Tyr Pro Pro Pro Ser Pro Val Glu Xaa  
20 25 30  
Lys Lys Ile Phe Thr Phe Val Thr Phe Leu Phe Pro Pro  
35 40 45

&lt;210&gt; 1585

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1585

Met Gly Pro Gly Gly Ala Leu His Gly Gly Met Lys Thr Leu Leu Pro  
1 5 10 15  
Trp Thr Ala Arg Ala Ser Arg Ser Pro  
20 25

&lt;210&gt; 1586

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1586

Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala Val Pro Ser Asp Ser  
1 5 10 15  
Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr Glu Tyr Leu Leu His  
20 25 30  
Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu Ser Glu Ile Arg Trp  
35 40 45

Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly Phe Leu His Ser Trp  
 50 55 60  
 Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala Pro Glu Arg Arg Glu  
 65 70 75 80  
 Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe His Asp Tyr Val Xaa  
 85 90 95  
 Asn Ile

<210> 1587

<211> 50

<212> PRT

<213> Homo sapiens

<400> 1587

Met Cys Leu Leu Glu Val Pro Gly Ala Thr Lys Leu Leu Ala Ala Arg  
 1 5 10 15  
 Arg Thr Leu Lys Arg Asn Gly Ile Ser Pro Pro Asn Gln Glu Gly Leu  
 20 25 30  
 Ala Leu Leu Leu Gly Glu Leu Thr Thr His Lys Gln Met Arg Thr Lys  
 35 40 45  
 Thr Glu  
 50

<210> 1588

<211> 32

<212> PRT

<213> Homo sapiens

<400> 1588

Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser  
 1 5 10 15  
 Xaa Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Xaa Ser  
 20 25 30

<210> 1589

<211> 58

<212> PRT

<213> Homo sapiens

<400> 1589

Met Ala Ser Ser Gly Ala Gly Asp Pro Leu Asp Ser Lys Arg Gly Glu  
 1 5 10 15  
 Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr Arg Glu Lys Leu Thr Pro  
 20 25 30  
 Glu Gln Leu His Ser Met Arg Gln Ala Glu Leu Pro Ser Gly Arg Arg  
 35 40 45  
 Ser Tyr His Gly Gly Glu Pro Gly Thr Ser  
 50 55

<210> 1590

<211> 98

<212> PRT

<213> Homo sapiens

<400> 1590

Met Ser Ser Asp Asp Lys Ser Lys Ser Asn Asp Pro Lys Thr Glu Pro  
 1 5 10 15  
 Lys Asn Cys Asp Pro Lys Cys Glu Gln Lys Cys Glu Ser Lys Cys Gln  
 20 25 30  
 Pro Ser Cys Leu Lys Lys Leu Leu Gln Arg Cys Phe Glu Lys Cys Pro  
 35 40 45  
 Trp Glu Lys Cys Pro Ala Pro Pro Lys Cys Leu Pro Cys Pro Ser Gln  
 50 55 60  
 Ser Pro Ser Ser Cys Pro Pro Gln Pro Cys Thr Lys Pro Cys Pro Pro  
 65 70 75 80  
 Lys Cys Pro Ser Ser Cys Pro His Ala Cys Pro Xaa Pro Cys Pro Pro  
 85 90 95

Pro Glu

&lt;210&gt; 1591

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1591

```

Met Cys Gly Gly Trp Asp Pro Val Ala His Pro Cys Arg Ser Cys Pro
1          5          10          15
Ser His Ala Arg Arg Arg Val Phe Val Val Thr Pro Cys Cys His Leu
          20          25          30
Phe Ser Ser Leu Cys Glu Asp Leu Asp Trp Gln
          35          40

```

&lt;210&gt; 1592

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1592

```

Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
1          5          10          15
Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
          20          25          30
Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
          35          40          45
Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
          50          55          60
Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
65          70          75          80
Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
          85          90          95
Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
          100          105          110
Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
          115          120          125
Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
130          135          140
Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
145          150          155

```

&lt;210&gt; 1593

&lt;211&gt; 119

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1593

```

Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys
1          5          10          15
Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg
          20          25          30
Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Val Pro Met Val Leu
          35          40          45
Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser Ser Ile Ala
          50          55          60
Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ala
65          70          75          80
Ser Gly Ser Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Thr Gly Leu
          85          90          95
Ser Gly Leu Thr Lys Xaa Ile Leu Gly Ser Ile Gly Ser Ala Ile Ala
          100          105          110
Ala Val Ile Ala Arg Phe Tyr
          115

```

&lt;210&gt; 1594

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1594

```

Met Tyr Ile Gln Cys Cys Glu Trp Leu Gln Ser Trp Arg Ser Lys Asp
1           5           10           15
Glu Phe Cys Leu Glu Glu Ser Gly Lys Ala Ser Trp Arg Arg Glu Gln
          20           25           30
Trp His Gly Pro Xaa Xaa Val Arg Ser Phe Gln Phe Ile Pro Phe Lys
          35           40           45
His Cys Ser His Val Ala Phe Lys His Ser Ile Val Leu Ala Val Thr
          50           55           60
Gln Ala His Ser Ala Lys Gly Ser Thr Ser Phe Ser Ala Met Arg Thr
65           70           75           80
Tyr

```

&lt;210&gt; 1595

&lt;211&gt; 65

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1595

```

Met Val Gly Val Ser Val Cys His His Ile Arg Val Gly Ile Lys Arg
1           5           10           15
Arg Lys Ala Ala Leu Leu Glu Leu Cys Gly Leu Leu Gln Val Arg Val
          20           25           30
Ala Gly Asn Arg Thr Thr Leu Leu Glu Glu Lys Arg Asn Ser Phe
          35           40           45
Ser Ala Xaa Thr Arg Lys Ala Val Phe Phe Ser Gly Asp Leu His Phe
          50           55           60
Ser
65

```

&lt;210&gt; 1596

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1596

```

Met Pro Ser Arg Thr Ala Arg Tyr Ala Arg Tyr Ser Pro Arg Gln Arg
1           5           10           15
Arg Arg Arg Met Leu Ala Asp Arg Ser Val Arg Phe Pro Asn Asp Val
          20           25           30
Leu Phe Leu Asp His Ile Arg Gln Gly Asp Leu Glu Gln Val Gly Arg
          35           40           45
Phe Ile Arg Thr Arg Lys Val Ser Leu Ala Thr Ile His Pro Ser Gly
          50           55           60
Leu Ala Ala Leu His Glu Ala Val Leu Ser Gly Asn Leu Glu Cys Val
65           70           75           80
Lys Leu Leu Val Lys Tyr Gly Ala Asp Ile His Gln Arg Asp Glu Ala
          85           90           95
Gly Trp Thr Pro Leu His Ile Ala Cys Ser Asp Gly Tyr Leu Thr
          100          105          110

```

&lt;210&gt; 1597

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1597

```

Met Ala Trp Gly Gly Trp Gly Ala His Ser Ala Cys Ser Glu Glu Arg
1           5           10           15
Ala Thr Arg Pro Val Glu Gly Ala Tyr Ser Gly Arg Trp Gly Gln Ala
          20           25           30
Gln

```

&lt;210&gt; 1598

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1598

```

Met Asp Pro Asn Pro Arg Ala Ala Leu Glu Arg Gln Gln Leu Arg Leu
1          5          10          15
Arg Glu Arg Gln Lys Phe Phe Glu Asp Ile Leu Gln Pro Glu Thr Glu
20          25          30
Phe Val Phe Pro Leu Ser His Leu His Leu Glu Ser Gln Arg Pro Pro
35          40          45
Ile Gly Ser Ile Ser Ser Met Glu Val Asn Val Asp Thr Leu Glu Gln
50          55          60
Val Glu Leu Ile Asp Leu Gly Asp Pro Asp Ala Asp Val Phe Leu
65          70          75          80
Pro Cys Glu Asp Pro Pro Pro Thr Pro Gln Ser Ser Gly Val Asp Asn
85          90          95
His Leu Glu Glu Leu Ser Leu Pro Xaa Ala Tyr Ile Arg Gln Asp His
100          105          110
Ile

```

&lt;210&gt; 1599

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1599

```

Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
1          5          10          15
Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Asp Thr Lys Tyr Ile
20          25          30
Ser Asn Gly Asp Ile Trp Asn Asn Ser Trp Phe Leu Trp Asn Ile Leu
35          40          45
Lys Leu Pro Val Gln Thr Leu Leu Gln Gly
50          55

```

&lt;210&gt; 1600

&lt;211&gt; 247

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1600

```

gaaaattact ttgacctttt gttagtgtc ccattcagct agtaccaagc tgaagattga      60
tattcggttaa tggtaatat aaatttactg ctctagggtta agcctaakat atgtaattgc      120
tactagccta ttacttttta gtccattggg aatcactaaa aaaagtagag gcttttagctt      180
cattcctcgg ctgcttaaat catattgtaa tgttttaaat tggtatgtcg tcctgtataa      240
ccttagg                                           247

```

&lt;210&gt; 1601

&lt;211&gt; 225

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1601

```

aaaattattt tgagacaaaa catgggaaag gagggagttg gccaggagtt tatcatgaag      60
catatacagg agtcatcccc tacgttgaca ctggttaagtt gacttcagtc acatgaaaca      120
tgtcaccttt ccataaatac tccattccct tttgtgattt tgttctttgc acatgttggt      180
ctatctctgc ctggaatgtg ttctccacct tttgattgtc tgcca                      225

```

&lt;210&gt; 1602

&lt;211&gt; 258

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1602

```

gtgaccacag tctgcagagg ccagagagag caggaaagga aatggaaagg aacctcacct      60
tcatgcttgg ggaaaaggag aaacctgtgt taatgtgtct tccaacatc ccactctctt      120

```

cagcaatcgc tggaaacagcc atggggccatc cctgctgagt caggaaagaa gctgagggaa 180  
gagtcgggat tgaaaagcag cagacaaggg aaatgtggac acaagcacat gaagagaaca 240  
ccatgtgaac ataaagat 258

<210> 1603  
<211> 341  
<212> DNA  
<213> Homo sapiens  
<400> 1603  
aagggttactt gactgggagt tctcagacct ccagtttcag ccctgccctc agcctccaat 60  
ccgtaagaga yacccagccc cagcaattgg attgggcagc ccgtcttgac acaccactgt 120  
gctgagtgtc tgaggacgtg tttcaacaga tggttggggg tagtgtgtgt catcacattc 180  
gagtggggat taagagaagg aaggctgcct tgctggagct gtgtggtcct ctccaagtga 240  
gagtcgcagg caatagaact actttgcttt tggaggaaaa ggaggaattc attttcagca 300  
gacacaagaa aagcagtttt tttttcaggt gctgacggcc a 341

<210> 1604  
<211> 292  
<212> DNA  
<213> Homo sapiens  
<400> 1604  
cactgggcgcg ggttgagttc cctgttgccc ttggtctcgg ggctcgtgtm ggcgctgagg 60  
ctgcagctat catggtgaac ttacttcaga ttgtcgggga ccactgggtt catgttcttg 120  
tccctatggg atttgtcatt ggatgttatt tagacagaaa gagtgatgaa cggctaactg 180  
ccttccggaa caagagtatg ttatttaaaa ggaattgca acccagtga gaagtacct 240  
ggaagtaag actggctaga ttatcgaatg ttcacatttt aaagtctctga ga 292

<210> 1605  
<211> 357  
<212> DNA  
<213> Homo sapiens  
<400> 1605  
ctgctctaag ctgcagcaag agaaactgtg tgtgagggga agaggcctgt ttcgctgtcg 60  
ggtctctagt tcttgacgc tctttaagag tctgcactgg aggaactcct gccattacca 120  
gtcccttct tgcagaagg agggggaaac atacatttat tcatgccagt ctgttgcatg 180  
caggcttttt ggcttcctac cttgcaacaa aataattgca ccaactcctt agtgccgatt 240  
ccgcccacag agagtctctg arccacagtc ttttttgctt tgcattgtag gagagggact 300  
aagtgtctaga gactatgtcg ctttcctgag ctaccgagag cgctcgtgaa ctggaat 357

<210> 1606  
<211> 293  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 13  
<223> n=a, g, c or t

<400> 1606  
attccctacc cancagccct cgcgcggtcc ggcacagcgg acaccaggac tccaaaatgg 60  
cgtcagttgg tgagtgtccg gccccagtac cagtgaagga caagaaactt ctggaggtca 120  
aactggggga gctgccaagc tggatcttga tgcggractt cagtcctagt ggcattttcg 180  
gagcgtttca aaraggttac accggtacta caacaagtac atcaatgtga agaaggggag 240  
catctcgggg attaccatgg tgctacccta ccacacattc gaagaaccg tat 293

<210> 1607  
<211> 361  
<212> DNA  
<213> Homo sapiens

<220>

<221> misc\_feature  
<222> 323  
<223> n=a, g, c or t

<400> 1607  
tggtgtcttt atcagactta cattgcctct gtgaatatca gccttggctct actccaagtg 60  
caggacaaac acaaagaact ctctgcacag ttcattactc cattaggtgg ttcagatgca 120  
attccagccc ttagtcaggt tctttccagt gtcctcaaac acagtaagga gagtgtctta 180  
agtgactctt tgtgtctcac acaatctctt gggttcccag gtcactgggt tagtagccag 240  
ctgcatccaa gaagccaggt gagcctgtgc caccaatcac agatactcct taccaaccat 300  
ctgccaaccc atgccagccc tgntgcccct ggatgtgctg ctgtccatgt gccacgccc 360  
c 361

<210> 1608  
<211> 305  
<212> DNA  
<213> Homo sapiens  
<400> 1608

aagacggaag ctcggttgat gtttctgcag aagttttccc ccttggctcg tggcggastg 60  
ctgagcgga tagtagcagc tccggcgga gcaacattga ctacgaggaa tggcggcggc 120  
tgccgcagga cctgcagcat cccagaggtg cagattttta tttcagtgc tgaattaaaa 180  
ggtgtcaaga agctcgaatg gtatgtaggc ctcccatggt atttcaattt aaaaagaagt 240  
aagcacttga aattttttgg ttttaagcaa tttgttttta cttttataat ttatttttaa 300  
taata 305

<210> 1609  
<211> 242  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 152  
<223> n=a, g, c or t

<400> 1609  
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tagaggcatt aaaggtcaga gttctgagac ctgctctgga gtgggcagtg tcaaaccggg 120  
aaatgcttat agctcaaaca gtccttgga anttaagcta cacagactgt attttattag 180  
cttgtaaatg ggtggaacca caaatcagcg agaggcatta caatatgcta aaaattttca 240  
gc 242

<210> 1610  
<211> 196  
<212> DNA  
<213> Homo sapiens

<400> 1610  
ggaagcgatt tcatagccac ggtttttggc tttcatcgct ttttctacat gtttttagcc 60  
tcaccagaag tctttcatct cggtgggtcca actcaggatc tcagcctcat tattttctta 120  
cccttctgga gtgcatatgt gcctttacag ttctgtttgc aaacgctgtc tagcatacta 180  
agaggatggt agcaaa 196

<210> 1611  
<211> 228  
<212> DNA  
<213> Homo sapiens  
<400> 1611

atattgaata agcgaccgg cctcctaggg ggtcgtcgtg gtgcagacag tttagcagaa 60  
cagcctccgc ggctccggg agaaggtgag gtcttgatg gatgggaagg gtgaggtgag 120  
tcggccagag gcttatttat tgacgggact gtttcctttg gccacgcga cgtagcttct 180  
gttgccttg actgggcgcc gcctccgcc ccgcgcctc ggaagccc 228

<210> 1612  
<211> 221  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 108  
<223> n=a, g, c or t

<400> 1612  
tatttttagag atggaacaaa gagaacacat agatattcaa taatttactc aaaagtctgt 60  
gaggagccct agaaagaaat tcagggtctcc tatgtactga tcacagcnca gaaccccagg 120  
aagccagagg tgttccaccc caatccttca ccttcacccc acatcatggt ggcccctggg 180  
acctggatgg aaaacctctg gcwtcctggg gttctgggct g 221

<210> 1613  
<211> 360  
<212> DNA  
<213> Homo sapiens  
<400> 1613

agttgcctgc agagcctgag gtcagggag gttcagatg gttcatacct tgggtgtatac 60  
atgagttcat aggcctggga ttaaggatta tccctgcaat cttgcctgcc ttgcagataa 120  
gctactttct gaatcctaaa gcgctcttcc agctttcaca tttgattccg tggcagaagg 180  
ctcacagcct cacaaagtgg agacaggcag acagtccac ctcatttcaa ctccagagtt 240  
ggggaacgtg ctgggggtgc tcagccagag cctctcagcc aggccttggt aggcagaggg 300  
atccttacca ggcagatggt ctggaggaga ggcagaccgg gagaaagcat agtgtgccag 360

<210> 1614  
<211> 171  
<212> DNA  
<213> Homo sapiens  
<400> 1614

cagtaaggta gcaggattca aattatTTTT tccagtattg acatttagaa tgtcatgttg 60  
gacattttaa atttttctgg ttgtagcctc attactgtat agaaatcaac taccagatga 120  
gtagttagaca gacacagcta gcttggttgc ttgcttgctg ttcttgccgc c 171

<210> 1615  
<211> 193  
<212> DNA  
<213> Homo sapiens  
<400> 1615

acatcttttag tagagacggg caatccaccc gcctcggctc ccagagtact gggatgacag 60  
gcgtgagcac cacgtccggc cacaaaagag ctttgatgca cacggtgaca gccacatggt 120  
gcacccggaa gaacaagggg cctgaagtta gttagaccct ccttgctggt tctaaccacag 180  
tcgcacgccc cac 193

<210> 1616  
<211> 349  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 99  
<223> n=a, g, c or t

<400> 1616  
atggttggaa tcatattcag caggagtaag ctgactaact tacaaaaaca ggtgtgtgct 60  
catattgtcc aagctattcg catggaagct accagagtnc gtgaagaatg ggaacatgct 120

atatcaagca	aagaaaaatgc	caattctcag	ccaaatgatg	aagatgcctc	ctctgatgcc	180
tactgctttg	agctgctctc	tatggtttta	gcactgagtg	gctctaactg	tggccggcaa	240
tatctggctc	aacagctaac	cctgcttcag	gatctcttcc	gctgcttcac	acagcctctc	300
ctagagtcca	gagacaggta	cctctttact	agaagagttt	gctgaagta		349

&lt;210&gt; 1617

&lt;211&gt; 155

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1617

atacacatat	ccatgggtttg	tgagaggctc	ctcactaccc	gtcctgtctc	agaatgtcag	60
aatgcctctg	ttccttccct	tttgtggaca	agtcaactct	atacaatatt	tgaagggatt	120
attctgaacc	catctgaatg	accaaggcct	gaggc			155

&lt;210&gt; 1618

&lt;211&gt; 185

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1618

cttgaaatgg	gctgagtccc	tcttgctcac	ccttgacttg	gaaaaaccag	tttctctttt	60
attgtctggt	actaatctct	attctaaaaa	ttcagctcaa	ttctcaacca	tactccaaac	120
tctctctttt	ccagctacct	ttactccctc	tccttcaatt	ccactttcct	ctgcttactt	180
ttttt						185

&lt;210&gt; 1619

&lt;211&gt; 169

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1619

ggcgcaatg	gcggtacgc	tgaggtcctc	gctggaggac	ccactgcgga	gtttgtgcga	60
gttttgagga	agcgggatgg	tacagtgcta	cgactacagc	agtatagctc	cggtggcgtg	120
ggtgcgttgt	gtgggacgct	gccattgtcc	tttctaaata	cctggaaac		169

&lt;210&gt; 1620

&lt;211&gt; 246

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 122

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 1620

cagagggtttt	gttttcttca	taatttttat	cactatctga	attattttga	ttctttgttt	60
atgtgtgcat	ttcacgttgt	ttcctatatt	ccgttcaatg	taagctctat	gagaccaaga	120
anstgggcag	ttttattcac	cataagtatt	ccaagcccta	gtggttcctg	gcacattttg	180
tattcacaat	aaatatttgt	taagtcaatg	accagatgaa	tggcttttaa	actcaagata	240
gtttttt						246

&lt;210&gt; 1621

&lt;211&gt; 280

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1621

agtctaggga	aagtcattca	gtggatgtga	tcttggtcca	caggggacga	tgtcaagctc	60
ttcctggctc	cttctcagcc	ttgttgctgt	aactgctgct	cagtccacca	ttgaggaaca	120
ggccaaagac	atttttggac	aagtttaacc	acgaagccga	agacctgttc	tatcaaagtt	180
cacttgcttc	ttggaattat	aacaccaata	ttactgaaga	gaatgtccaa	aacatgaata	240
atgctgggga	caaattggtct	gcctttttta	aggaacagtc			280

&lt;210&gt; 1622

<211> 400  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 43  
<223> n=a, g, c or t

<400> 1622  
agggagggac agagagcgaa ctgtcagatc ggagcgagag cngcgcccg agagagggag 60  
agagagagag ggagggagag gaaaagtgag agagggaaag agagcgcgaa cgagggcgca 120  
gagcgagctc ctgctgcaac tctgctccag cacggccagc gccagcgccc gccgtcgggtg 180  
cactctacga gccgtgcagc gtgcccactg gagttgttgt gtatcaagga tcgatccctt 240  
atatgcacac acacacctcc acctccacca atgcactctt cttcctcctc cttctccaga 300  
caactgctgg gaaaaaata aaacaccaac cccaaccgtc agcaacaagg taasmgagcg 360  
attcgacatc attttttttc ctgttcaatt ttttccttgt 400